

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: November 6, 2004, 05:32:16 ; Search time 2909 Seconds

(without alignments)
5791.302 Million cell updates/sec

Title: US-09-482-788-2

Perfect score: 16128
Sequence: 1 MEYLAVDGRQDLPTPTPASF.....RVHLLBEVSKTEPEGLNSL 3129

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3611042 segs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seg length: 0

Maximum DB seg length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-FEAPOP=6 -FEAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA: *
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22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2364	14.7	61944	15 US-10-329-079-34	Sequence 34, Appl
2	2325.5	14.4	37360	15 US-10-329-079-6	Sequence 6, Appl
3	2191.5	13.6	18876	15 US-10-329-079-42	Sequence 42, Appl
4	2160.5	13.4	7788	15 US-10-329-079-8	Sequence 8, Appl
5	2011	12.5	47988	15 US-10-402-842-1	Sequence 1, Appl
6	1897.5	11.8	9748	16 US-10-282-122A-11388	Sequence 31388, A
7	1867.5	11.6	15450	16 US-10-282-122A-1449	Sequence 7449, Ap
8	1838.5	11.4	31263	16 US-10-282-122A-25447	Sequence 25447, A
9	1831	11.3	9590	16 US-10-282-122A-33351	Sequence 33351, A
10	1824.5	11.3	88421	9 US-09-976-059-1	Sequence 1, Appl
11	1804.5	11.2	9025608	15 US-10-156-761-1	Sequence 1, Appl
12	1770.5	11.0	10296	15 US-10-282-122A-33665	Sequence 33665, A
13	1752	10.9	6288	16 US-10-282-122A-33846	Sequence 33846, A
14	1749.5	10.8	939	15 US-10-369-493-42604	Sequence 42604, A
15	1749	10.8	15738	15 US-10-329-079-46	Sequence 46, Appl
16	1743.5	10.8	10002	16 US-10-282-122A-14471	Sequence 14471, A
17	1722	10.7	15738	15 US-10-329-079-12	Sequence 12, Appl
18	1713.5	10.6	7347	9 US-09-815-242-7773	Sequence 7773, Ap
19	1713.5	10.6	7347	16 US-10-282-122A-7467	Sequence 7467, Ap
20	1713.5	10.6	7347	17 US-10-324-967-17	Sequence 17, Appl
21	1702.5	10.6	7155	16 US-10-282-122A-10403	Sequence 10403, A
22	1696.5	10.5	7155	9 US-09-974-300-2171	Sequence 2171, Ap
23	1694.5	10.5	8244	15 US-10-402-842-3	Sequence 3, Appl
24	1690.5	10.5	13029	9 US-09-815-242-4052	Sequence 4052, Ap
25	1690.5	10.5	13029	16 US-10-282-122A-7240	Sequence 7240, Ap
26	1685	10.4	12951	16 US-10-282-122A-31678	Sequence 31678, A
27	1670.5	10.4	7617	16 US-10-282-122A-25471	Sequence 25471, A
28	1666.5	10.3	8649	16 US-10-282-122A-26001	Sequence 26001, A
29	1641.5	10.2	11100	15 US-10-329-079-5	Sequence 5, Appl
30	1641.5	10.2	13315	15 US-10-329-079-1	Sequence 1, Appl
31	1613.5	10.0	8138	15 US-10-369-493-35302	Sequence 35302, A
32	1612.5	10.0	9683	15 US-10-369-493-38492	Sequence 38492, A
33	1607	10.0	8268	9 US-09-974-300-2169	Sequence 2169, Ap
34	1605.5	10.0	7925	16 US-10-282-122A-33350	Sequence 33350, A
35	1588	9.8	7185	15 US-10-329-079-48	Sequence 48, Appl
36	1548	9.6	6408	15 US-10-329-079-44	Sequence 44, Appl
37	1524	9.4	6522	16 US-10-282-122A-31533	Sequence 31533, A
38	1522	9.4	6432	15 US-10-329-079-10	Sequence 10, Appl
39	1493.5	9.3	7155	15 US-10-329-079-14	Sequence 14, Appl
40	1486	9.2	6465	9 US-09-974-300-2166	Sequence 2166, Ap
41	1464	9.1	5127	15 US-10-156-761-31630	Sequence 31630, Ap
42	1451.5	9.0	9723	16 US-10-282-122A-13740	Sequence 13740, A
43	1428	8.9	7161	16 US-10-282-122A-35022	Sequence 35022, A
44	1428	8.9	29555	8 US-08-781-986A-206	Sequence 206, App
45	1428	8.9	29555	16 US-10-329-624-206	Sequence 206, App

ALIGNMENTS

RESULT 1
US-10-329-079-34 Application US/10329079
; Sequence 34, Application US/10329079
; Publication No. US20030198981A1
; GENERAL INFORMATION:
; APPLICANT: FARNET, Chris
; APPLICANT: ZAZOPOULOS, Emmanuel
; APPLICANT: STAPFA, Alfredo
; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
; FILE REFERENCE: 3002-11US
; CURRENT APPLICATION NUMBER: US/10/329, 079
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 61944
; TYPE: DNA
; ORGANISM: Streptomyces refuineus
; US-10-329-079-34
Alignment Scores:

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Qy 657 lAphSerSerCyS-----AlaLeuIyAspPheGlyIleSerLeuGlyIleAsnSerAspT 675
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Qy 675 hArGAlaLeuGlnPheGlyThrHsAlaPheGlyAlaCysLeuLeuGlnIleMetThrt 695
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Qy 695 hIleuIleAsnGlyIy---CysAlaCysAlleProSerAspAspAspAspMet---AsnS 713
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Qy 713 erIleProSerPheIleAsnArgTyraAsnValAsnTrpMetMetAlaThrProSer---- 731
Db 18307 ACCTCTGAGAGCTGTGGCGCGCGCGAGCGCTCACGGTCTCAGCCAGACGCTTCGGCCT 18366
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Qy 747 -----LeuValIleuValGlyIleGlnMetSerSerValAsnAlaIleTrpAlaP 764
Db 18427 TGAAGTACGTCGCTTCCTCGCGGCGAGCGCGCTGACACCGCCAGCTCGCCCTCGGCGG 18486
Qy 764 roIyS---LeuGlnLeuLeuAsnGlyTyrgIyGlnSerGlnSerSer---SerIleCysP 782
Db 18487 GCCGCGCGCTGCTGT 18546
Qy 782 heIaSerAsnMetSerThrgIyProAsnAsnMetGlyArgAlaValGlyAla----- 799
Db 18547 ACTTGAGAGCTGACGACGCGCGCGGTGAGCGCGCGCGCACCTCATCGCTCCCGCTG 18606
Qy 800 -----HisSerTrpValIleAspProAsnAspIleAsnAlaGlyLeuValProIleGly 817
Db 18607 ACAGACTGCGCGCGCGCGCTGCTGAC-----GAGCGCGCTGCGCGCTGCTGCGGCG 18660
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Db 18661 TGTGTGCGAGCTGTACGT 18720
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Db 18721 GCCTGACGCGCGCGCGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 18761
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Db 18762 -----GCGCGCGCGAGATGTACCGGACCGCGCATCTGTGTGTGTGTGTGTGTGT 18816
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Db 18817 TCACACTGAGCGCGCGCTGCGAGCGCCAGGTCAAACTGCGCGGTACCGATGTAGCGG 18876
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Db 18877 GAGAGGTGTAGAGCGCGCGCGCGCGCAC---CCGAC----- 18911
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Db 18912 -----ATCGGCGCAGG 18921
Qy 937 er-----TyPheGlyAsnArgProSerAspAlaHsIleLeu----- 949
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Qy 1006 lmgIyAlaIleValGlnAlaProAlaProIleProValPheAlaAspThrAlaAla 1026
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Db 19201 TCGCCGAGCTCTCCGCTGTGAGAGGTACAGCGGAC-----G 19239
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Qy 1066 rGSer---ValGlyMetAspLeuIyValSerAsnIleTyrgIleHsProThleuAlaG 1085
Db 19300 GTGTGCGCGCTGTGAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 19359
Qy 1085 lYlSer-----AlaValValIyGlyAspProLeuSerTyThrLeuIleP 1101
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Db 19411 CGCAGCG 19464
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Db 19465 TCTCTGCGAGCTGTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19524
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Db 19525 GCGGTCCCTGTGAGCTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 19584
Qy 1160 lUnThrLeuArgThrTrpPheGlnIyAspGlyValGlyValGln-----IleValH 1178
Db 19585 AGCGCGCTGCGCGCGCGCTTCCCGCGAGACGAGAGTCCCCCAGCAGCAGTGTCCGCG 19644
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Db 19759 GGGCGGT 19818
Qy 1238 lAileSerAspGlyTrpSerIleAspValLeuArgArgAspLeuAsnGlnIleuTySer 1258
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Db 19930 CCGACTTACCTCTGTGTGAGAGAGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 19989
Qy 1293 -----LysGlnLeuAsnTyTrpIyIySgIleuIyAspSer---SerProAlaIyS 1310
Db 19990 TCGCAGCGCGCTGTGCTGT 20049

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Db	20050	TGCCACCGAGCGGGCCGGCCCGCCGATGGAGAC---CACCGGGCGGATACACCGCT	20106
OY	1329	alThriLeaSPglYgLeuTyTrGlnSerLeuAaTgaLpheCyValaGlnHISaThrT	1349
Db	20107	TCACCTCCGCGGACAGGCTGGGGACCGGCTGCGTGTTGGGACCTCCCGACAGCGCA	20166
OY	1349	hTrSerPheValValLeuLeuAlaLaLpheaRgLaLaHISaTyTrAglLeuThAlaValG	1369
Db	20167	CCCTGTTCATGACCTCTCAGCGGGCCCTGGCGCGGCTTGGCCCAAGTTGGGGCCGGCC	20226
OY	1369	luAaPaLaValIleGlyThProIleLaAaHnRgaAaHnTgProGlnLeuAaPLeIle	1389
Db	20227	GGGACATCGTCCTGGGACACCCGGTCGCCGGCCGGCGGACGAGGGGCTGACAGACTGG	20286
OY	1389	legLYCySPheValaAaThTrGlnCyMetARgllaEaHISaPheHISaThrPheG	1409
Db	20287	TCCGCTTCTTCGTACAAACCTCTGGCTCCGACCCGACCTCGCGGGGACCCCACTTGG	20346
OY	1409	lyThriLeuIleAaRgLaValValaLaThThThThAlaLaPheGluAaGlnAaPLeIle	1429
Db	20347	AGGAGCTCTGACCCGGGTAGGAGAGCGGACCTGTCCGCTTCCGCCACAGAAATAC	20406
OY	1429	roPheGluAaTgValValSerAlaLeuGlnProGlySerAaPLeuSerSerThProL	1449
Db	20407	CGTTCGAGACACTGTGAGGCGCTCAACCC--ACCGCTCCCTCCCGGACACCGG	20463
OY	1449	euaLaGlnLeuIlePheAlaValHISerGlnlySPaPLeuGlyAaPheLyPheGlnG	1469
Db	20464	TCTTCACAGTGTCTGTGCTCCCTCCAGAAC--AACGAATCTGGCGAGGCGGTATCCGG	20520
OY	1469	lyLeuGln---SerValProValProSerLyValATyThTrARgPheAaMetGluPheH	1488
Db	20521	GTCGAGAGTCAACGTGGAAAGCCCGCCGACAGGTGGCGGCAAGTACACTCTTGCTGA	20580
OY	1488	ISleuPheGlnGlnThAsp-----SerLeuLyGlySerValaAsp	1502
Db	20581	ACCTGTGAGATCCCGGAGACCCGGCCGGCGGACCGGACCGGACGAGGGCGCTGTGAGT	20640
OY	1502	heaLaAPaRgLaLeuPheLyMetGlnThThValGluAaHnValAaTgValaPhePheGlnT	1522
Db	20641	ACGCGACCGACTTTCGACCGCGGAAACGTCGACGAGCTGGCGCGGACGCTACAGAGAC	20700
OY	1522	leLeuAaTgAaGlnLyLeuGlnSerSerARgThThProValSerIleLeuProLeuThr---	1540
Db	20701	TGCTCTGTGGCGGTACACGAGGAGGCCCGGACGCGCTCAACCGGAACTCCGATGCTAGCG	20760
OY	1541	-----AaPGLyIleValThThLeuGlnLyLeuA	1550
Db	20761	GGCGCGAACCGGCACTGCTGGCGGCGGACGAGACCGGCGGGCGCCGGCGAGG	20820
OY	1550	SPValaLeuAaHnVallyeHISaValaSPtyrProARgGlnSerSerLeuAaAPValaPheG	1570
Db	20821	ACGG-----GCCACCTCTCC	20838
OY	1570	lInThRglnValSerAlATyTrProAaSPSerLeuAlaValaAaSPSerSerCyValaGlnT	1590
Db	20839	GCGCGCGCGGACCGGACGCGCGGAGCGGTGGCGGTCCCTGCGCGGGGAGAGGCTCA	20898
OY	1590	hTyTrThGlnLeuAaPArGlnSerARpIleLeuAlaGlyTrPLeuAaTgAaTgSerM	1610
Db	20899	CGTACCGGAGCTCGCGAGCGGGCCGACCGGGGTGGCGGCGCTGGCCGGCGGGGG	20958
OY	1610	eTProAlaGlnThThLeuValaLaValaPheaLProARgSerCySGlnThIleValaLaP	1630
Db	20959	CCGCGCGCGGACCGGAGTCCGGGTGGCTGTGCTGCGGCGGACCGGCACTGTGTGGCTGCG	21018
OY	1630	hePheGlyValaLeuLyAlaAsnLeuAlATyTrLeuProLeuAaPValaAaTgSerProSerA	1650
Db	21019	TGCTCGAGTCTCTGGGCGGGCGCGCTACGCGCGCTGAGACCGGAGTACCCGAGCG	21078

QY	1550	laaYaaIaGlnAaPrlaLeuSerGlyLeuSerGlyProThrIleValIleuIleGlyHisA	1670
Db	21079	AGCCATCCGCCGCGATCTCTCC-----G	21100
QY	1670	spRThaIaProAaPrlaIleGluValaThrAaValaGluPheValaArgIleArgAaPaLaL	1690
Db	21103	ACACCCGCCCGCGTGGCGCTGTCAACG-----GGGACTGCCGCCCGCGCA	21155
QY	1690	euaNaAaPserAaNaIa-----AaPglyPheGluValIleGluHisAaPserThiLys-	1707
Db	21151	TCACCGCTGCCCGCGCGCTGCCGTGCCCAACCCCTCCGGCGCGCGAAGCGGCACAGG	2121
QY	1708	-----ProSerIaIaThrSerLeuAaIaTyValLeuT	1718
Db	21211	CGCCCGGAGCCCTCCGAGAGTCCCGCGCGCTCCGCCGACACAGCGCGTAAGTCTGC	2127
QY	1718	yrThrSerGlySerThiGlyArgProLysGlyValMetIle-----	1731
Db	21271	ACACCTCGGGGTCCAGGGAGCGGCCCAAGGGCGTGGTGGTCAAGCGCGGACCACTGGCA	2133
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Db	21331	ACCTGCTGCCGACATCGGGAGCGGCTGGCG-----CTACCGCGCGG-----	2137
QY	1748	yrProSerGluThiArgMetAlaHisMetIaThiIleAlaPheAaPglAaIaSerTyrg	1768
Db	21375	-----GACCGGCTGGCGCTCCACACAGGCACTTCGATCATCGCGCTCGG	2142
QY	1768	IuIleTySerAlaLeuLeuPheGlyArgThiLeuValCysValAspTyrMetThiTrL	1788
Db	21424	AGCTGTTCTCGCCCTGTGGCGCGCGGACCACTGGTCTGGCGGACCGCGGACCGGCAC	2148
QY	1788	euaAaPaIaArgAlaLeuLysAaPValaPhePheArgGluHisValaNaIaIaSerHisV	1808
Db	21484	GGGACCGGAGGCGACTG-----GCGGCACTCG	2151
QY	1808	aIaThrSerSerSerGluAaPValaProLeuArgValaProArgAaGlyLeuSerArgThiLeu	1828
Db	21511	TCACCGGAGCGCGGACCACTCTCCAGGCCACCCGACCACTGGCGAG-----	2156
QY	1828	etPhePhePheLeuValaIaThrAaPserThiAlaProAaPaIaLeuAaPaIaGlnGlyL	1848
Db	21561	-----CTGCTGCCGAGACCGCGCCGACGCGCTG-----CGCGGCG	2159
QY	1848	euTyrgIn-----	1850
Db	21598	TGCCCAAACTGTGGCGGCGGAAGCGCTCCCGCGCTCCGTGCCCTCCGCGCTCACAGGCC	2165
QY	1851	--GlyValGlnCysTyraAaGlnGlyTyrgIaProThiGluAaGlnGlyValMetSerThiLeT	1870
Db	21658	TGGCGGCGCACTGCTCAACGTCTACCGCGGCCACCGAAGCAACCACTGGTCTCAACCGCGC	2171
QY	1870	yrProIleAaPserThiGlySerPheIleAaGlnGlyValaProIleGlyArgAlaLeuAaNa	1890
Db	21718	CCGACCTCGAGCGGCGCACCGGG-----AGCGCAACGCCCAATGGCGCGGCGCTGGCA	2177
QY	1890	anSerGlyAlaTyraValaIaAaPProGluGlnGlnLeuValaGlyIleGlyValaMetGlyG	1910
Db	21772	ACACCCGCGGCTAGTGTCTGAGACAGAGGCTCGACCCGCGTCCCGCGCGGTCCCGGCGG	2183
QY	1910	IuLeuValaIaIaThrGlyAaPglYleuAaIaArgGlyTyrgSerAaPlys--AlaLeuAaP	1929
Db	21832	AGCTCTACTCGCGCGCGCGCGGTGGCGCGCGCTACTCGGCGCGCGGCGCTTACCG	2189
QY	1929	IuaAaAaPserPheValaHisIleThraValaAaNaPrgIaThiValaTyraTyrgThiGlyA	1949
Db	21892	CCGAGCGCTTACCGCGGACCCCTTCCGCGCGCGCGCGGACCCGCAATGATCCGACCGGGCG	2195
QY	1949	spArgValaArgTyraGlnIleGlyAaPglYleuIleGluPhePheGlyArgMetAspThrg	1969
Db	21952	ACCTGCTCCGCGCGCGCG-----CGCGACGGGAGAGTGAAGTTCTTCGAGCGACGACGACAC	2200
QY	1969	IaPheLysIleArgGlyAaNaArgTlleGluSerAlaGluIleGluAlaIaLeuLeuAaArgA	1989

[illegible]

D	23037	-----GAGGTCCGAGAC-----CGCGCGCGGTGGCCGACGCTCGCGGGACACC	23082
O	2332	ysllePhepNegluillethralaPheglu-----ArglnvalValAlaSerL	2348
D	23083	CGCGCGCGCTGCGCGCACCGCGATCCCAACCGCGGGTGGCGCGACGCGCGCC	23142
O	2348	eumanserAmilleapnguITPrglnLeuserthrlaPgserseralagluIyAps	2368
D	23143	TCGCGCGGCTGGAGAGCGCGCGCGCTGGCGCGGCGCGCGCTGGACGGCCCCG	23202
O	2368	er---SerLeuserValProAsnillePheargillelaIygluIaIleuCyAspValG	2387
D	23203	CCGCGCGAGTGGACCCGAGAGACCTGTACAGCTGGCGCGCGCGCGCGCCACCGCT	23262
O	2387	IuValserSerAlaargIINTPserSerIaasnIyAlaIeupAlaValPheNIshISc	2407
D	23263	GGGTGTCC-----TGGTGGCGCGAGGACCGCGCGACACCTG-----	23300
O	2407	ysCyserIingIyAgtThrIleuValAsnPheProthrAer-----	2420
D	23301	-----GACGTGTCTGGCCCCCGCGACCGGGCGCGCGCGGAGG	23343
O	2421	-----HisIleuIyargIySerIaPleuIleuThraAsnA	2432
D	23344	TGGCACCGCGCGCGGAGCTGGCCGTACAGCCGCGACCGCGACCGCGCGACACCAAG	23400
O	2432	rgProIeugIaArgIyLeugIaasnIaArgIleAlaIlegluValaArgIuaArgIeuaRS	2452
D	23404	ACCGGTCCGCGCGCGGTGGCGMACCGGGAACGTGCGCGCGGCTGCGCGGTACTGGCGG	23463
O	2452	erIeuleuProserTYrMetIleProserAsnIleValIalleuapIySmetProIeua	2472
D	23464	GACGCGCTGCGGACCTCATGTGTCCCTCGGCGCGTCTGTCTCGCGCGCTCCCGCTCA	23523
O	2472	snAlaasnIyIyValaAspArgIyGluIeuserIaArgIaIyValaValProIySg	2492
D	23524	CCGCGAACGGAGAGTGGACCGGCGCGCGCTGCCGAC-----CCGACCC	23566
O	2492	IngIINThrAlaIaIa-----ProIeuprothrPheProIleSerIuValgluValI	2509
D	23569	CGCGCGCGCGCGCGCGCGCGCGCA-----CGCGACAGCCCGGAGAGAC	23616
O	2509	IeIeuCySgluIuaIaThrgIuValaPheglYmet---IySValaPrlIethrAerPhIer	2528
D	23617	TGCTGTGTCGCGCTTTCGCGACCTCTGCGCTGAGCGGGTGGCACCGAGACAGCT	23676
O	2528	hePheAsnIeugIyglYhISerIeIeuaIaThryIeIeuserArgIleAerPglA	2548
D	23677	TCCTTCACCTCGGGCGGACAGCATCTGTCTCGCTCGTCAACCCCGACCGGGAAC	23786
O	2548	rgIeulYsValaArgIleThrValIyAspValaPheAsnIserProvalaPheAlaAspIeua	2568
D	23737	AG---GGGCTCGCGTTGACACCGCGGACGTCTTCAGACACCAACCGTGGCGCGCTGG	23799
O	2568	IaservalIle--ArgIingIyIeugIyIeugIingIINprovalSerAspGlyIingIyGI	2587
D	23794	CGGCGCGCTTGGACCGGACG-----GGAGCCGAGAC	23822
O	2587	naAspArgSerAlaIshIeMetAla---ProArgThrgIuThngIuaIaIleuCyAspIer	2606
D	23824	AGACCGCGCGGACGCGCGCGGACCGCGCGCGCGCGCGCGCGCGCC-----	23865
O	2606	uPheAlaIyValIeugIyPhegluValaIglYleThraAsnPhePheAspIeugIygl	2626
D	23869	-----	23865
O	2626	yhISerIeueMetAlaThryIeIeuaIaValaArgIleglYhISaArgIeuaSpThrThrya	2646
D	23870	-CATCAACGCGCGAGAACTGCG-----CGAGCTGGAGAGAACTCGCGCGCGACT	23919
O	2646	IserValIyAspValaPheAsnIserProvalIeuePhegluIeuaIaIleuAspAs	2666
D	23920	GGGA-----	23923

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QY 2666 nleuValGlnSerlyThrAngluileValGlyArgGluMetAlaGluTrpSerPr 2686
Db 23924 -----GGAGATGCATGTCAGAGCGGCTCG----- 23944
QY 2686 orpheGlnLeuLeuPheThrGluAerProGluGluPheMetAlaSerGluileysProG 2706
Db 23944 ----- 23944
QY 2706 nleuGluLeuGlnGluileileGlnAerileTyProSerThrGluMetGlnlyAer 2726
Db 23945 -----CACGCGATGTCAGAGAGTCCTTCGCGTACACCCGCTCCAGAGGGGCT 23994
QY 2726 eleuPheAerPheThrThrAlaArgProArgProPheValProPheTyrlleAerPhePr 2746
Db 23995 GCTCTTC--CACGCGGCTC-----TTGACAGAGAGCGTCCC 24027
QY 2746 oSerThr-----SerGluProAerAlaAlaGlyLe 2756
Db 24028 CGACGCGCTACGTACGCGCGGTGCTCGCTCCGCGCGAGCTGACCGCGCGGCT 24087
QY 2756 uilelyValACyAGluSerleuValAerHileAerPheAerThrValPheAlaG 2776
Db 24088 GAGACGGGCGCGCGAGCGCTGAGAGCGGACCGCGCGCTGCGCTCCGCGCA 24147
QY 2776 u--AlaSerGlyGluLeuTyrglnValAlleuSerCyAlyAerleuAerProileGlnVa 2795
Db 24148 GCGGCGCTGCGGGGAGTGTTCAGCTGTGCGGTCCGCGCGGCTGCGCGAGGA 24207
QY 2795 lileGluThrGluAerAerHileAerHileAerHileAerHileAerHileAerHile 2810
Db 24208 GCTGAGACTGCGGTCCGCGCGGCGCGCGCGCGAGCGGACGAGCTGAGCGCTCT 24267
QY 2810 uAerGluPheAlaAlyGluPheProValArgleuGlyHile--ProleuileAerPheThr 2829
Db 24268 GAGCGAGACCGCGCGAGCGCGGTTCAGCTCCGCGCGCGCGCTGCTGCGCTTCGCT 24327
QY 2829 eilelyGlnThrlySerMet--ArgValileAerArgileSerHileAerlyAer 2848
Db 24328 CGCGAGAGCGGGGAGAGCGCGCGCGCTGCGCGTACCTACACACATCATCTCGA 24387
QY 2848 rGlyLeuSerleuGlnHileValAlaArglyAlyMetleuTyrglnly----- 2865
Db 24388 CGGCTGCTCATCCGCTGCTGAGAGAACTGCTGCGCTGAGCGAGCGCGGCGGA 24447
QY 2865 --ArgSerleuLeuProProHileGlnPheSerArgTyrglnTyrglnAla----- 2882
Db 24448 CCCCTCGCGCTCGCGCGGTGCTCGCGCGCGCGAGCGGACCTGAGCTGCGCGCGAG 24507
QY 2883 -AerGlyArgGluSerGlyHileGlyPheTrpArgAerValileGlnAerHileProMet 2902
Db 24508 CGGTCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 24553
QY 2902 rileLeuSerAerPheThrValAla-----AerGlyAerAerAlaThrCyAly 2918
Db 24554 ---CTGTCCGAGCCGAGCTGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 24601
QY 2918 salAlaLeuHileLeuSerlyrileValAerHileProSerGlnVal----- 2932
Db 24602 -----CTGCGCGAGAGGTGTGAGCGCGCGCTGAGCGCGCTGAGCGCG 24633
QY 2933 -----LeuArglySerAerAerHileleTh 2941
Db 24634 ACGGAGACCGCGCGCTGACCGCGTGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 24681
QY 2941 rGlnAlaThrValPheAerAlaAlaCyAlyAlyAerValleuSerArgGluSerAer 2961
Db 24682 GGTGAATCGCGCGGTGAGCGCGCTGCGCGAGCGGTCTGCGCGCTGCGCGCGCG 24741
QY 2961 sAerPheValAlaPheGlyArgGlyValleuAerGlyArgGlnGlyLeuProAlaGluTy 2979
Db 24742 CGAGTCGTCTTGGAGAGCGAGCGGTGCGGCGG-----CGCGGAGGCTGCCCG 24792

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QY 2980 ----GlnAerPheValGlyProCyThrAerAlaValProValArgAlaHileGluSe 2998
Db 24793 TGCGGAGGACATGTGTGGGTCTTCATCAACGCGCGCGCGGTGCGAGTGGCGC 24852
QY 2998 rSerAer---TyrglnLeuLeuHileAerPheleGlnAerGlnTyrlleuLeuSerleuPr 3017
Db 24853 GAGCGAGCGGATGGGAGACTGTGCTCCGCGAGTCCAGCGCGAGACACCGCGCTCATGA 24912
QY 3017 ohileGluThrileGlyPheSerAerleuAerAerAerAerAerAerAerAerAer 3037
Db 24913 GACGAGACAGTACAGTGTCCGAGATCCAGCGCG-----TGCGGAGACAGCG 24960
QY 3037 eThrAerPheSerCyAlyleThrTyrglnAerPheGluTyrglnPheProGluSerGlnPr 3057
Db 24961 CGAATCTTCGACCTCCAGCGCGCTTCAGAGACTAC----- 24997
QY 3057 eGluGlnArgValGluMetGlyValleuThrlyPheValAerHileGluMetAerP 3077
Db 24997 ----- 24997
QY 3077 uProleuTyrglnAerleuAlaileAlaGlyGluValGluProAerGlyAlyleuAly 3097
Db 24998 -CGCGCGAGAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 25050
QY 3097 1 3097
Db 25051 G 25051

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RESULT 2

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US-10-329-079-6
; Sequence 6, Application US/10329079
; Publication No. US20030198981A1
; GENERAL INFORMATION:
; APPLICANT: FARNET, Chris
; APPLICANT: ZAZOPOLOS, Emmanuel
; APPLICANT: STRAPA, Alfredo
; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
; FILE REFERENCE: 3002-11US
; CURRENT APPLICATION NUMBER: US/10/329, 079
; CURRENT FILING DATE: 2002-12-24
; NUMBER OF SEQ. ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ. ID NO. 6
; LENGTH: 37360
; TYPE: DNA
; ORGANISM: Streptomyces fradiae
US-10-329-079-6

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Alignment Scores:
Pred. No.: 5,77e-187 Length: 37360
Score: 2325.50 Matches: 887
Percent Similarity: 41.70% Conservative: 502
Best Local Similarity: 26.63% Mismatches: 1212
Query Match: 14,42% Indels: 734
DB: 15 Gaps: 131

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US-09-482-788-2 (1-3129) x US-10-329-079-6 (1-37360)

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QY 51 ProCyThrProPheGlnleuAerMetileAerCyAerAlaAlyAerlyGlnSerAla 70
Db 62 CCCCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 121
QY 71 ileGlyHile-----AlaValTyrglnAerValProThrAerPheleAerAerPheAla 88
Db 122 GGTACACATACAGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 181
QY 89 leuAlaTrlyGluileValAerGlnThrProAlaAerAerAlaPheAlaPheThrSer 108
Db 182 GCGGACACTGGGAGACTGACCGCGCGCGCGCGCGAGAGCGCTGCGAGCG--GTCCTCCGCGAG 228
QY 109 AarSerGlyAerThrAerGlnAlaileuAlyAerSerPheAlaPheSerTrpMetCy 128
Db 239 GACGAAACAGGCGCGGACGAGGTGCTGAGACCG----- 274

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QY 129 TrpSerSerSerPro-----AspGluVal 138
 Db 275 ----GGGGCCCCCGACCGCCGTCGTCGCCGTCGCCGCCACCGCATGACGCCCTG 331
 QY 139 ValArgAsp-GluAlaAlaAlaAlaSerGlyProArgCysAsnArgPheValLeu 158
 Db 332 GTCCGGAAGCCGCGCCCTTCGACCTGGCCGACGACATCCCGCTGCCACACC 391
 QY 158 uGluAap---MetGlnThrIleCysGlnLeuValTrrPheSerIleAlaLeu 177
 Db 392 CTCTTCACGCTCCCGACCGGCAACGTCCTGCTCTGTCATC-CACACATCGCCG 450
 QY 177 IAspValThrPheGlnGlnArgValLeuSerArgValAlaAlaTyrIleHisGlu 197
 Db 451 CGACGCGTGTGCATGGGCGCGCTGGACGGGACCTGGCCGCCCTACCGCCCGCCG 510
 QY 197 sAePThrHisArgProGluThrPro----- 205
 Db 511 CGCCGCGCGCGCCGACTGCGCCCGCCGCGCCCGCCCGCCGACACCGCCCGG 570
 QY 206 ----GluSerSerAspAlaThrAspThrAspSerGlnSerValSerValSerMetSe 224
 Db 571 ACAGCAGCGGACGACGTGGACGACGATGACCGCCGCTGCC----- 616
 QY 224 rCysGluAspAsnAlaValSerAlaThrHisPheTrrPglThrHisIleuAsnAspLeuAs 244
 Db 617 -----CACTGGGCGGAGAACTGGCGGA----- 640
 QY 244 nAlaSerValPheProHisIleuSerAspHisIleuMetVal-----ProAsnPr 260
 Db 641 -----CTGCCCGACGAATCGCGCTGCTGCTACGACGCGCGCGCC 681
 QY 260 oThrThr----- 262
 Db 682 CAGACACACCCCGGCTACCGGACGCGGATCCCTTCGCGGTGACGCGCGCTGTACCG 741
 QY 263 -----ThrAlaGlnHisArgIleThr-----PheProLeuSerGlnIleVal 276
 Db 742 GAGACGTGGGCGCTGGCGCGCCGACCGGCGACCCGCTTATGATGCTCCACGCGCG 801
 QY 276 aLeuSer----- 278
 Db 802 CTGAGCGCGCTGTGGACACCGGCTCGGCGCGCGGACATCCCGTGGGACACCGCGTC 861
 QY 279 -----AsnSerAlaIle 282
 Db 862 CGCCGCGCGGACCGCGCCGACCGCGCATCTGTCGCGCTTCCTGTGTCAACACCTGAT 921
 QY 282 eCysArgThr-----AlaLeuSerIleLeuLeuSerArgTyrThrHis 296
 Db 922 CTGCGGACCGAACCCTCGGCGGACCGCGCTTCGCGGAATGCTTCACCGGGTGGCGCA 981
 QY 296 sSerAspGluAlaLeuPheGlnValAlaThrGlnGlnSerLeuProPheAspIleHisTyr 316
 Db 982 GACGAC-----CTGCGGCGCTTACGCGCAACGAGAGTGCCTTCAGAGCG----- 1027
 QY 316 rLeuAlaAspGlyThrTyrGlnThrValAlaProLeuArgValHisCysGlnSerAsnLe 336
 Db 1028 -CTGGTGGAGGCGGTCAACCGCGCGCTGCCCGACAGG----- 1066
 QY 336 uArgAlaSerAspValMetAspAlaIleSerSerTyrAspAsp-----ArgIle 352
 Db 1067 -----CACCGCGCTGTCCAGACGATGCTCACTTCGACACGCGCCACGAGCGCT 1119
 QY 352 uGlyHisIleuAlaProPhe---GlyLeuArg---AspIleArgAsnThrGlyAspAsnG 370
 Db 1120 CGATGACCTTCGTGACCTGCGGCGCGCGCGGGAACCTGCTGCCACCGCCGAG---GG 1176
 QY 370 ySerAlaAlaCysAspPheGlnThrValIleuLeuValThrAspGlySerHisValAsnAs 390
 Db 1177 CACCGCGCACACGACATCGAATGACCTTCACCGAGACGAGCGGACCGACGCGCGA 1236

QY 390 nGlyIleAsnGlyPheLeuGlnGlnIleThrGlnSerSerHisPheMetProCysAsnAs 410
 Db 1237 CGAATCTGACGCGCTTCGCG----- 1258
 QY 410 nArgAlaLeuLeuLeuHisCysGlnMetGluSerSerGlyAlaLeuLeuValAlaTyr 430
 Db 1259 -----TA 1260
 QY 430 rAspHisAsnValIleAspSerLeuGlnThrArgGlyLeuGlnGlnPheGlyHisIle 450
 Db 1261 CGCGCCCGACCTGTTGACCGGACGACGACCGCGCGGCTCTGGCGGAGCGGTTACGCGCT 1320
 QY 450 uIleIleCysLeuGln-----SerProLeuAspLeuSerMet 463
 Db 1321 GTCCTGACCGTACCGCGGACCGCGCCGCTGCGGCTGCGGACGCTGACGTCACACCGC 1380
 QY 463 tAlaGluValAsnLeuMetThrGluTyrAspArgAlaGluIleGluSerTrrAsnSerG 483
 Db 1381 CGGGAACCGCGCGGCTGGCCGACGCGGACGCGCGGCACGGAGCGACGCGCCGAC 1440
 QY 483 nProLeuGluValGlnAspThrIleHisIleGlnMetLeuValAlaSerHisSe 503
 Db 1441 CGCGTGCCTGCTGCGCGCTTC-----GCCGCTTCGCGCA 1482
 QY 503 rProThrIleThrAlaIleGlnAlaTrrAspGlyAspTrrThr-----TyrSerGluLe 521
 Db 1483 TCGCACGCGCGCGCGCGCGCGCTCACACGACGCGCGGCGACCTGAGCTACCGGAACT 1542
 QY 521 uAspAsnValSerSerArgLeuAlaValHisIleIleCysSerGlyLeuArgAlaGlnG 541
 Db 1543 CGACGCGCGCTCCACCGCTGCTCGCGCGCGCTGCTGAGCTGCGCGCTG---GGCGCGGA 1599
 QY 541 nAlaIleIleProValTyrPheGlnIleCysSerIleTrrValIleAlaSerMetLeuAla 561
 Db 1600 GACTTCGCGCTGCGCGCTGCGCGCTGCGCGACCTGCTGTGCGCTTCGCGGT 1659
 QY 561 lLeuIleSerGlyAsnAlaPheThrIleuIleAspProAsnAspProAlaArgThrAl 581
 Db 1660 GCTGAATCGCGGCGCGCGCTTACCTGCGCGCTGACACCGGACCGCGCGGACGACTC 1719
 QY 581 aGlnValValThrGlnThrArgAlaThrValAlaLeuThrSerIleCysLeuHisArgGlu 601
 Db 1720 GTACATCTTCACGACGCGCGCGCGCGCTGCTTCACGACGCGCGCTGCGCGGAGAC 1779
 QY 601 rValGlnIleLeuValGlyArgCysVal-----ValValAspAspG 615
 Db 1780 CTTCACGCGACGATGGCGGACGCGGTGCGGAGTCCGATGCTGTGACGAGGCC 1839
 QY 615 uLeuLeuGlnSerValSerAlaSerAspAspPheSerSerLeuThrIleSer----- 632
 Db 1840 CGGCACCGCGGCGGCGACGCGCGCGCATCTGCGCGGACCGGTACGACGCGACCGCGCG 1899
 QY 633 -----GlnAspLeuAlaTyrValIlePheThrSerGlySerThrGlyAs 647
 Db 1900 GTGCGCCCTGCTCCCGACACCGCGCGCTTACACATCTACACCTCGCGCTGACCGGACG 1959
 QY 647 pProIleGlyIleMetIleGlnHisArgAlaPheSerSerCysAlaLeuIleAspPheGly 667
 Db 1960 GCCCAAGGCGGTGTGCTGATGACGCAACGTTCTACGATCTGACGATCGGCGCGCGC 2019
 QY 667 aSerLeuGlyIleAsnSerAspThrArgAlaLeuGlnPheGlyThrHisAlaPheGlyAl 687
 Db 2020 GCGCGTGAATTCGGGCGGACGACGATGAGAGCTTTCACATCCAGCGCTTCGACTT 2079
 QY 687 aCysLeuLeuGluIleMetThrThrIleuIleangIlyIle---CysValCysIleProse 706
 Db 2080 CTGCGTGTGGAGATGTGGGCGCGCTGCGGCGACGCGCGCGCTGCTGCTCCCGCA 2139
 QY 706 rAspAspAspArgMet---AsnSerIleProSerPheIleAsnArgTyrAsnValAsnTr 725
 Db 2140 CGACGTGGCGACATCACCGCGGACCTTCGACCTGTGCGCGCGCGGCGCGGCTGACGCT 2199
 QY 725 pMetMetAlaThrProSerTyr-----MetGlyThr 735

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Db      2200 GCTCAGCCAGACGCGCCCTCCCTCCAGCTCTCGGCGGAGTCCGACCTCGCGCT 2259
Qy      735 rPheserProgluaapValProgluLeuAlaThrLeuValGluGlnMetSe 755
Db      2260 C---CCCCAGAGACACCGCGCGCTCGGCTAGCTCTCTCGGCGGAGAGAGCGCTGGA 2316
Qy      755 rSerSerValaAaAlaLeuTrpAlaProlyS---LeuGlnLeuLeuAnglyTrgyl 774
Db      2317 CACCGCCCAACTCGCCCGCTGGCGGGGCGCGCGCTGGCTGATCAATGTACGGGAT 2376
Qy      774 nSerGluSerSer---SerIleCySPheAlaSerAsnMetSerThrGluProAsnAmMe 793
Db      2377 CACCGAGACGACGCTCCACGCTACCCACCTGAGCTGAGACGCGCGCTGAGCCGCG 2436
Qy      793 rGlyAaGAlaValGly-----AlaHiserTrpValIleAspPr 806
Db      2437 CCGCAGCCCGCATGGGACACCCCTGAAAGACCTCGGCGCCAC-----GTGCTCGACCA 2490
Qy      806 oAenAspIleAsnArgLeuValProIleGlyAlaValGlyLeuValIleGluSerPr 826
Db      2491 GGGGCTGCTCC-----GTGCGGTGGGCGTGTGGGCGAGCTGTACGTCGCGCGCC 2544
Qy      826 oGlyIleAlaArgAspTrpIleValProProProProGluLysSerPro-PhePheThra 846
Db      2545 CGGCTGTGGCGCGGCTACCG-CGCGCGCGCGCTGAGCGCCACCGCTTCGTCGCG 2603
Qy      846 sPileProSerTrpTrpProAlaAsnThrPheProAspGlyAlaValLeuTrpArgThg 866
Db      2604 AC-----CCGTTCCAGACCGCGCGCGCGCATGTACCGGACCG 2659
Qy      866 lYAspLeuAlaArgTrpAlaSerAspGlySerIleValCyLeuGlyArgIleAspSerg 886
Db      2640 GGCACCTCGCTCGGCGGACCGACCGCGCGCTCCACTAGCGCGGTCCCACTCCC 2699
Qy      886 lValIlySileArgGlyGlnArgValGluLeuGlyAlaIleGluThrHisLeuArgGln 906
Db      2700 AGGTGAACGCGCGCTACCGCATGAGCGCGCGAGTCGAGCGCGCGCGCGCGCC 2759
Qy      906 lMetProAspAspLeuThrIleValAlaGluAlaThrIlyAspSergIleSerAlaAsn 926
Db      2760 AC---CGGAC-----GTGCGCGGACGG----- 2779
Qy      926 exrThrSerIleuAlaPheLeuIleGlySerSerTrpPheGlyAsnArgProSerAsp 946
Db      2780 -----GCCACCGCGCTGACAGCGGAGAGACCGGAGAGACC 2813
Qy      946 lAlaIleLeuAspHisAspAlaThrIlyAla-----IleA 958
Db      2814 GGTACCTGTCTGTCTACGTGTGCGCGCGCGGCGGACACCGACCCGACCCGACCGAGTGC 2873
Qy      958 snIleuYsLeuGlnGlnValLeuProArgHisSerIleProSerPheTrpIleCyMetL 978
Db      2874 GCGCCACCTCGCGCGAGCGCTGCGCGCTATATAGTCCCGCGCGCTGTGTCGCTGA 2933
Qy      978 euGluLeuProArgTrpAlaThrGlyIlySileAspArgArgGlyLeuArgIleMetGly 998
Db      2934 CCGCGCGCTGAGACCCCAACGCTGAGCGGACGCGCGCTG----- 2980
Qy      998 yAspIleLeuAspIlyGlnThrGlnIlyAlaIleValGlnGlnAlaProAlaProIleP 1018
Db      2981 -----CCGCGCGCC----- 2989
Qy      1018 roValPheAlaAspThrAlaAla----- 1025
Db      2990 -----GACCGGCGCGCGCGGCGGACCGCGCGCGCGCGCGGACCGGCGGAG 3038
Qy      1026 --LysLeuHisAspSerIleTrpValGlnSerLeuGlyIleAspProAlaThrValaAsnValG 1045
Db      3039 AACGCGCTGCGCGCGCTGCGCGGACGCTCGCGCGCTGAG-----GAGTTCGCGCGG 3092
Qy      1045 lYAlaThrPhePheGluLeuGlyIlyAsnSerIleThrAlaIleLeuMetValaAsnMetA 1065

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Db      3093 AGCCGCACTTCTTCCCGCTGGAGGCCATTCTCTCGGCGGCTCGGCTCATACGCCGA 3152
Qy      1065 lAaArgSer---ValGlyMetAspLeuLeuYsAlaSerAsnIleTrpGlnHisProThrLeuA 1084
Db      3153 TCAAGTTCGGCGCTCGGAGGTGGAGATCGGACCGCTTCCTCGAGGGCGCCACGCCGCG 3212
Qy      1084 lAglYIleSer-----AlaValAlaYsGlyAspProLeuSerTrpThrLeuI 1100
Db      3213 CCGCGCTGTCTCCGCGCTCGACACCGCGGACCGGACCGGCC-----CGCTCC 3263
Qy      1100 lProIlySerThrHisGluGlyProValGluGlnSerTrpSerGlnGlyArgLeuTrp 1120
Db      3264 TCGCGCGCGCGGACCGGAC---CGGCTCCGCTCTCTCTCCGCGGACCGGAGCTGTGT 3320
Qy      1120 heLeuAspGlnLeuAspValGlySerLeuTrpTrpIleuIleProTrpAlaValArgMetA 1140
Db      3321 TCCTCGAGAACTGGAAGGACCGAGCGGACCTAACAACATCCGCTCGCTCGCTCGCTGC 3380
Qy      1140 rGlyLProValaAsnValaAspAlaLeuArgArgAlaLeuAlaLeuGlnGlnArgHisG 1160
Db      3381 GCGCGCGCTCGACGCTGAGCGCTGCGACCGCGCTGCGGACGCTGTGGCGGCGGACG 3440
Qy      1160 lThrLeuArgTrpThrPheGluAspGluAspGlyValGlyValGln-----IleValH 1178
Db      3441 AGGCTTCGCGCACCTCTCTCTCGGAGACCGGCGCGCTTCACGACAGTGTGCGCG 3500
Qy      1178 lGluLysLeuSerGluGlnMetLeuValIleAspLeuCyGlySerAspLeuAspProP 1198
Db      3501 CCGAAGCGGCGCGCGCGCTGACGCTGAGCTGACGCTACCGAAGAGACTGCC----- 3556
Qy      1198 heGluValLeuAnglnGlnGlnThrThrProPheAsnLeuSerSerGluAlaGlyTrpA 1218
Db      3557 --CGCGCTCGCGCGGCGCGGCGGACACGCTTCACCTTCACCGAGAGACTTCGCTGC 3614
Qy      1218 rGAlaThrLeuLeuArgLeuGlyIlyAspAspHisIleLeuThrIleValMetHisI 1238
Db      3615 GGGCGCTACTGTGCGGACCGGCGCGCGGACCAACAGCTCTCTCTCTCTCACACCA 3674
Qy      1238 lAlleSerAspGlyTrpSerIleAspValLeuArgArgAspLeuAsnGlnLeuTrpSera 1258
Db      3675 TCGCGGCGGACGCTGTGTGCTGCGCGCTCGCGCGGACCTGACGACCGCTAC---G 3731
Qy      1258 lAlaLeuLysAspSerLysAspProLeuSerAlaLeuThrProLeuProIleGlnTrpS 1278
Db      3732 CCGCAGCTCGGAGGCGCGCGCG-----CAGTGGCGCGCGCTGCGCTGACAGTACG 3785
Qy      1278 exAspPheAlaLysTrpGlnLysAspGlnPheIleGlnGlnIly----- 1292
Db      3786 CCGACACACCTCTGGAAGAGAGATGCTCGCGCGCGGAGACACCCGAGAGCTTC 3845
Qy      1293 ----LysGlnLeuAsnTrpTrpLysLysGlnLeuLysAspSerSerProAlaLysIle- 1310
Db      3846 TCGCGCGCAACTCGCTTGTGCGGAGGCGCTG---GAGGCGCGCGCGGACAGATCG 3902
Qy      1311 ----ProThrAspPheAlaArgProAlaLeuLeuSerGlyAspArgIlyCyValHis- 1328
Db      3903 AGCTTACCCACGACCGCGCGCGCGCGCATGAGAGC---CACCGGCGGCGATCCAC 3959
Qy      1329 --ValThrIleAspGlyGluLeuTrpGlnSerLeuArgAlaPheCyAsnGlnHisAsnTr 1348
Db      3960 GCTTACCTCTCCCGGCTGCTGCGGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4019
Qy      1348 hYThrSerPheValIleLeuLeuAlaAlaPheArgAlaAlaIlyValGlyLeuThrAlaV 1368
Db      4020 CCACTCTTCAAGGCTCTCAGGCGGACTCGCGCGGACGCTTGCACACCTGGGCGCG 4079
Qy      1368 alGluAspAlaValIleGlyThrProIleAlaAsnArgAsnArgProGluLeuGluAspI 1388
Db      4080 GCGGAGACATGCTCTCGGACCGCTGTGCGCGCGCGCGCGGACGAGCGCGGACGAC 4139
Qy      1388 lAlleGlyCySPheValAsnThrGlnCyMetArgIleAsnIleAspHisIleAspThrP 1408
Db      4140 TCGTGGCTTCTGTGTCACACCTCGCGCTCGGACCGACCTCGCGGCGGACCCGACCT 4199

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Db	6185	CTGGACGAGATCCACCACTGAGCGGGCGGCACGCGTGGACCCGCAATCCGGGCGCTCGCGCC	6244
Oy	2089	AsnArgSerLeuGlyAsnValLeuGluIleGlyThrGlySerGlyMetIleLeuPheAsn	2108
Db	6245	ACGGCG-----GTGCTGGAGATCGGAGTCCGACCGCGGCTGTCTCTCGGAG	6292
Oy	2109	LeuAspSerAlaGlyLeuGlySerTyrValGlyLeuGluPheSerAlaAlaAlaPhe	2128
Db	6293	CTGGCGGAGAGACTGCACCGCTTACCGACGACCGACCTGTCTCGCGGCGCATCGAGCG	6352
Oy	2129	ValAsnLeuValAlaThrGlySerIleProSerLeuAlaGlyValAlaValValGlu	2148
Db	6353	CTGGCGGACAGTGTGACGCGCGAACCCTGGCTGAAGAGAGAGGTGACGTGCACGTCCG	6412
Oy	2149	ThrAlaThrAspIleGlyGlnValAspAspLeuHisProAspLeuValValLeuAsnSer	2168
Db	6413	CCGGCGCCACGACTTGACGCGCGCTGCGGGGGCTTCTACACACATGTCTCACTCC	6472
Oy	2169	ValIleGlnTyrPheProSerSerGlyTyrLeuAlaGluIleAlaAspThrLeuIleHis	2188
Db	6473	GTCTGTCAGATCTTCTCCGACCGACCACTCACCCGCGTACGCGCGCGCTCCAC	6532
Oy	2189	Leu-----ProAsnValGlnArgIlePhePheGlyAspValArgSerGlnAlaThrAsn	2206
Db	6533	CTGCTCGCCCCCGGC--GGGGGCTCTTCTGTGGCGACGTCCGAGCTGTGCACCTGTG	6589
Oy	2207	GluHisPheLeuAlaAlaArgAlaIleHisThrLeuGlyGlyAsnAlaThrGlyAspAsp	2226
Db	6590	CGCGCGCTT-----CGCGCGCTGGTGGAGACCGGCAACAGCGCGCTCTCGGAAC	6640
Oy	2227	ValArgGlnValMetAlaGluLeuGlu-----AspMetGluGluLeuLeuVal	2243
Db	6641	CCCGCGCGCGTACTTGTCCGCGCGCCGACCGACGCGCGCGGAGAACGAACTGTCTATC	6700
Oy	2244	GluProAlaPhePheThrSerLeuLys-----AspArgPheProGlyLeuValGluHis	2261
Db	6701	GCCCCGCACTACTTGTCCGCGGTGGGGGAGAGCGCCCGAACCCTCTG-----	6751
Oy	2262	ValGluIleLeuProLysAsnMetGluAlaValAsnGluLeuSerAlaTyrArgTyrAla	2281
Db	6752	CTGACGCGTCCGATCCGCGCGCGGACCGCGCTTACACGAGTGTACGCGTACCGTCA--	6808
Oy	2282	AlaValValHisValArgGlySerLeuGly-----Asp	2292
Db	6809	GACGCTCTGTGTCAAAACAGAGACCGGACGCGCGCTCGCTCCCGCGGCAC	6868
Oy	2293	GluLeuValLeuProValGluLysAspAspGlyPheAspPheGlnAlaAsnGluLeuAsn	2312
Db	6869	GACATCGCTGCACGCGCGGAGACCGGCAT-----GCCGGCGCGCTGCG	6913
Oy	2313	GlnLysSerLeuGlyAspLeuLysSerSerSerAlaAlaIleMetAlaValSerLys	2332
Db	6914	GAG-----ATCTCGCGCGGCGACCCCGCGCGCTCGCGTCAACCGC	6955
Oy	2333	IleProPheGluIleThrAlaPheGluArgGlnValValAlaSerLeuAsnSerAsnIle	2352
Db	6956	ATCCCAACGCGCGCGGTGGCGGCGACACCGCGCTCGCGCTGAG-----	7006
Oy	2353	AspGluTyrGlnLeuSerThrIleArgSerSerAlaGlu-----GlyAspSerSerLeu	2370
Db	7007	GACGCGGACGCGGTACCGAGGTGGCGCGCTGTGAGGAAACCGCGGTGAC--GAGATC	7063
Oy	2371	SerValProAspIlePheAspArgIleAlaGlyGlnAlaGlyPheArgValGlnValSerSer	2390
Db	7064	GATCCGAGAGACTTGTACACGCGCGGACCGCGCGCGGACGACCGCTGGTGTAC--	7120
Oy	2391	AlaArgGlnTyrSerGlnAsnGlyAlaLeuAspAlaValPheHisLeuSerSerGln	2410
Db	7121	-----TGGTGGCGCGACGACCGCGGACCGCG--	7150
Oy	2411	GlyAlaGlnThrLeuValAsnPheProThrAspHisHisValAspArgGlySerAspLeuLeu--	2429

Db	7151	-----GACCTCGTGGCGCCGCGGCGG-----	-----GGCGGGAGACGGCGTCCGCG	7169
QY	2430	-----	-----Thr	2430
Db	7190	CCGGTGGCGCGCGCGCGACCTGTGGCGCGCGCGCGCTGACCGCGCGAGACG		7249
QY	2431	AsnAtrProLeuGlnArgLeuGlnAsnArgArgIleAlaIleGluValArgGluArgLeu		2450
Db	7250	AACGACCCGACCGCGCGGTGGCGACCAACGACGACCTGGCGCGCGCGCTCCGCTCCACCTG		7309
QY	2451	ArgSerLeuLeuProSerTyrMetIleProSerAsnIleValIleuAspLysMetPro		2470
Db	7310	GCCGACGGCGCTCGCGGACTACATAGTGTCCCTCGGCGCGTGGTCTTCGACGCGCTCCGCG		7369
QY	2471	LeuAsnAlaAsnGlyLysValAlaAspArgLysGluLeuSerArgArgAlaLysValValPro		2480
Db	7370	CTGACCGCGCAACGGGAGAGGTGACCGGACCGCGCTG-----		7405
QY	2491	LysGlnGlnThrAlaAlaProLeuProThrPheProIleSerGluValGluValIleLeu		2510
Db	7405	-----		7405
QY	2511	CysGlnGluAlaThrArgLysAlaPheGlyMetLysValAspIleThrAspHisPhePheAsn		2530
Db	7405	-----		7405
QY	2531	LeuGlyGlyHisSerLeuLeuAlaThrLysLeuIleSerArgIleAspGlnArgLeuLys		2550
Db	7405	-----		7405
QY	2551	ValArgIleThrValLysAspValPheAspHisProValPheAlaAspLeuAlaSerVal		2570
Db	7405	-----		7405
QY	2571	IleArgGlnGlyLeuGlyLeuGlnGlnProValSerAspGlyGlnGlyGlnAspArgSer		2590
Db	7406	-----CCGACCCCGACCCGGCGCGGACCGGACCGGAC-----		7432
QY	2591	AlaHisMetAlaProArgThrGluThrGluAlaIleLeuGlyAspArgGluPheAlaLysVal		2610
Db	7433	GCCGAGCGCGCGCGCGGACCGCGCGGAGGAGCTGCTTCGACGCTTCGCGCGGACCTG		7492
QY	2611	LeuGlyPhe---GlnValGlyIleThrAspAsnAspPheAspLeuGlyGlyHisSerLeu		2629
Db	7493	CTGGAGCTGGCGCGGAGTGGAGTGCAGACAGCTTCTTGGCTTCGCGCGGCGGACGCTC		7552
QY	2630	MetAlaThrLysLeuAlaValAlaArgIle---GlyHisArgLeuAspThrThrValSerVal		2648
Db	7553	CTGTCCGTCGCGCTTCGTACGCGCGCGCGCGCGGACGACGCGGCTGCGCGTACC-----ACC		7606
QY	2649	LysAspValPheAspHisProValIleuPheGlnLeuAlaIleuAspAsnLeuVal		2668
Db	7607	CGCGACGCTTCGAGACCAACACCGCGCGCGCTGGCGCGCGCGCTGGAGCGC-----		7666
QY	2669	GlnSerLysThrAsnGluIleValGlyGlyArg-----		2679
Db	7661	AGGGAAACCGGACGGAACCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG		7720
QY	2680	-----GlnMetAlaGluTyrSerProPheGlnLeuLeuPheThrGluAspProGluGlu		2697
Db	7721	CCCATCACCTTCGACGAACCTCGCGAGCTCGAGCCGACGATTCGCGACCGAGCTGGAGGAG		7780
QY	2698	PheMetAlaSerGluIleLysProGlnLeuGlnGlnGluIleIleGlnAspIleTyr		2717
Db	7781	AC-ACAGTGAAC-----GTCGCCGACGCCAAGTTCGAGAGAGTCTCGT		7821
QY	2718	ProSerThrGlnMetGlnLysAlaPheLeu-----PheAspHisThrThrAla		2733
Db	7822	GCGGTACACCGCGCTCCAGAGAGGAGCTGCTTCACGCGCGTTCGACGAGAACGTC--		7878
QY	2734	ArgProLysArgProPheValProPheTyrIleAspPheProSerThrSerGluProAspAla		2753
Db	7879	---CCGACGCGCTACGTCACCGCGGTGGCT---CTGGCGCTTTCGAGAGACTGGACCC		7932


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QY 2774 PheAlaGlu---AlaSerGlyLeuLeuValValaValaLeuSerCysLeuAspLeuPro 2792
DB 7993 TTCGCGACGGCGGCTGGGAGAGTGTTCACACTGTGTCCACCGCCCGCGGTGCC 8052
QY 2793 IleGlnValIleGluThrGluAspAsnIleAsnThrAlaThrArgGlu----- 2808
DB 8053 TGGCAGAGCTTCACCTGCGCGCGCTGGAGCGCGGAGCGGAGCAAGACCTGGAG 8112
QY 2809 ---PheLeuAspGluPheAlaValaValaValaValaValaValaValaValaVala 2826
DB 8113 GCGCTGTGGACAGACACACCGCGGCTGCACTCGCGCGCGCGCGCGCGCGCGCGCG 8172
QY 2827 PheThrIleIleLeuVala---ThrLysSerMetArgValaIleMetArgIleSerHisAla 2845
DB 8173 TTCCTGTGGCGACAGACCGCGGAGACACACCGCGGCTGGCGCGGTTCACACCTC 8232
QY 2846 LeuTyrAspGlyLeuSerLeuGluHisValaValaArgLysLeuHisMetLeuTyrAsnGly 2865
DB 8233 GTCCTGACGCGCTGTGCTCATGCGCATGTGATGGGAGACTGGCGCGTGTACGGGAGC 8292
QY 2866 ---ArgSerLeuLeuProProHisGlnPheSerArg---TyrMetGlnTyrThr 2881
DB 8293 GCGGCGACCGCTGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 8352
QY 2882 Ala---AspValaArgGluSerGlyHisGlyPheThrArgAspValaIleGlnAsnThrPro 2900
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QY 2901 ---MetThrIleLeuSerAspThrValaValaAspGlyAsnAspAlaThrCysValaAla 2919
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QY 2920 LeuHisLeuSerLysIleValaAsnIleProSerGlnVala----- 2932
DB 8452 -----CGGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 8490
QY 2933 -----LeuArgGlySerSerAsnIleIleThrGln 2942
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QY 2963 ValValaPheGlyArgIleValaSerGlyArg---GlnGlyLeuProValaGluTyrGlnAsp 2981
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QY 3041 SerCysCysIleThrTyrHisAspHis 3049
DB 8824 GACACCTCCACCGCGCTTCGAAACCTAC 8850

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; GENERAL INFORMATION:
; APPLICANT: FARNET, Chris
; APPLICANT: ZAZOPOULOS, Emmanuel
; APPLICANT: STRAFA, Alfredo
; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
; FILE REFERENCE: 3002-1105
; CURRENT APPLICATION NUMBER: US/10/329,079
; CURRENT FILING DATE: 2002-12-24
; NUMBER OF SEQ. ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 18876
; TYPE: DNA
; ORGANISM: Streptomyces refuineus
; US-10-329-079-42

Alignment Scores:
Pred. No.: 6,26e-176 Length: 18876
Score: 2191.50 Matches: 795
Percent Similarity: 43.91% Conservative: 445
Best Local Similarity: 28.15% Mismatches: 1069
Query Match: 13.59% Indels: 517
DB: 15 Gaps: 110

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QY 71 IleGlyHis-----AlaValaTyrAspValaProThrAspIleAspIleSerArgPheAla 88
DB 11185 GCGTACCACTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11244
QY 89 LeuAlaTyrLysGluIleValaLeuGlnThrProAlaLeuValaAlaPheAlaThrSer 108
DB 11245 GCGGCGTGGCGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11301
QY 109 AspSerGlyLysThrSerGlnValaIleLeuLysAspSerPheValaPheSerTrpMetCys 128
DB 11302 GACGAGAGAGGCGCTTACACAGTGTCTG----- 11331
QY 129 TrpSerSerSerSerPro----- 1136
DB 11332 ---CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11388
QY 137 GluValaValaArgAsp---GluAlaAlaAlaAlaAspGlyProArg----- 151
DB 11389 GCGCTGGTGGCGAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11448
QY 152 ---CysAsnAspPheValaLeuLeuGluAspMetGlnThrLysLysCysGlnLeuVala 169
DB 11449 CACACCTGTTCGCGC-----TCCCGGACCGCGAGCAGCTCTGCTC 11490
QY 169 ITrpThrPheSerHisAlaLeuValaAspValaThrPheGlnGlnArgValaLeuSerArgVala 189
DB 11491 CTGGTG-ATCCACACATACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11549
QY 189 ILeuAlaAlaTyrLys----- 194
DB 11550 GCGCGCGCGCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11609
QY 195 -----HisGlyLysAspThrHisArg---ProGlnThrProGluSerArg 209
DB 11610 GACCGACCGCGATCAGTGTCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11663
QY 209 AlaThrAspThrAspSerGlnSerValaSerValaSerMetSerCysGluAspAsnAla 229
DB 11664 GCGCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 11694
QY 229 AlaSerAlaThrHisPheTrpGlnThrHisLeuAsnAspLeuAsnAlaSerValaPhePr 249
DB 11695 -----CACTGGCGCGGAGAGCTGCGCGA----- 11718

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249 OHISLeuSerAspHisLeuMetVal-----ProAsnProThrThr----- 263
11719 -----CTGCCGAGAGAGTCCCGCTCCCTACGACCGGCGCGCCACGACACCCCGG 11774
264 ----AlaGluHis-----ArgIleThrPheProLeuSerGlnLysAlaLeuSerAs 279
11775 GTACGCGGAGCGGATCGGCTTCCGGATGACGCGGAGCTGACCGGATCGTGGCCCT 11834
279 nserAla-----IleCysArgThrAlaLeuSerIleLeuLe 291
11835 GGGGCGCGCGGACCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11894
291 userArgTyrThrHisSerAspGlnAlaLeuPheGlnAlaValThrGlu----- 307
11895 GACCGG-----CTGGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11930
308 ----GlnSerLeuProPheAspLysIleTyrLeuAlaAsp-----GlyThrTyrGlnm 324
11931 CACCCCTCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11990
324 ValAlaProLeuArgValHisCysGlnSerAsnLeuArgAlaSerAspValMetAspAl 344
11991 CACCCCTCGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 12050
344 ailesSerTyrAspAspArgLeuGlnHisLeuAlaProPheGlnLeuArgAspIleAr 364
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364 gaenThrGlyAspAsnGlySerAlaAlaCysAspPheGlnThrValLeuLeuValmra 384
12101 AACGCGTGTGAGGCGGCTCAACCCCGCGCTCGCCACAGGCGACCCGCTGTGAGA 12160
384 gLySerHis-ValAsnAsnGlyIleAsnGlyPheLeuGlnIleThrGlnSerSerh 404
12161 CCACTCCACCTCGACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 12213
404 iAsPheMetProCysAsnAsnArgAlaLeuLeu-----HisC 417
12214 -----CTGCCG---GGGTGCGAGCGGAGCTGTGCGGCGGCGGCGGCGGCGGCGG 12265
417 yAsnIleMetGlu-----SerSerGlyA 424
12266 CCGACCTCGACCTGACCTTCGCGGAGACCGGCTCGCGCGGCGGCGGCGGCGGCGGAG 12325
424 lAlaLeuValAlaTyrTyrAspHisAsnValIleAspSerLeuGlnThrThrArgLeu 444
12326 TCACGCGGAGACCTCGACATACCGCCGACCTGTTCGACCGGCGGAGACCGCGGAGCTTGG 12385
444 euGlnGlnPheGlnHisLeuIleLysCysLeu---GlnSerPro----- 457
12386 TGGAGCGGCTGTGCGGCGGCTGTGCGGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGG 12445
458 --LeuAspLeuSerSerMetAlaGluValAsnLeuMetThrGlyTyrAspArgAlaIu 477
12446 GGGTTCGACGTCACCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 12501
477 leGluSerTrpAsnSerGlnProLeuGluValGlnAspThrLeuIleHisIleGluMet 497
12502 -----GCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 12547
497 euLysAlaValSerHisSerProThrLysThrAlaIleGlnAlaTrpAspGlyAspTrp 517
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517 hr-----TyrSerGlnLeuAspAsnValSerSerArgLeuAlaValHisIleLysSer 535
12608 CCGTGCATCTACCGGAGTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAG 12667
535 euGlyLeuValArgAlaGlnAlaIleIleProValTyrPheGlnLysSerLysTrpVal 555
12668 TCGGCGTG---GGCGCGGAGAGCTTGTGCGGCGGCGGCGGCGGCGGCGGCGGAGCTGG 12724

555 leAlaSerMetLeuAlaValLeuLysSerGlyAsnAlaPheThrLeuIleAspProAsn 575
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575 spProProAlaArgThrAlaGlnAlaValThrGlnThrArgAlaThrValAlaLeuThr 595
12785 ACCCGCGGAGCGACCTCTTACATCTCGGAGCATGCGCGGCGGCGGCGGCGGCTCTCCA 12844
595 erLysLeuHisArgGluThrValAlaGlnLysLeuValGlyArgCys----- 609
12845 CGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGTCCCT 12904
610 --ValValValAspAspGlnLeuLeuGlnSerValSerAlaSerAspAspPheSerL 629
12905 GGGTGTGCTGACATGCGCGCGGAGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 12964
629 euThrLysSer-----GlnAspLeuAlaTyrValIlePheT 641
12965 TCACCGAGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTACA 13024
641 hrSerGlySerThrGlyAspProLysGlyIleMetIleGluHis-----ArgA 657
13025 CTTGCGGATGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 13084
657 lAsPheSerCys-----AlaLeuLysPheGlyAlaSerLeuGlyIleAsnSerAspT 675
13085 TGGTGCATCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 13129
675 hrArgAlaLeuGlnPheGlyThrHisAlaPheGlyAlaCysLeuLeuGluIleMetThrT 695
13130 TGTGAGACGCTC---TTCACCTCAGCGGCTTCACATCTTCGAGTGGAGATGGGAGAG 13186
695 hrLeuIleAsnGlyGly---CysValCysIleProSerAspAspArgMet---Asn 713
13187 CCTGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 13246
713 erIleProSerPheIleAsnArgTyrAsnValAsnTrpMetValThrProSer--- 721
13247 ACCTCTGAGCGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 13306
732 -----TyrMetGlyThrPheSerProGluAspValProGlyLeuAlaThr----- 746
13307 TCCTCCAGCTCTCGGCGGCGGAGACCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 13366
747 -----LeuValLeuValGlyGlnIleMetSerSerSerValAsnAlaIleTrpAlaP 764
13367 TGAAGTACGTGCTTGTGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 13426
764 rOlyS---LeuGlnLeuLeuAsnGlyTyrGlyGlnSerGlnSerSer---SerIleCysP 782
13427 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 13486
782 heAlaSerAsnMetSerThrGluProAsnAsnMetGlyArgAlaValAlaIleGlyAla 799
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800 -----HisSerTrpValIleAspProAsnAspIleAsnArgLeuValProIleGlyA 817
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13661 GCCTGACGCGGCGGCGGCTGTGCGGCGGAC-----CGTCCGAGCGC--- 13701
857 rObAspGlyAlaLysLeuTyrArgThrGlyAspLeuAlaArgTyrAlaSerAspGlySerI 877
13702 -----GGCGGCGGAGTACCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 13756
877 lAlaValCysLeuGlyArgIleAspSerGlnValLysIleArgGlyGlnArgValGluLeuG 897

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QY 897 |YAlAlleGIuThrHISleuArGIuGlnImeTProAspApleuThrIleValValGluA 917
Db 13817 GGAAGGTTCAGAGCGCGCCGACGCGCAC--CCGAC----- 13851
QY 917 |aThrIyAsrGerGIuSerAlaAsnSerThrSerIleuIleAlaPheIleuIleGIySer 937
Db 13852 -----ATCGGCGACG 13861
QY 937 er-----TyrPheGIyAsnArGProSerAAspAlaHISleu----- 949
Db 13862 CGGCGCGCGGTCTGACAGCGGGACGACCGGACCGGTACTGCTGTCTACGCGGTG 13921
QY 950 --AspHisAspAla-----ThrIyAlAlleAsnIleIySleuGIuGlnValLeuP 966
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QY 966 roArGIISerIleProSerPheTyrIleCySmetIleuGIuLeuProArGIyThrAlaThrg 986
Db 13982 CGGCTCATATGATGTCCTCGCGCGGTGTGTCTGTCTGCGCGCTGCGCTGACCCCAAG 14041
QY 986 |YLyAlleAspArGArGArGIuArGIleuArGIyAspArIleuAspIySleuThrg 1006
Db 14042 GCMAAGTCGACGCGAGGCGCTGCGCGCGCGCGCGCGCGGACGCTGCGCGCGCTG 14095
QY 1006 |ngIyAlAlleValGIuGlnAlaProAlaProIleProValIleAlaAspThrAlAla 1026
Db 14096 GCGCGC-----GCTCGCGCGCGACCGCGCGAGGAGGCGCTGCGCGCGCT 14140
QY 1026 yArIeHISerIleTProValGIuSerIleuGIyIleAspProAlaThrValAsnValGIyA 1046
Db 14141 TCGCCACAGTCCTCGCGCTGAGAGGTGACCGCGGAC-----G 14179
QY 1046 |aThrPhePheGIuLeuGIyGIyAsnSerIleThrAlAlleIySmetValAsnMetAla 1066
Db 14180 CCGACTTCTTCCGCTGCGCGCGCGCACCTCGCTGCGCGCGGTGCATCAGCGGATCC 14239
QY 1066 rGser---ValGIyMetAAspLeuIyValSerAsnIleTyrGlnHISProThIleuA 1085
Db 14240 GGTTCGCGCGCTGCGGAGATCGGATCGGACGCGCTTTCGAGCGCGCGCGCGCGCG 14299
QY 1085 yIleSer-----AlaValValIySleAspProIleuSerTyrThrIleuIleP 1101
Db 14300 CGCTGCGCGCGCGGTGAGACACCGCGGACCGGACCGGCGCC-----CGCTGTGTC 14350
QY 1101 ro---LysSerThrHISleuGIyProValGIuGlnSerTyrSerGIuGIyArGIleuIleP 1120
Db 14351 CGGAGCGCGCGCGCGCACCGCGCTCCGCTC-----TCTCGCGCGCGCGCGGTGTGCT 14404
QY 1120 heIeAspGIuLeuAspValGIySerIleuTyrIleuIleProTyrAlaValArGIyMe 1140
Db 14405 TCTTCGCGGAGCTGAGGCGCGCGCGCGGACGATCAACATTCGCTCGCGCGCGCTG 14464
QY 1140 rGIyIyProValAsnValAspAlaAspAlaAspArGIaIleuAlaIleuGIuGlnArGI 1160
Db 14465 GCGGTCCCGCTGAGCGTGCAGCGCGCTGCGCGCGCGGTGAGCGAGTGTGCGCGGACG 14524
QY 1160 |uThrIleuArGIyThrPheGIuAspGIuAspGIyValGIyValGln-----IleValH 1178
Db 14525 AGCGCGCTGCGCGACGCTTCCCGCGCGAGAACGAGTCCCGCACGACGAGTGTGCGCG 14584
QY 1178 |eGIuIySleuSerGIuGIuMetIyValIleAspIeCySleuAspIySerAspIeAspP 1198
Db 14585 CCGAGAGAGCGCGCGCGGACCGGCGCGCTGAGAGTGTGCGCGGAGAGAGCTGCC--- 14640
QY 1198 heGIuValleuAsnGIuGlnIleThrThrProPheAsnIleuSerGIuAlaGIyTrpA 1218
Db 14641 --CGCGCGCTGCGCGAGCGCTGCGCATACCGCTTACGCTGACGAGGACCTCCGCTGC 14698
QY 1218 rGIaThrIleuLeuArGIleuGIyGIuAspAspHISleuThrIleValIleMetHISle 1238
Db 14699 GGGCGGTGCTGTGCGCACCGGCGCGGACCGGACCGAGCTGTCTCTGCTGTGACACCA 14758
QY 1238 |eIleSerAspGIyTrpSerIleAspValIleuArGIyAspIeAsnGIuLeuTyrSerA 1258
Db 14759 TCGCGCGCGAGCGCTGTGTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 14818
QY 1258 |aAlaIleuAspSerIyAspProIleuSerAlaIleuThrProIleuProIleGIuTyr 1278
Db 14819 CACGCTG---GAGGCGCGCGCGCGCG-----CGGTGCGCGCGCGGTGCGGTGAGTACG 14869
QY 1278 erAspPheAlaIyTrpGIuIyAspGIuPheIleGIuGlnIu----- 1292
Db 14870 CCGACTTCAACCTGTGAGAGAGCGGCTGTGCGGAGCGGACGACCGCGACGCTCT 14929
QY 1293 -----LysGIuLeuAsnTyrTrpIySleuGIuLeuIyAspSer---SerProAlaIy 1310
Db 14930 TCGCACGCGACGCTGCGCTTGTGCTGTGACACCTTGGCGGGGCGCGGAGCAATGAGC 14989
QY 1310 |eProThrAspPheAlaArGProAlaIleuIleuSerGIyAspAlaGIyCySvalHIS--V 1329
Db 14990 TCGCCACCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 15046
QY 1329 aThrIleAspGIyIuLeuTyrGIuSerIleuArGIaPheCySAsnGIuHISAsnThr 1349
Db 15047 TCACCTGTGCGCGACGCGCTGCGGACCGGCTGTGCTGTGCGCGCGCGCGCGCG 15106
QY 1349 hSerPheValValIleuLeuAlaIlePheArGIaIleHISyArGIyLeuThrAlaValG 1369
Db 15107 CTTTGTTCATGCGCTGCGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15166
QY 1369 |uAspAlaValIleGIyThrProIleAlaAsnArGIyAsnArGProGIuLeuGIuAspIle 1389
Db 15167 GGGACATCGCTCGGAGACCGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 15226
QY 1389 |eGIyCySAspPheValAsnThrGIuCySmetArGIleAsnIleAspHISAspThrPhe 1409
Db 15227 TCGGCTTCTTGTTCACACCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15286
QY 1409 |yThrIleuIleAsnGIuValIyAlaIleThrThrAlaIlePheGIuAsnGIuAspIle 1429
Db 15287 AGGAGCTGTGACCGGAGTGAAGAGCGGACCTGTGCGCTTGTGCGCGCGCGCGCG 15346
QY 1429 roPheGIuArGIyAlaIleSerAlaIleuGIuProGIySerArGIyAspIleuSerThrPro 1449
Db 15347 CGTTTCAGACGCTGTGTGAGGCGGCTCAACCC---ACCGCTCTCTCTCCGCGCACCCG 15403
QY 1449 euAlaGIuIleuIlePheAlaIleHISerGIuIyAspIleuGIyArGIyPheIyPheGI 1469
Db 15404 TCTTCAGGTCGTGCGCGCTCCAGAAC---AACGAACCTCGCGGAGCGCGGTATGCGCG 15460
QY 1469 |yIleuGIu---SerValProValProSerIyAlaTyrThrArGIyAspMetGIuPheH 1488
Db 15461 GTCTGAGGTCACTGTGGAACGCGCGCGCGCGGAGTGCAGGTCACTTGTGTA 15520
QY 1488 |sIeAspPheGIuThrAsp-----SerIleuGIySerValAsp 1502
Db 15521 ACCTGTGTGAGTCCCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 15580
QY 1502 heAlaAspGIuLeuPheIySmetGIuThrValGIuAsnValValArGIyAlaPhePheGI 1522
Db 15581 AGCCACCGACCTTTCAGACGCGGAAAGCTGCGACGCGGTGCGCGAGCGCTTACAGAG 15640
QY 1522 |eIleuArGIyGIuGlnIleSerIyArGIyThrProValSerIleuProIleuThr--- 1540
Db 15641 TGTCTGTGCGGTACCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 15700
QY 1541 -----AspGIyIleValThrIleGIuIySleuA 1550
Db 15701 GGGCGGACCGCGGATGCTGCGCGCGCGGAGGAGCGGACCGCGCGCGCGCGCGAGG 15760
QY 1550 spValIleuAsnValIySHISValAspTyrProArGIuSerIleuAlaAspValPheG 1570
Db 15761 ACCTG-----GCCGACCTCTTCC 15778
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Qy	1570	lntHngInValSerA1TyProApsertleuAlaValA1ApserserCyAaGlent	1590
Db	15779	GGCCCCGGCCACCGGCACACCGAAGCGGGTGGCGCTGGCCGGGGAAGAGCTTA	15838
Qy	1590	hTyrThrgInLeuApsaPargInSerApsrIleuAaIaGlyTrpLeuAArgAArgSerH	1610
Db	15819	CGTACCGCGAGCTCGCGAGCGAGGCGACCGGGGTGGGGCGGCGCTGGCCGGGCGGGCG	15898
Qy	1610	etProlaG1uThrIleuValAlaValPheAlaProAgsersCyAaG1uThrIleValAlaP	1630
Db	15899	CCGGCCCCGAAACGGCGGGGTGGCGGTGGCTGGCCGGCCACCGCCACCTGGTGGCTGCC	15958
Qy	1630	hePheG1yValIleuLyAlAAsmleuAlaTrpLeuProleuApsAValAArgSerProserA	1650
Db	15959	TGCTCGGAGTCTCTCGGGCGCGCGCGCCCTACGTCGCGCTGGACCCGGAGTACCGGAGC	16018
Qy	1650	laArgValGlnApsrIleuApsrG1yLeuAserG1yProthrlleValIleuIleGlyH1A	1670
Db	16019	AGCGCATTCGCGCGCATCTGTCTCC-----G	16042
Qy	1670	epThrlAlaProProApsrIleG1uValThraAmtAlaG1uPheValAaG1eAArgAAla	1690
Db	16043	ACACCCCGCGGTGGCGCTGTACACAG-----GGGAGTGGCGCCGGCA	16090
Qy	1690	euaApsaPserAAsm1A-----ApsrIyPheG1uValIleG1u1ApsaPserTh1y-	1707
Db	16091	TCACCGCTGCCCGCGCGCGCTGGCGTGGCCACACCTCTGGCGGCGACGCGCGCACAG	16150
Qy	1708	-----ProserAlaThrsrleuAlaTrpValleuTr	1718
Db	16151	GCGCCGGAGCCCTGGCCAGAGTGGCGCGCGCTGCCCGGACAGCGCGCGTACGTGCTGC	16210
Qy	1718	yrThrsrG1ySerThrg1yAArgProAaG1yValMe1le-----	1731
Db	16211	ACACCTTGCGGTCCACAGGACCGGCCAAGGCGGTGTGTCTGACCGCGGGGACCTGGCA	16270
Qy	1732	-----G1uH1AArgValIle1leArgThrValThrsrG1yCyA1leProAent	1748
Db	16271	ACCTGTGGCGGCATGCGGAGCGGCTGGCC-----CTCACCGCGCGG-----	16314
Qy	1748	yrProserG1uThrAArgMeAlaH1eMeAlaThrlleAlaPheApsrG1yA1aserTrg	1768
Db	16315	-----GACCGCGTGGTGGCGCTACACAGCTTGCACATCGCGCCCTGG	16363
Qy	1768	Iu1eTrysrAlaLeuApsheG1yAArgThrIleuValCyAValApsrTrmeThTrH1r	1788
Db	16364	AGCTGTCTCTGCCCTGTGCGCGGCGCCGAACTGTGCTGGCGGACCGCGGACCGGCAC	16423
Qy	1788	euaApsrAlaArgAlaLeuApsAValPhePheArgG1uH1sValAaAla1AAserH1eV	1808
Db	16424	GGGACCGCGAGGCACTG-----GGCGCACTGC	16450
Qy	1808	alTrhsrSerSerG1aApsValProleuArgValProAArgLeuAserAArgThrlleuH	1828
Db	16451	TCACCGGAGGCGGCGCACATCTCCAGGCGACCCGACCACTGGAG-----	16500
Qy	1828	etPhePhePheLeuValValThraPserThrlaProApsrAlaLeuApsrAlaGlnG1yL	1848
Db	16501	-----CTGCTGGCCGAGACCGCGCCGACGCGCTG-----CGCGGGCG	16537
Qy	1848	eutYrGln-----	1850
Db	16538	TGGCGAACTGTGGGCGGGAAGCGTCCCGCGTCCCTGGCGCTCCCGCTGACAGGC	16597
Qy	1851	--G1yValGlnCyATrysAaG1yTrg1yProThrgIuAaG1yValMe1SerThrl1er	1870
Db	16598	TGGCGGCGGAACGTGTCAAGCTTACCGGCGCCACAGACCAACATCTGTGTACACGCGCG	16657
Qy	1870	yrPro1leApsrThrlcluserPhe1leAaG1yValPro1leG1yAArgAlaLeuAAsA	1890
Db	16658	CCACCTGTGACCGGCGCACCGGG-----AGCGACCGCCCATCTGGCGGGCGCTGCGCA	16711

[illegible]

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Qy 2252 ysaapargpheprogluleuvalglunihisvalgluleuproulysaammetglualav 2272
Db 17822 GC---CGGAGAACCGGCGAACCCTCGTCTGGACGCGGGCGCGCGGAGAGCGCG 17878
Qy 2272 alahngluleuseralatyargtlyalalavalahisvalarglyserleuglya 2292
Db 17879 TCACCGAGCTGAGCGCGCTACCGCTAC---GACGTCTGTGCGCAACCGGAGCGCGGGA 17935
Qy 2292 epgluleuvalleuprovalglulysahapargtripleaphneginalahnglileua 2312
Db 17936 CCGCGCGTCCGCGCCCGGCGCGGAGATGCGCTGGCGGAG--- 17976
Qy 2312 snnglyuserleuglyaspleuleuylusersearhpalalalemetlavalserly 2332
Db 17977 -----GAGTCCGAGAC-----CGCGCGGCGTGGCGAGGTGCGCGGACACC 18022
Qy 2332 ysalleprohegluliethralapheglu-----Arglnvalvalalaserly 2348
Db 18023 CGCGCGCGCTGCGCGTACCGCGATCCCAACGCGCGGTGCGCGCGAGACCGCGCGCC 18082
Qy 2348 euahnsersanilleaprglutrgluleuserthrtleargseaserlagnlgluayrs 2368
Db 18083 TCGCGCGCTGAGAGACGGCGCGCGCTCGCGCGCGCGCGCGCTGAGAGCGCGCG 18142
Qy 2368 er---Serleuservalproaspllepheargllealagllyualagllypheargvalg 2387
Db 18143 CCGCGCGAGTGAACCGCGAGACCTGTACGACGCGGGCGCGCGCGCGCGACCGCGT 18202
Qy 2387 luvalserserlalarglnttrserglahngllyalaleuapralavalphenishic 2407
Db 18203 GGGGTGTC-----TGGCGCGCGAGGACCGCGCGACCGCTG----- 18240
Qy 2407 yscysserglnglyargthrleuvalasnhetrothrar----- 2420
Db 18241 -----GACCTGAGTGTGCGCCCGCGGACGGGGCGCGCGCGGAG 18283
Qy 2421 -----Hislyleuarglyseraspleuleuthrasna 2432
Db 18284 TGGACCGCGCGCGGAGCTGGCGCGTACGACCGCGGACCGCGCGCGCGAGACCAAG 18343
Qy 2432 rgrproleuglnargleuglnasnarargtllealilegluvalArggluargyleuayrs 2452
Db 18344 ACCGCTCGCGCGCGCTGCGCAACCGGAGACTGGCGCGCGGCGCTACCTGCGCG 18403
Qy 2452 erleuenuprosertrymetilleproserksnillevalleleuapulysmeproleua 2472
Db 18404 GACGCGTGGCGGACTACATGATGTGCTCGCGCGTGTGCTCTCGCGCGCTCCGCTGA 18463
Qy 2472 snalalenglylyvalaspargluysleuserargatrgalylavalprolyug 2492
Db 18464 CCGCGCAACGGGAGGTGACCGGCGCGCGCTGCCGAC-----CCGAC 18508
Qy 2492 lnglnthralaia-----ProleubProthrhpheroillesergluvalglual 2509
Db 18509 CGGCGGCGCGCGCGCGCGCGCGCA-----CGCGACGACCGCGGAGAGAG 18556
Qy 2509 leleucyrglulglualathrglulvalphehlymet---lyvalasparlletthrahnier 2528
Db 18557 TGGCTGTCGCGGCTTTCGCGACCTGTGGGCGCTGAGCGCGGAGGACACGAGACGT 18616
Qy 2528 hepheanleuglygluylhiserleuenualathrhlyleuilleserarglileaprglna 2548
Db 18617 TCTTCAGCTGGGCGGAGACGACATCTGTTCGCTCGCGCTGTCAAGCGCGGACCGGAAAC 18678
Qy 2548 rgleuylvalarglyethrvallyasparvalpheasphisprovalphealaspyleua 2568
Db 18677 AG---GGGCTGCGGTGACACCGCGGACGCTTTCGAGACCAACCGTGGCGCGCTGG 18733
Qy 2568 laservalilleahrglnglyleuclnglntglnprovalserarpglyngllyglua 2588

Db 18734 CGGGCGCCCTG---GACGGCAGAGAGCGGAGAGACCGCGCGCGACCGCGCGGAC- 18789

Qy 2568 spaySerAlaHisMetAlaProArgThrGluThrGluAlaIleLeuCyAspGluPheA 2608

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Qy 2608 lalyVal 2610

Db 18830 CCGAGCTG 18837

RESULT 4
US-10-329-079-8
; Sequence 8, Application US/10329079
; Publication No. US20030198981A1
; GENERAL INFORMATION:
; APPLICANT: FARNET, Chris
; APPLICANT: ZAZOPOULOS, Emmanuel
; APPLICANT: STAFFA, Alfredo
; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
; FILE REFERENCE: 3002-11US
; CURRENT APPLICATION NUMBER: US/10/329, 079
; CURRENT FILING DATE: 2002-12-24
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 7788
; TYPE: DNA
; ORGANISM: Streptomyces fradiae
US-10-329-079-8

Alignment Scores:
Pred. No.: 7,4e-174 Length: 7788
Score: 2160.50 Matches: 783
Percent Similarity: 43.05% Conservative: 441
Best Local Similarity: 27.54% Mismatches: 1059
Query Match: 13.40% Indels: 563
DB: 15 Gaps: 110

US-09-482-788-2 (1-3129) x US-10-329-079-8 (1-7788)

Qy 51 ProCysThrProPheGluLeuAspMetIleAspCysAsnAlaLeuAspLysGlnSerAla 70

Db 61 CCCCTGTGCCCCCGCCAGCGGAGCGCTGTGTTCTTAAACCGCTACAGACAGGAGCGCGC 120

Qy 71 lIeGlyHis-----AlaValTyraAspValProThrAspIleAspIleSerArgPheAla 88

Db 121 GGCTACCAACATCAGAGGTGCGCTGCGGCTCACCGGAGATCTGACGTCGACGCGCTCAC 180

Qy 89 LeuAlaTrpLysGluIleValAsnGlnThrProAlaLeuArgAlaPheAlaPheThrSer 108

Db 181 GCGGCGAGCGGCGACCTGACCGCGCGGACAGAGAGCTGCGCACCC---GTCTCCGCGAG 237

Qy 109 AspSerGlyLysThrSerGlnValIleLeuLysAspSerPheValPheSerTrpMetCys 128

Db 238 GACGAAACAGGGGCGCGACCGAGTGTCTGTGACCCG----- 273

Qy 129 TrpSerSerSerSerPro-----AspGluVal 138

Db 274 ---GGGGCGCGCGCGCACCGCGCGTGTGTCGCGCGCGCGCCACCGCATCGACGCCCTG 330

Qy 139 ValArgAsp-GluAlaIleAlaIleAlaIleAlaSerGlyProArgCysAsnArgPheValLeu 158

Db 331 GTGCGCGAAGCGCGTCCGCGCGCTTCGACCTGCGCGGACGACATCCCGTCCGCGCACACC 390

Qy 158 wGluAsp---MetGlnThrLysLysCysGlnLeuValTrpThrPheSerHisAlaLeuVal 177

Db 391 CTCTTACAGCTCCGAGCGGCGAACAAGTCTGCTCTCTGTATC-CACCACTACGCCGC 449

Qy 177 lAspValThrPheGlnGlnArgValLeuSerArgValPheAlaAlaTyrlHisGlu 197

Db 450 CGAGCGCGTGTGATGGGGCGCGCTGGACAGGAGACCTGGCGCGCTACCGCGCGCGCGC 509

Qy 197 sAspThrHisArgProGluThrPro----- 205

Qy 806 oAenAsp1LeuAsnArgLeuValPro1IleGlyAlaValGlyGluLeuVal1IleGluSerPr 826
Db 2490 GGGGGCTGCTTCC-----GTGCCGCTGGGCTGTGGCGAGCTGAACGTGCGCGGCC 2543
Qy 826 og1y1LeuAlaArgAspTyr1LeuAlProProProProGluLysSerPro-PhePheThrA 846
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Qy 846 sp1LeProSerTyrTyrProAlaAsnThrPheProAspGlyAlaLysLeuTyrThrG 866
Db 2603 AC-----CCGTTGCACCGCGCGCGGATGTAACGAGACCG 2638
Qy 866 1yAspLeuAlaArgTyrAlaSerAspGlySer1LeuAlaCysLeuGlyArg1LeuAspSerg 886
Db 2639 GCACACCTCGTCCGCGCGACCGACCGCGCGCTCCACCTACGTGCGCGCGCTCCACCTCC 2698
Qy 886 1nVal1yS1LeArg1yG1nArgValG1uLeuG1yAla1IleG1uThr1S1LeuArg1ng 906
Db 2699 AGGTGAACCTGCGCGCTACCGCATCGACCGCGCGAGATCGAGCGCGCGCGCGCGCC 2758
Qy 906 1nMetProAspAspLeuThr1LeuValG1uAlaThr1ySArgSerG1nSer1aAsnS 926
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Db 2779 -----GCCACCGCGCTGCACCGCGGAGACCGACGAC 2812
Qy 946 1aH1S1LeuAspH1S1AspAlaThr1ySAla-----1Lea 958
Db 2813 GGTACCTGCTGTGTAGTGGTGGCGGCGCGACACCGACCGCGACCGCGACCGACGAG 2872
Qy 958 sn1LeuS1LeuG1uG1nValLeuProArgH1S1Ser1LeProSerPheTyr1IleCysMetL 978
Db 2873 GCGGCCACCTGGCGCGACCGCTGCGCATATGATGCTCCGCGCGCTGTGGCGCTGA 2932
Qy 978 euG1uLeuProArgTyrAlaThrG1yLys1LeuAspArgArgArg1uLeuArg1IleMetG1yL 998
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Qy 998 yAsp1LeuAsp1ySg1nThrG1nG1yAla1IleValG1nG1nAlaProAlaPro1IleP 1018
Db 2980 -----CCGCGCCCC----- 2988
Qy 1018 roValPheAlaAspThrAlaAla----- 1025
Db 2989 -----GACCGGCGCGCTGGCGCACCGCGCGCGCGCGACCGCGCGAG 3037
Qy 1026 --Lys1eUuH1S1Ser1LeTyrValG1nSer1eUuG1y1LeuAspProAlaThrValaAsnValG 1045
Db 3038 AACGCGCTGTGGCGCGCTTGCAGCATCTCTGGCGCTCGAG-----GAGTTCAGCGCG 3091
Qy 1045 1yAlaThrPhePheG1uG1uG1yG1yAsnSer1eThrAla1IleuMetValaAsnMetA 1065
Db 3092 ACGCGCATCTTCTGCGCTGGAGCGCATCTCTGCGCGCTCGCGTCACTACCGCGA 3151
Qy 1065 1aArgSer---ValG1yMetAspLeu1ySValSerAsn1LeTyrG1nH1S1ProThr1eUa 1084
Db 3152 TCAGGTGGCGCTGGAGTGAATCGCATCCGACGCGCTTTCAGAGCGCGCACGCGCG 3211
Qy 1084 1aG1y1LeuSer-----AlaVal1ySg1yAspProLeuSerTyrThr1eU 1100
Db 3212 CCGCGCTGTCCCGCGCTCGACACCGCGCGGACCGGCGCC-----CGCTCC 3262
Qy 1100 1ePro1ySerThrH1S1G1uG1yProValG1uG1nSerTyrSerG1nG1yArgLeuTyrP 1120
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Qy 1120 he1eUuAspG1nLeuAspValG1ySer1eUuTyr1yLeu1IleProTyrAlaValaArgMetA 1140
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Db 3380 GCGCGCTGTCCAGCTGAGCGCTTGCACCGCGCTGCGCGAGCTGATGGCGCGGACG 3439
Qy 1160 1uThr1eUa1yG1nThrPheG1uAspG1nAspG1yValG1yValG1n-----1LeValH 1178
Db 3440 AGGCGCTGCGCACCGTCTCCGTCCGAGACCGCGCGCTTACACAGAGTGTCTCCG 3499
Qy 1178 1eG1y1yS1eSerG1uG1uMet1ySVal1IleAspLeuCysG1ySerAspLeuAspProp 1198
Db 3500 CCGAGCGCGCGCGCGCGCTCGACGTCTGAGCATCGACAGAGAGAGAGTGTCC----- 3555
Qy 1198 heG1uVal1eUuAsnG1nG1uG1nThrThrProPheAsnLeuSerSerG1uAlaG1yTyrA 1218
Db 3556 --GCGCGCTCGCGAGCGCGCGACACCGCTTACCTCACCGAGAGACTTCCGCTGC 3613
Qy 1218 rGAlaThr1eUuAspArgLeuG1yG1uAspAspH1S1LeuThr1IleValMetH1S1S1 1238
Db 3614 GGGCGTACTGTGCGGACCGCGCGCGCGACGAGCTCTCCCTGCTCTCCACCA 3673
Qy 1238 1e1IleSerAspG1yTyrSer1IleAspVal1eUuArgAspAspLeuAsnG1nLeuTyrSerA 1258
Db 3674 TCGCGCGCGAGCTGT 3730
Qy 1258 1aAlaLeu1yAspSer1yAspProLeuSerAlaLeuThrProLeuPro1IleG1nTyrS 1278
Db 3731 CCGGACGTCCGAGAGCGCGCGCGCG-----CAGTGGCGCGCGCTCGCGGTGAGTACG 3784
Qy 1278 eAspPheAla1yTyrG1n1yAspG1nPhe1IleG1uG1nG1u----- 1292
Db 3785 CCGACACACCTCTGGAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3844
Qy 1293 -----LysG1nLeuAsnTyrTyr1ySg1nLeu1ySAspSerSerProAla1yS1Ile 1310
Db 3845 TCGCGCGCGACCTGCTCTGTGCGCGAGCGCTG---GAGGCGCGCGGAGACAGATCG 3901
Qy 1311 ----ProThrAspPheAlaArgProAlaLeuLeuSerG1yAspAlaG1yCysValH1S- 1328
Db 3902 AGCTACCATCGACCGCGCGCGCGCGCGCATGAGAGAC---CACCGGCGCGCATTCAC 3958
Qy 1329 --ValThr1IleAspG1yG1uLeuTyrG1nSer1eUuArgAlaPheCysAsnG1uH1SAsnT 1348
Db 3959 GCTTACACCTCCCGCGCTGACGCGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4018
Qy 1348 hrThrSerPheValaVal1eUuLeuAla1aPheArgAla1aH1S1TyrArgLeuThr1a1y 1368
Db 4019 CCACCTCTTATAGCCCTCCAGGCGGAGCTCGCGGACCTGCTGCGACCTTGGGAGCG 4078
Qy 1368 alG1uAspAlaVal1IleG1yThrPro1IleAlaAsnArgAsnArgProG1uLeuG1uAsp1 1388
Db 4079 GCGGAGACATCTCTCTGCGACGCTCTGCGCGCGCGCGCGCGAGAGCGCGACGAC 4138
Qy 1388 1e1IleG1yCysPheValaAsnThrG1nG1nSerArg1IleAsn1IleAspH1S1AspThrP 1408
Db 4139 TCGCGGCTTCTGTCAACACCTGCGCTCCGACCGACGCTGCGCGCGCGACCCACT 4198
Qy 1408 heG1yThr1eUu1eUuAsnG1nVal1ySAlaThrThr1a1a1aPheG1uAsnG1uAsp1 1428
Db 4199 TCGGAGAACTGCTGACCGGCTCAGGAGACCGACGCTGCTGCTGCTGCTGCTGCTGCTG 4258
Qy 1428 1eProPheG1uArgValaValaSerAlaLeuG1nProG1ySerArgAspLeuSerSerThrP 1448
Db 4259 TCCGCTTGCAGCAACTGTGTGAGCGCTTCAACCC---ACCGCTCTCTTCCAGGAC 4315
Qy 1448 roLeuAlaG1nLeu1ePheAlaValaH1S1SerG1n1ySAspLeuG1yArgPhe1ySPhg 1468
Db 4316 CCGCTTCCAGAGTGTCTGCGCTCCAGAAC---AACGAGCGCGCGAGCGCGCTTATGC 4372
Qy 1468 1nG1y1LeuG1u---SerValProValProSer1ySAlaTyrThrArgPheAspMetG1uP 1487
Db 4373 CCGGCTGTGAGTCACTGTGAAAGCGCGCGCGCGCGCGCGCGCGCGCAAGACTCTTGC 4432
Qy 1487 heH1S1eUuPheG1nG1u-----ThrAspSer1eUu1ySg1ySerValA 1501

[illegible]

Oy	379	ValLeuLeuVal1ThrArgGlySerHisValValAsnAsnGly1LeuAsnGly1PheLeuGlnGln	398
Db	16144	TGCGTGGCCCAAGGTGCAGAGCGCTGGAGCGCCGAGACGGGGCCGACGGCGGAGCTGTTCACAGCC	1620303
Oy	399	IleThrGlySerSerHisPheMet-----ProCysAsnAsnArgAlaLeuLeu	414
Db	16204	GTGCTGGACCTTTCAGAAATTTCCCGCGCGAGCATCTCGGTCCCGCGAGAAATTACGGGCTGGCGG	1626303
Oy	415	LeuHisCysGlnMetCysLeuSerGlyAla-----	424
Db	16264	CTGCAGCGC--ATCAGAGCGCGAGCAACACTTCCAACTACCCGCTCAAGCGCATCGTTCAAG	1632003
Oy	425	-----LeuLeuValAlaTyrTyrAspHisAsnVal1LeuSerLeuGln	439
Db	16321	CTCAAGCAAGAGCTGACCGCTGCTGGCTGAGGCTAGACACCGCGCTGTTCAGCGGAGCACCC	1638003
Oy	440	ThrThrArgLeuLeuGlnGlnPheGlyHisLeu1Leu1CysLeuGlnSerProLeuAsp	459
Db	16381	GTGGCGGGCTGGCC-----GGCAGCATCTGCACACCTCTGGAGGAGACCGCCGAG	1643103
Oy	460	LeuSerSer-----MetAlaGluValAsnLeuMetThrGlyTyrAspArgAlaGlu1Le	477
Db	16432	AACCCGACCGCGCGGGCTGGCGAGAGCTGCCCTCTGATCCGCGCGGAGCGAGCACACATC	1649103
Oy	478	--GluSerTyrAsnSerGlnProLeuGluValGln--AspThrLeu1LeuHisGlu	495
Db	16492	GTGCACACCTGGACCGACACCGCTCGAGCATCTCGGTGCAGACCGCGCTGACGACCGCTC	1655103
Oy	496	MetLeu1ValAlaValSerHisSerProThrTyrValHis1LeuGlnAlaTyrAspGlyAsp	515
Db	16552	ATGCGCCAAAGAGCGCGCGCGCGCGCGCGCGAGCCGAGATCGCGTGTGTCGACGCTGAAGCGCAG	1661103
Oy	516	TyrThrTyrSerGluLeuAsnAsnVal1SerSerArgLeuAlaValHis1Leu1CysSerLeu	535
Db	16612	CTGAGTTACGGGCAAGTTTGAACCGCGCGCGAGCAACAGCTGCACACATCTGGCGCGCGG	1667103
Oy	536	GlyLeuAspArgAlaGlnGlnAla1Leu1ProValTyrPheGlu1CysSerTyrTyrVal1Le	555
Db	16672	GGGGTGG--GGCGGGAGCGCCCTCGTCGGAGATCGCGGTGCAGACGCGCGGAGGCTGCTC	1672803
Oy	556	AlaSerMetLeu1ValLeu1Leu1CysSerGlyAsnAlaPheThrLeu1LeuAspProAsnAsp	575
Db	16729	GTGGCATCTCTCGGACACGCTCAAGGGGGCGCGCGCGCTATGTGTCGCGTCAACCCGAAATTC	1678803
Oy	576	ProProAlaArgThrAlaGlnValVal1ThrGlnThrArgAlaThrValAlaLeuThrSer	595
Db	16789	CCGCGGACGAGCGTCCGACCAACATGCTGTCCGAGTCCCGCGCGCGCTCTGCTTCAACCCAG	1684803
Oy	596	LeuLeuHisArgGlu1ThrValGln1CysLeuVal1GlyArgCysValVal1ValAsnArgGlu	615
Db	16849	GAACACCTGCTGGCGGGGCGCTCGCGCGAGACGAGCGCGGAGTGTGTGCTGAACCGGAGAC	1690803
Oy	616	Leu-----LeuGlnSerVal1SerAlaSerAsnAspPheSer	627
Db	16909	CTGGCGGACATCGAGGCGGACCCCAACGCGCGCGCGCTCTCCGCGCGGAGC-----	1695903
Oy	628	SerLeuThr1CysSerGlnAsnLeuAla1TyrVal1LeuPheThrSerGlySerThrGlyAsp	647
Db	16960	-----CCGCGGACCTGGGCTGTATGTCACTTACCACTTGGGGCTTCCACGAGCGCG	1700703
Oy	648	ProLeuGly1LeuMet1LeuHisArgAlaPheSerSerCysAlaLeuAspPheGlyAla	667
Db	17008	CCCAAGGGGCTCATGTGTCAAGCACCGCTGCTGTTCACATATCATCAACGAGCGCGAGCGG	1706703
Oy	668	Ser1LeuGly1LeuAsnSerAspThrArgAlaLeuGlnPheGly1ThrHisAlaPheGlyAla	687
Db	17068	CTCTACAGACCTGGGCGCCCGACAGCGCGAGTGTCTGACATGTCACAAATGACTTTCAGAGCG	1712703
Oy	688	CysLeuLeuGln1LeuMetThrThrLeu1LeuAsnGly1CysValCys1LeuProSerAsp	707
Db	17128	GGCGTGTGGAGGTCTTCTTGAAGCTGCAGCGCGCGGCGGCAACCTCTCATTCGCGGAGCCCC	1718703

Qy 708 AspAspArgMetAsn-----SerileProSerPheileAsnArgTyraAsnValAsnTrp 725
Db 17188 GAGGCCCGGAGAGCCCGGCCCACTGCGGAGAGCTGGCGGAGTGCATGACCGCG 17247
Qy 726 MetMetAlaThrProSerTyrmGlyThrPheSerProGluAspValProGlyLeuAla 745
Db 17248 CTGACGCTGCGCGCGGCTGAGCTGCGTGGACCGGCTGCGCGCGGATGACG 17307
Qy 746 ThrLeuValLeuValGlyGluGlnMetSerSerValAsnAlaIleTPAlaProLys 765
Db 17308 AGCGTGGGCTGCGCGGAGATGCTGCGCGGACACTGCGCGGAGTGGCGCGG 17367
Qy 766 LeuGlnLeuLeuAsnGlyTyrglyGlnSerGlySerSer---SerileCysPheAlaSer 784
Db 17368 CGCGGCTGTTCACATCTACAGGCGCCAGAGGCGGACCTGTCTCGTGGCGCTG- 17421
Qy 785 AsnMetSerThrGluProAsnAsnMetGlyArgAlaVal----- 797
Db 17422 ---CACCGCTGCACCGCGGCGCGCGCGCGCGCGCTGCGGACCGCGGTC 17478
Qy 798 GlyAlaHisSerTrpValIleAspProAsnAspIleAsnArgLeu-----ValProIle 815
Db 17479 AACACCGCTTCCATGCTGCAC-----GAGCGGCTGGCGCTGCTCGGCT 17526
Qy 816 GlyAlaValGlyLeuValIleGluSerProGlyIleAlaArgAspTyriLeValPro 835
Db 17527 GGGGTGACCGGCGAGCTCTACATGCGGCTGCGGCTGGCGCGGCTGACCTGGG-CCG 17585
Qy 836 ProProGluLysSerPro-PhePheThrAspIleProSerTrpTyProAlaAsnTh 855
Db 17586 CCGGACCTGACCGCGGAGCGCTGCTGCGCGAC-----CCGTCGGA-- 17628
Qy 855 rPheProAspGlyAlaLysLeuTyraGlyThrGlyAspLeuAlaArgTyriAlaSerAspG 875
Db 17629 ---CCGCGCGGATCCCGCTCTACCGCACCGGAGCTGATCGCGGACCGCGAGG 17684
Qy 875 ySerIleValCysLeuGlyValArgIleAspSerGlnValLysIleArgGlyGlnArgValG 895
Db 17685 GCGGCTGAGATTGCGCGGCGGCGGCGGAGACACAGTCAAGATCCGCGCTACCTGCGA 17744
Qy 895 uLeuGlyAlaIleGlyThrHisLeuArgGlnGlnMetProAspAspLeuThrIleVal 915
Db 17745 GCCCGCGAGTGAAGAGCGGACGCTGCGCGAG---CCGCGCGCTCGGAGGCGGTG 17801
Qy 915 lGluAlaThrLysArgSerGlnSerAlaAsnSerThrSerLeuIleAlaPheLeuIle-- 934
Db 17802 GATCGCC---CGGAGCAGCAGCACCGGCGCACAGCGGCTGCTGCTATGCTGAC 17855
Qy 935 ---GlySerSerTyriPheGlyAsnArgProSerAspAlaHisIleLeuAspHisAspAl 953
Db 17856 GAGCGGAGGAC-----GGAACCGCGCGGAGACCGCGCGCTGCTGCGC----- 17898
Qy 953 arThrLysAlaIleAsnIleLysLeuGlnGlnValLeuProArgHisSerIleProSerPh 973
Db 17899 -----GCCCTGGGCGGCGAACCTCCGCGCTACATGGCGCTGCGC 17939
Qy 973 eTyriLeCysMetLeuGlnLeuProArgThrAlaThrGlyLysIleAspArgAlaGly 993
Db 17940 CCGTGCACCTGCGCGGAGCTACCGCTGCGGAGCAGCAGGAGTGCATGCGCGGCGCT 17999
Qy 993 uArgIleMetGlyLysAspIleLeuAspLysGlnThrGlnGlyAlaIleValGlnGlnAl 1013
Db 18000 G----- 18000
Qy 1013 aProAlaProIleProValPheAlaAspThrAlaAlaLys----- 1026
Db 18001 -CCGCGACCGGATCCGCGCGGCGGACCGCGGCGGATCCCGCGCGCACCCCGAC 18059
Qy 1027 -----LeuHisSerIleTyriValGlnSerLeuGlyIleAspProAlaThrValAs 1043
Db 18060 GGAAGAGCACTGGCGCTCATCTGGGTGAGAGTGGCTGGCGCTGCA-----CACGTCGG 18113
Qy 1043 nValGlyAlaThrPheGluLeuGlyLysAsnSerIleThrAlaIleLysMetValAs 1063

Db 18114 CGTGAAGACAACTTCTTGCACCTCGCGCGGAGCTCCATCAGACAGCTGCGGTTGATGTC 18173
Qy 1063 n---MetAlaArgSerValGlyMetAspLeuLysValSerAsnIleTyriGlnHisProTh 1082
Db 18174 GCGGATGGGCGGCGCTTGGTGTGAGAGCTCAACCCCGGCACTTCTTGAACGCCCGCAC 18233
Qy 1082 rLeuAlaGlyIleSer-----AlaVal 1089
Db 18234 CATCGCGCGCTTGGCGGAGCGCTAGAGAAAGATCTGGCGCATGGAGAGAGCGT 18293
Qy 1089 lValLysGlyAspProLeuSerTyriThr----- 1098
Db 18294 CGAGGCGGCGC-CTATGACAGACTTGTGAGCGGACACCGCGGACAAACCGGACAC 18352
Qy 1098 ----- 1098
Db 18353 CACCGCGCTGCGCTGCGGAGCGCACCGCGCGCTGCGGCGCATGTGAGAGAGTCT 18412
Qy 1099 -----LeuIleProLys 1103
Db 18413 GCGCGCGCGCTGCGCGGCGCGCGCGCGCGCGCGCGCGGAGACACATCCCGCAT 18472
Qy 1103 rThrHisGlyLysProValGlnGlnSerTyriSerGlnGlyArgLeuTrpPheLeuAspG 1123
Db 18473 CGGCGACAGAGCGCGCGCTGCGCTGCGCGCGCGCGCGCGCGCGCGCTGTGATCGTATGA 18532
Qy 1123 nLeuAspValGlySerLeuTyriTyriLeuIleProTyriAlaValArgMetArgGlyProVa 1143
Db 18533 GCTGGAACCGGAGAGCAACAGTACAAACCTGCGCGCTGCGGTGGCGCGCGCACT 18592
Qy 1143 lAsnValAspAlaLeuAspArgAlaLeuAlaIleLeuGlnGlnArgHisGlnThrLysu 1163
Db 18593 GAGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCG 18652
Qy 1163 gThrThrPheGluAspGlnAspArgIleValGlyValGlnIleValHisGlnLysLysuSerG 1183
Db 18653 CACCACTTGGGCTCCCGGAGGCGGACCGCGGAGACAGCGTGCATCCGCGCGTACCGAC 18712
Qy 1183 uGluMetLysValIleAspLeuTyriGlySerAspAspLeuAspProPheGlu----- 1199
Db 18713 ACCGCTGCCCTGTGCACCTGTGCGGCGGAGACAGCGGAGCGGAGCGGCGCTGCG 18772
Qy 1200 ---ValLeuAsnGlnGlnGlnThrThrProPheAsnLeuSerSerGlnAlaGlyTrpAr 1218
Db 18773 GACCTGCTGCAAGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCG 18832
Qy 1218 gAlaThrLeuLeuArgLeuGlyLysAspHisIleLeuThrIleValMetHisHisI 1238
Db 18833 GCGGAGCTGATCGCGCTGCGGCGGCGGAGCAGACATGCTGCGCGCTGCGCGTGCATCAT 18892
Qy 1238 eIleSerAspGlyTyriSerIleAspValLeuAspArgAspLeuAsnGlnLeuTyriSerAl 1258
Db 18893 CGTCAACCGAGCGGTGTGATGGCGGTGCTCACCGGAGGAGACCGCGCACATACCGCGC 18952
Qy 1258 aAlaLeuLysAspSerTyriAspProLeuSerAlaLeuThrProLeuProIleGlnTyriSe 1278
Db 18953 GAGCGTGGCGGTGCGC-----GCCGTACTGCGCGAACTTCCGAGACTGACT 19003
Qy 1278 rAspPheAlaLysTrpGlnLysAspGlnPhe-----IleGlnGlnLysLysGlnLys 1296
Db 19004 CGATGTCGCGCTGCGGAGGTACACAGCTGAGCTCGCGCGCGGTGCGGAGGCGTCA 19063
Qy 1296 nTyriTrpLysGlnLeuLysAspSerSerProAlaLysIleProThrAspPheAlaAr 1316
Db 19064 CCACTGGCGCGGAGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 19123
Qy 1316 gProAlaLeuLeuSerGlyAspAlaGlyCysValHis---ValThrIleAspGlyLys 1335
Db 19124 GCGCGCGCTGCGGAC---AGCGCGGAGCGCTGCACTCTTGCAGATCCCCCGCGGT 19180
Qy 1335 uTyriGlnSerLeuArgAlaPheCysAsnGlnHisAsnThrThrSerPheValValLeu 1355

Oy	2032	GLYTPRGLINAspHisphGluSerGlyMetCysrAspIle-----	2046
Db	21254	GGTGTCTGGCCGAGCAATGCTGCTTCGCTTCGTCGCGTACGCGCTGCTGAA	21313
Oy	2047	-----GLGluIleAspProSerThrIleGlySerAspPheIleGlyTrpHisSerme	2064
Db	21314	CGCCACCGCAAGTTCGACCGCGCGGCGTG-----	21344
Oy	2064	CTyrAspGlySerGlnIleAspPheAspGluMetHisGluTrpLeu-----	2079
Db	21345	-----CCGCGACCCGACATCCGCGCGCGACGAGGCGAGCGCCGATGCGCGCGACCC	21400
Oy	2080	-GLYGLuThrTrpArgHisIleHisAspAsnArgSerLeuGlyAsnValLeuGluIleG	2099
Db	21401	GGCGGAGAGACCGTGGCGCGCATCTGTGCGAGAGTCTTGCGC---GTACCGGACATCGG	21457
Oy	2099	YThrGlySerCylMetIleLeuPheAsnLeuAspSerArgLeuGluSerTyraValGlyLe	2119
Db	21458	CGTGGAGGACACTTCTTCGACCTCGCGCGCGGCGACTCATCTTACGCTTCAGGTGTGGC	21517
Oy	2119	UGluProSerArgSerAlaAlaAlaPheValAsnValAspIleThr-----GluSerI	2136
Db	21518	GGGGGCGCGGCGCGGACCTGCGGCTGACCGCGCAACAGACCTTCTCGCGGACAGCAT	21577
Oy	2136	eProSerLeuAlaGlyValAlaValValGlnVal-----GlyThrAlaHis	2151
Db	21578	CGCGGATCTGCGCGCGCGACCGCTGCGCGGACCGACCGCGCGCGACCGTGGCGGCA	21637
Oy	2151	AspIleGlyGlnAlaAspAspLeuHisAspAspLeuValValLeuAsnSerValIleG	2171
Db	21638	CGAC---GGCGCGGTACCGCGGACGTGGC-----	21665
Oy	2171	nTyrPheProSerSerGluTrpLeuAlaGluIleAlaAspThrLeuIleHisLeuProAs	2191
Db	21666	-----CTACGCC	21673
Oy	2191	nValGlnArgIlePhePhe-----GlyAspValArgSerGlnAlaThrAsnGluHis	2208
Db	21674	CATCCAGACTGTGTTCTTCAACTCTCGCGCGACGCTGACAGTTCACCAAGTCGCT	21733
Oy	2208	sPheLeuAlaAlaArgAlaIleHisThrLeuGlyLysAsnAlaThrLysAspAspAlaAr	2228
Db	21734	GTATCTG-----	21740
Oy	2228	gGlnIleMetAlaGluLeuGluAspMetGluGluGluLeuValGluProAlaPheHis	2248
Db	21741	---GAGTGGCGGAGGCGCCGACCTC-----CCGCGC-----	21770
Oy	2248	eThrSerLeuLysAspArgPheProGlyLeuValGluHisValGluIleLeuProLysAs	2268
Db	21771	-----CTCGGCGCGCCCACTGCGCGCGCTGACCGAACAACAGACGCGACTG-----CG	21817
Oy	2268	nMetGlnAlaValAsnGluLeuSerAlaTyraArgTyraAlaAlaValAlaHisValArgI	2288
Db	21818	GCTCGCGGCGGTATCCAGAGACGGCGAGTGGCGCTGCACACGCGCGCGGACGCGG	21877
Oy	2288	YSerLeuGlyAspGluLeuValLeuProValGluLysAspAspTrpIleAspPheGlnAl	2308
Db	21878	TCAACTCTCTGAAACACTCATCTGTCTCGCGCGTGTGCGCGGAC-----	21920
Oy	2308	aAsnGlnLeuAsnGlnLysSerLeuGlyAspLeuLeuLysSerSerAspAlaAlaIleMe	2328
Db	21921	-----GACACAGGACCGCGCGATGCGC	21940
Oy	2328	tAlaValSerLysIleProPheGluIleThrAlaPheGluArgGlnValAlaSerIe	2348
Db	21941	GGCGCGCC-----GTCCAGCGCGCGCACCGG-----	21965
Oy	2348	uAsnSerAsnIleAspGluTrpGlnLeuSerThrIleArgSerSerAlaGluLysAsp	2368
Db	21966	-GACTTCCGCGTGTCCAGAGGCGCGCTGTCGCGGCGCGCGCTTACCTCGGCGACCC	2202
Oy	2368	rSerLeuSerValProAspIlePheArgIleAlaGly-----	2380

[illegible]

Db 22881 -----ACGGCGCGCGCTGGAGTTCACCTGACGATCTCGGTGAAC-- 22922
Qy 2638 eglyHsArgLeuAphThr-----ValserVallyAsa 2650
Db 22923 -CGGACCGCGGACAGACCGCTGCGCGCGGCTTCATGACCGCGTGAAC 22981
Qy 2650 pvalPheAphHs-----ProValLeuPheGlnLe 2660
Db 22982 GATCGTGGCCACATCGCGCGCGCGCTCGCGCGCGCACCGCGTCCGACCTCCGCGT 23041
Qy 2660 ualHsLeuAphAspHsLeuValGlnserLeuThraGlnLileValGly---GlyAr 2679
Db 23042 GGGC---GCCCTGAC-----CAGGCCACCGTGCACAGATCCCGCGACGGCGC 23089
Qy 2679 ggluMetAlaGluTyrSerProPheGlnLeuLeuPheThrcLysAProGluGluPhe 2699
Db 23090 C----- 23090
Qy 2699 talAserGluLileYserProGlnLeuGluGlnLileGlnAphLileTyrProse 2719
Db 23091 -----ACGGTCCAGGACATCTACCGCGCT 23113
Qy 2719 rThrGlnMetGlnLysAlaPheLeuPheAphHsThrThraAlaArgProArg---Proph 2738
Db 23114 CACCGCGATCGACGCGGACATGCTCTTCACGCGCTGACGAGTCCGAGCGACCGCTA 23173
Qy 2738 eval---ProPheTyrLileAphPheProserThrSerGluProAphAlaAlaGlyLeu 2757
Db 23174 CACCGGCGACTTCGGCGCTCGCGCTGCAGCGGATACCGACCGCGGGGCA-----CTGGC 23227
Qy 2757 elyAlaCyseGlnserLeuValAphHsLysLeuAphLilePheArgThryAlPheAla---G 2776
Db 23228 CGCGGCGCTGCAGGACGCTCGTGCACCGGACCGCGCGCTGCACCGCGCTGCTGCA 23287
Qy 2776 ualAserGlyGluLeuTyrGlnValValLeuSerCyLeuAspLeuProGlnValL 2796
Db 23288 GAGCGTGCAGAACCCCTTCAGGTGTGTGCACGCGCGCGCGCTGTCGGGACCATCA 23347
Qy 2796 eglyu-----ThrcLysAphAphLileAphThraLileThraGlnLilePheLeuAph 2812
Db 23348 CGACCTGCGGCTCCCTGACCGACGAGAACGCGACCGCGCTGACCGCGCTGGAGCG 23407
Qy 2812 upheAlaLysGluProValArgLeuGly---HisProLeuLileArgPheThrLileLe 2831
Db 23408 GCGCGAGGACACCGTCACTCGCTGCGCGCGCGCGCTGCGCGCTGACCGCTGCGCG 23467
Qy 2831 sGlnThrLysSer---MetArgValLileMetArgLileSerHisAlaLeuTyrAph 2850
Db 23468 GCTGACCGACGCGCGCTGATGCTTGTGACCTCGACCATCTGATGAGCGCTG 23527
Qy 2850 user-----LeuGlnHisValValArgLysLeuHisMetLeuTyrAphGlyAr 2866
Db 23528 GAGCTTGGCGGGGTGTGTGTGAGAGTGTGCGCCAGTACACCGCGGTGACCGCGCGCC 23587
Qy 2866 gSerLeuLeuProPro-----HisGlnPheSerArgTyrMetGlnTyrThraAph 2883
Db 23588 CCGGCTGCGCGCGCGCGCGCGCGCGCTGACCGGACTATGCTGCGTGTGCGCGGACA 23647
Qy 2884 -GlyArgGlnserLysHisGlyPheTyrArgAphValLileGlnAsn-----Th 2899
Db 23648 GAGACCGCGCGCGCGCGCGCGCGCTGCGCTGCGTGTGACGCGGTTCACGCGTCCGAC 23707
Qy 2899 rProMetThrLileuserAphAphThraValValAphGlyAphAphAlaThrcYlsAl 2919
Db 23708 CCGCGTCCG 23746
Qy 2919 aleuHsLysSerLysLileValAphLileProserGlnValLeuArgLysAr----- 2936
Db 23747 CACCGGCTGCTCGCGTGTGAGGCGCGTGCAGCTGCGCGCGAGCGCTCCGCGCGCTGTC 23806
Qy 2937 -----SerAsnLileThrcGlnAlaThraValPheAsnAlaAlaCyseAlaLe 2952
Db 23807 CGAGCGAT 23866

Qy 2952 uValLeuSerArgLysSerAphSerLysAphValValPheGlyArgLileValserGlyAr 2972
Db 23867 CTGCTGCGCGCGCTGACG 23926
Qy 2972 gGlnGlyLeuProValGluTyrGlnLysAphLileValGlyProGlyThraAphAlaProVa 2992
Db 23927 TCCCGCGACCGTCCCG 23986
Qy 2992 lArgAlaHsLileGlnserSerAphTyrAph-----GlnLe 3004
Db 23987 ACCGGGACCATGACGAGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 24046
Qy 3004 uLeuHsAphLileGlnAphGlnTyrLeuLeuSerLeuProHsGlnThrcLysLileGlyPhe 3024
Db 24047 GCTGCGCGCGCTGACAGCGAGCGAGCTGCACTCCGCGACGACGAGATGCTCGCTGCG 24106
Qy 3024 rAphLeuLysArgAphAphSerThraPhe-----ProGlnAlaLileThraAphPhe 3041
Db 24107 GCAGATCCAGCGC-----TGAAGCGCGTACCGCGCGCGCGCGCGCGCGCGCGCGCG 24154
Qy 3041 rCyseValLeuThrcTyrHisAphPheGlnTyrHisProGlnser----- 3055
Db 24155 CAGCATGCTGCTTGTGAGAACTACCTTACGACGAGGATCGCGCGCGCGCGCGCGCGCT 24214
Qy 3056 -----GlnPheGlnGlnGlnArgValGlnMetGlyValLeuThr----- 3068
Db 24215 GACCTGCGGACGCTTCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 24274
Qy 3069 -----LysPheValAphLileGlnMetAphGlnProLeuTyrAphLeuAla 3083
Db 24275 CTGGCGCGACGACGCTGACATCTCACTCGCGCTACGACCGGATGTTGACAGAGCG 24332

RESULT 6
US-10-282-122A-31388
Sequence 31388, Application US/10282122A
Publication No. US2004029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zykkind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308

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; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ. ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31388
; LENGTH: 9748
; TYPE: DNA
; ORGANISM: Pseudomonas putida
US-10-282-122A-31388

Alignment Scores:
Pred. No.:      3,65e-151      Length:      9748
Score:          1897.50      Matches:      762
Percent Similarity: 36.18%      Conservative: 469
Best Local Similarity: 22.40%      Mismatches: 1100
Query Match:    11.77%      Indels:      1073
DB:             16      Gaps:      95

US-09-482-788-2 (1-3129) x US-10-282-122A-31388 (1-9748)
QY      46  IlegluAlaIlelyspProcyThrProhGlnleuaspmetIleapcyAsnAlaLeu 65
DB      4  ATGGAACACTCTATCTGTTGCGCGATGCGAGAGCGCTGCGATGCACACCTTCTC 63
QY      66  AspLysGlnSerAlaIle-----GlyHisAlaValTyrAspValProThrAspIleAsp 83
DB      64  GAACCGGCTTCGGGCACTATCTGATGCAGATTGCTACCGCGTCGACACCGCATTTGAT 123
QY      84  IIserrArgPheAlaLeuAlaTPrLYsgluIleValanglnThrProAlaLeuArgAla 103
DB      124  GTCGGCGCGTTACGAGCAAGCGTGAAGCGGTTCATTCGCGCCATGACGTGCTCGCACC 183
QY      104  PheAlaPheThrSerAspSerGlyLysThrSerGlnValIleLeu-----LysAspSer 121
DB      184  ---TCGTTTGGCTGGAGCTGGTGAGCGCATGGTGACGATGCCATCCCGCCGACCGAG 240
QY      122  PheValPheSerTrpMetCysTrpSer-----SerSerSerProAspGluValVal 139
DB      241  CCGGCAATGGCGCTGCTGACCTGCGCTCACCCTGACCTGAAGATCATGACGAAGCCCTT 300
QY      140  ArgAspGluAlaAlaIle-----AlaAlaSerGlyProArg 151
DB      301  CAGGCGCAACTGGAAGCGAGAGCTGCGCAGGCTTCGATATGCGCAAGAACTCCGCTTC 360
QY      152  CysAsnArgPheValIleLeuGlnAspMetGlnThrLysCysGlnLeuValTPrThr 171
DB      361  CGCCTGGCGCTGATCGCTGCGAT-----GCCGACCACTTCGCTTCCTTACG 411
QY      172  PheSerHisAlaLeuValAspValThrPheGlnGlnArgValLeuSerArgValPheAla 191
DB      412  AACCAACATGTGCTGCTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 471
QY      192  AlaTyrIleHis-----GluLysAspThrHisArgProGluThrProGluSerSer 208
DB      472  GTCTACACAGAGCTGACACCGGTGTCGGGTACACATGCGCAGACCGCGCGCTTACGCG 531
QY      209  AspAlaThrAspThrAspSerGlnSerValSerValValSerMetSerCysGluAspAsn 228
DB      532  GAC-----TTTCATCGCTTCGCTGCGAT----- 561
QY      229  AlaValSerAlaThrHisPheTrpGlnThrHisIleuAsn----- 241
DB      562  CGTGAAGGCTTCGGGTATTTCTGGCGCAATGAGCTGCAAGTTTCGACCGGCGCACCGCG 621
QY      242  -----AspLeuAsnAlaSerValPheProHisLeuSerAspHisIleuMetValPro 258
DB      622  CTGCGCGTTACCGCAGCGCGCAGCGCC---GAGCAC-----AACCATGACAGCAGTGCGC 672
QY      259  AsnProThrThrThrAlaGluHisArgIleThrPheProLeuSerGlnValAla----- 276
DB      673  GATGAGCTGTGTACTGACCGCGGACCAAGCGCGGAGGTGCGCGCGCGCGCGCAGCGCG 732
QY      277  -----LeuSerAnSerAlaIleCysArgThrAlaLeuSerIleLeuLeuSerArgTyr 294

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DB      733  GCACAGTTACGGTCAACACCTGTGTGCAAGCGCGCTGCGACACTGTACTGCAACGCTAC 792
QY      295  ThrHisSerArgGluAlaLeuPheGly---AlaValThrGluGlnSerLeuProPheAsp 313
DB      793  AGCGGCGACCGGTGATCGTGTTCGGGGTGACCGGTGCGCGCGGTGAATTCCTCC 852
QY      314  LysHisTyrLeuAlaAspGlyThrTyrGlnThrValAlaProLeuArgValHis----- 331
DB      853  GAGATGACAGCTACCGTGGGCTGTTTATCAACAGCATCCCGTGGCGGTCCGTTGCGG 912
QY      332  ---CysGlnSerAnLeuAlaSerAspValMetAspAlaIleSerSerTyrAspAsp 350
DB      913  GCGCGCGACCGCGGCTCAAGCGCAAGCGGTGCTCAAGTCACTGCTTGACCAACCACTC 972
QY      351  ArgLeuGlyHisIleuAlaProPheGlyLeuArgAspIleArgAnThrGlyAspArgGly 370
DB      973  AACCTGCGCAGACGACGACATTCCTTGTGTGATATCCAGGCGGTGACGAGTTCGCT 1032
QY      371  SerAlaAlaCysAspPheGlnThrValIleuLeuValThrAspGlySerHisValAsnAsn 390
DB      1033  AGCGGTGAGCGCTGTTGACAGC---CTGTTGCTTTCAGAAAGCGCGCGGTGAGATCC 1089
QY      391  -----GlyIleAngIyPheLeuGlnGlnIleThrGluSerSerHisPheMetProCys 408
DB      1090  AGCGTTGCGCGCCAGCGCTTGACCATGAGTGAAGCTGAGGCTGCGCGACGACACACC 1149
QY      409  AsnAsnArgAlaLeuLeuLeuHisCysGlnMetGluSerSerGlyAlaLeuValAla 428
DB      1150  AACCTACCGGCTCACCGGTGTGTGTATCCCGGTGAGGTGCTGGGCG-----CTGCACCTG 1203
QY      429  TyrTyrAspHisAnValIleAspSerLeuGlnThrThrArgLeuGlnGlnPheGly 448
DB      1204  TCGTATGACCAAGCGCTGTTGACAGCGCAACCATCAAGCTGCTGCTGCTGCTGCTGCT 1263
QY      449  HisLeuIleLysCysLeuGlnSerProLeuAspLeuSerSerMetAlaGluValAsnLeu 468
DB      1264  GCTTGTGTGCTGGCGTTGACGAGCAGCTGAGCGGCGGACTTCATGCTGTGGCGCGGCC 1323
QY      469  Met-----ThrGluTyrAspArgAlaGluIleGluSerTrpAsnSerGlnPro 484
DB      1324  CTTCTGCGAGTGGCGCGCGGAGTGCCGACCGCGCTGCGCAGGCTTACGACGAGGCTAT 1383
QY      485  LeuGluValGlnAspThrLeuIleHisGlnMetLeuLysAlaValSerHisSerPro 504
DB      1384  GCGCGGCTGTTCAAGCC-----ACTGTCCAGCGTCCGCGG 1419
QY      505  ThrLysThrAlaIleGlnAlaTPrAspGlyAspTPrThrTyrSerGlnLeuAspAsnVal 524
DB      1420  CAATGCTGTCGGCGCGCTGCCAGGCGCGGTGATGAGCTACCGCGAGCTGATCAACGG 1479
QY      525  SerSerArgLeuAlaValHisIleLysSerLeuGlyLeuArgAlaGlnAlaIleIle 544
DB      1480  GCGGACGCTGCGGAGGTGTACTGACGAGGCAATGTTGTGACGCTGACACAC---CTGCTC 1536
QY      545  ProValTyrPheGluLysSerLysTPrValIleAlaSerMetLeuAlaValLeuLysSer 564
DB      1537  GCTGTGCTGCTGAGCGTGAACCTGTCTGCTGCGCATGTGTGTGGGGGTTCACAGCG 1596
QY      565  GlyAsnAlaPheThrLeuIleAspProAsnAspProProAlaArgThrAlaGlnValVal 584
DB      1597  GGTGCGCGTATATCTCTGCTGATCCCTCTTCCGGTGGCGCGCGCGCATGTGCTG 1656
QY      585  ThrGlnThrArgAlaThrValAlaLeuThrSerLysLeuHisArgGluThrValGlnLys 604
DB      1657  CGCTTGAAGCAGCGCGGTGTGTGTGTGTCGATAG----- 1692
QY      605  LeuValGlyArgCysValValValAspAspGluLeuGlnSerValSerAlaSerAsp 624
DB      1693  -----CATTGTGCGGCTGGCCCAAGCATGCTCAAGGCTTCAAGCGCGCGCG 1743
QY      625  AspPhe-----Ser 627

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Dh 1744 ACCTTGTTGGCTGGAGCAGGTGACGACACCGCCGCGGACAGATGTCACCTG 1803
Qy 628 SerLeuThrIysSerGlnAAspLeuAlaTyrValIlePheThrSerGlySerThrGlyAsp 647
Dh 1804 CCCATCAATGCCGCAAGCTGCTGGCTTACCTTCACTTCTGTTGCAACCGGCTG 1863
Qy 648 ProIleGlyIleMetIleGluHisArgAlaPheSerSerCysAlaIleuLysPheGlyAla 667
Dh 1864 CTTAAAGGCGTCAATGCTGCAACAGGCGGCATGCTCAACCAACGCTGACGACGCTACCG 1923
Qy 668 SerLeuGlyIleLeuSerAspThrArgAlaLeuGlnIleGlyThrHisAlaPheGlyAla 687
Dh 1924 TACTTGGGCTGCGGGCAGCAGCATGATCGCCCAAGCGCTTCGACAGAGCTTGATATC 1983
Qy 688 CysLeuLeuGluIleMetThrThrLeuIleAsnGlyGlyCysVal----- 702
Dh 1984 AGCGTCTGGCAATTGCTGACGGCGCCCTGTGTGTTGCCCGGTGAAATCTTCCCGAC 2043
Qy 702 ----- 702
Dh 2044 GCCGTGCGCAGATCCGACAGCGCTGTCACAGGTGACAGCGCAGCGGTGACCATC 2103
Qy 703 -----CysIleProSerAspAspAspArgMetAsnSerIleProSerPheIleAsnArg 720
Dh 2104 CTGGAATGCGTACCGGC-GATGAT----- 2126
Qy 721 TyrAsnValAsnTrpMetMetAlaThrProSerTyrMetGlyThrPheSerProGluAsp 740
Dh 2127 -----CAGGCCATGCTGAACTGCCAGCCGCG--CA 2157
Qy 741 ValProGlyLeuAlaThrLeuValLeuValGlyGluIleMetSerSerSerValAsnAla 760
Dh 2158 TTGCGACGCGCTGCTACCTGCTCACACCGGCGCAACCATGTGACCGGACCTGGCCCGC 2217
Qy 761 IleThrAla-----ProLysLeuGlnLeuLeuAsnGlyTyrGlyGlnSerGluSer 777
Dh 2218 CGCTGGCGGACGCGCTACCAAGGTGAACTGTTCAACGCTTACCGCGCGGAGTGT 2277
Qy 778 SerSerIleCysPheAlaSerAspMetSerThrGluProAsnAsnMetGlyArgAlaVal 797
Dh 2278 TCCGACGACGTCGCGCTGACCGGCTGCGTGAATCCCAAGACTCCGTGACCTGCCATC 2337
Qy 798 GlyAla-----HisSerTrpValIleAspProAsnAspIleAsnArgLeuValPro 814
Dh 2338 GGTGCTCCGACCGGACCAACCGCTGATGTCTCAACGACTGCTGCAACCGATGCCG 2397
Qy 815 IleGlyIleValGlyIleuValIleGluSerProGlyIleIleAspArgTrpIleVal 834
Dh 2398 GCCCGGCGCACCGGCGATGTCATGTGACCGGCTGAGTGTGCGGCGCGTTACCTTGGG 2457
Qy 835 ProProProProGluLysSerProPhePheThrAspIleProSerTrpTyrProAlaAsn 854
Dh 2458 GATCCGCTGGCGACCGGATGAGCTTGTCCCGAT-----CCGTTGCC 2502
Qy 855 ThrPheProAspGlyAlaLysLeuTyrArgThrGlyAspLeuAlaArgTyrAlaSerAsp 874
Dh 2503 AGCGGCGCG--GGTGAAGCGCTGTACCGGAGTGGCCACCTGGCGGACGTTGGCGCGAT 2559
Qy 875 Gly-----SerIleValCysLeuGlyArgGluLeuSerGlnValIleArgGlyGlnArg 893
Dh 2560 GGGGACGCGCTGAGTATGTGGGGCGGCGGACCTTCCAGGTGAAGATCCGGGGCTACCG 2619
Qy 894 ValGluLeuGlyAlaIleGluThrHisLeuArgGlnGlnMetCProAspAspLeuThrIle 913
Dh 2620 ATGAATCGGGGCAATCGAATCGCGGCTGTGCGCATGAAGTGTGACAGGCGCGGTG 2679
Qy 914 ValValGluAlaThrLysArgSerGlnSerAlaAsnSerThrSerLeuIleAlaPheLeu 933
Dh 2680 GTGGTGATGCG-----CAGATGGCGCGGTGACGACGAGCTTGTGGCTTACTGG 2727
Qy 934 IleGlySerSerTyrPheGlyAsnArgProSerThrAspIleHisIleLeuAspIleAspAla 953
Dh 2728 GTGGCC-----CGCATGCTCGGTCGTCGCGGACCGGACGATG 2763

Qy 954 ThrLysAlaIleAsnIleLysLeuGlnGlnValLeuProArgHisSerIleProSerPhe 973
Dh 2764 CGCAGCGCTGTGGCCGACATCTGCGGCGACGCTTCCGGGCTACATGTGGCGGACATG 2823
Qy 974 TyrIleCysMetLeuGluLeuProArgThrAlaThrGlyLysIleAspArgAlaGlyLeu 993
Dh 2824 TGGGTGGCTGCACAGCGCTGCGCTGACCTGCATGTGCAATGTGCAAGGTGACCGCAAGCAT 2883
Qy 994 ArgIleMetGlyLysAspIleLeuAspLysGlnThrGlnIleAlaIleValGlnAla 1013
Dh 2883 ----- 2883
Qy 1014 ProAlaProIleProValPheAla-----AspThrAla 1024
Dh 2884 CCGGACCGGACCGGACCGGCTGACAGCGGTACAGGACCGGACCGGAAAGTGTTCAG 2943
Qy 1025 AlaLysLeuHisSerIleTrpValGlnSerLeuGlyIleAspProAlaThrValAsnVal 1044
Dh 2944 CAGCAATTGGCGGAGCTGTGAGCGAGGTGCTGGGCTGCGAG--CGGATCAGTCTG 2997
Qy 1045 GlyAlaThrPhePheGluLeuGlyIleAsnSerIleThrAlaIleLysMetVal--Asn 1063
Dh 2998 GCGATGACTTCTTCAAGCTGGGTGGGCACTCTCTGCTGTGTGACAGTGTGGCGCT 3057
Qy 1064 MetAlaArgSerValGlyMetAspLeuLysValSerAsnIleTyrGlnHisProThrLeu 1083
Dh 3058 GTGGCGCGGACATGGGCAATCGAAGTCAGCTCGATCGTGTTCGACGACCGGACCTTG 3117
Qy 1084 AlaGlyLysSer-----AlaValValLysGly-----AspPro 1094
Dh 3118 GAGCGCTTCAGCGAGCGCTGCGAGGTGCAAGGGGCGGCGCTGATTCAGAGACGAG 3177
Qy 1095 LeuSerTyrThrLeuIle-Pro-----LysSerThr----- 1104
Dh 3178 TTGGCTAAATCTTGGCGCGCTTGGAAACGCTTACTGACAGAGAGATCGACAGTTGACC 3237
Qy 1104 ----- 1104
Dh 3238 CAGTAGCGTCTGCGGCGCGGTATGACCGGCGCGGCTGTCACCTTACATACACCCAG 3297
Qy 1105 -----HisGlu----- 1106
Dh 3298 AGCGGACCGGCTCGGCTCTTTCATTGTTGCGACAGATCATGAGCTGTGCGGCGCTG 3357
Qy 1106 ----- 1106
Dh 3358 GCACGTTCCGACGCAAAAGCCGCTGCTGTGAGAGATGTTCAAGTCAAGCATTTCT 3417
Qy 1106 ----- 1106
Dh 3418 CGATTCGAGATCACTGTGCTCCGGAGCGCAAGGCCCTGGCGGCTTGTCTCAAGCA 3477
Qy 1107 -----GlyProVal 1109
Dh 3478 GACAGGTGTCAACTTACGCGGCTGACCGGCACTTTCGCGGACCGGCGGACCGGAC 3537
Qy 1109 IGlunSerTyrSerGlnIleArgLeuTrpPheLeuAspGlnLeuAspValGlySerIle 1129
Dh 3538 CCGGCTCTTCAAGCGCCAGAGCGGACAGTGTCTTCTGCAACTGACCCCGGCGGCGG 3597
Qy 1129 uTrpTyrLeuIleProTyrAlaValArgMetArgGlyProValAsnValAspAlaLeuArg 1149
Dh 3598 AGCCTAACATCGATCGGCTGCGGCTGACGCTGACAGGCGGCGGCTGGAATTCAGAGGCTTGGC 3657
Qy 1149 gATgAlaLeuAlaIleuGluGlnArgHisGlyIleuThrLeuArgThrPhe---GluAs 1168
Dh 3658 CGGTGCTCGGACGCGGTATTCAGCGGCAAGAGTGTGCGGACCAAGTGTGGACAAAGA 3717
Qy 1168 pGlnAspGlyValGlyValGlnIleValHisGlyLysLeuSerGlnGluMetLysValIle 1188
Dh 3718 CAGCGACGCGGTG--GTGCAATCATCCACCGGCAAGTGCCTGTGAGTTCCTCATCGA 3774

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QY 1188 eAerPLeuCySgLYSerAerPLeuAerProPheGluValLeuAerGlnGluIn----- 1205
DB 3775 GCGGCTCATGCGATGAGCGCGACCGACGCGCTTGCGGAGAGACGTGACGGGCTGCAT 3834
QY 1206 -ThrThrProPheAerLeuSerGluValAGLYTPArgAlaThrLeuLeuArgLeuG1 1225
DB 3835 CGCGAAGCGCGTTCATCTTGACACAGGGCGCGTTCGCGGTGACCACTGCTGCGCGCTTGG 3894
QY 1225 YGluAerAerPheAerLeuThrLeuValMetHisHisLeuSerAerGlyTPSerL1 1245
DB 3895 CGAAGACGACACGCTGCTGCTGCTGACGCGACCAATATGCGCTGACGCGCTGCTGAT 3954
QY 1245 eAerValLeuArgArgAerPLeuAerGlnLeuTySerAlaAlaLeuTyAerSerLys 1265
DB 3955 GCGGATCTTGATCAACGATTTGGTACAGTCTGACGAA-----CGCTGACCGACGG 4005
QY 1265 pProLeuSerAlaLeuThrProLeuProLLeuTySerAerPheAlaLysTPGlnL 1285
DB 4006 GCAGGACCGCAATCTGCGCGCGCTGCGGCAATACCGCACTATGCACTTGGCAGCG 4065
QY 1285 sAerP-----GlnPheLeuGlnGlnLysGlnLeuAerTyThrLysLysGlnLeuL 1303
DB 4066 CAATGATGATGAGCGGAGTGAAGCGCGCGACGCTGCTTACTGAAAGACACCTTCGCG 4125
QY 1303 sAerSerSerProAla---LysLLeProThrAerPheAlaArgProAlaLeuLeuSerG1 1322
DB 4126 CGGAGGACCAACCGGCTGCTGACGCTGCGCAATCGCTCCGCGCGGTGGCGCCACGCG 4185
QY 1322 YAerAlaGlyCySValHisValThrLLeaArgLysLysLysLysLysLysLysLysL 1342
DB 4186 GCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 4245
QY 1342 eCySValGlnHisAerThrSerPheValValLeuLeuAlaAlaPheArgAlaAlaHis 1362
DB 4246 GCGCAATGCCCGACGGGTGAACCTTGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 4305
QY 1362 sTyArgLysLeuThrAlaValGluAerAlaValLLeuGlyThrProLLeaAerAerAer 1382
DB 4306 GCACCGCTACAGCGCGCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4365
QY 1382 pProGluLeuGluAerLLeuLLeuGlyCySValHisValThrLLeaArgLysLysLys 1402
DB 4366 CAGTGAAGTGCAGAGGTTGATCGGTTCTTCGTCACACCGGATCTCAAGCGCGCAT 4425
QY 1402 eAerPHisLeaSerThrPheGlyThrLeuLeuLeuAerGlnValLysAlaThrThrAla 1422
DB 4426 CGGCTGCACAGCGCGCTTCATGATGCTGCAACAGTGCAGGAAACCGCTTGCAGCG 4485
QY 1422 aPheGluAerGluAerLLeuProPheGluArgValLLeuSerAlaLeuGlnProGlySer 1442
DB 4486 CGAGCGCGACACGAGCTTACCGTTCCAAACGCTGCTGAGGCGCTTCAACCG--GAGCG 4542
QY 1442 gAerLeuSerSerThrProLeuAlaGlnLeuLeuPhe-----AlaVal 1456
DB 4543 CACATGAGCGACAGTCCGCTGTTCCAGTGAATGTTCAACACCGGCGGAGGCTGCGAG 4602
QY 1456 HisSerGlnLysAerLeuGlyArgPheLysPheGlnGlnLysLysLysLysLysLys 1476
DB 4603 CGACGCGCATGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4651
QY 1476 oSerLysAlaLysThrArgPheAerMetGluPheHisLeuPheGlnGlnLysLysLys 1496
DB 4652 -GACACCGCGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4710
QY 1496 LysLysGlySerValAerPheAlaAerGluLeuPheLysMetGlyThrValGluAerVal 1516
DB 4711 GTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4770
QY 1516 LysValPhePheGluLysLeuArgAerGlnLysLysLysLysLysLysLysLysLys 1536
DB 4771 GCGGCACTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4830
QY 1536 eLeuProLeuThrAerGlyLysLysLysLysLysLysLysLysLysLysLysLysLys 1556

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DB 4831 GCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4890
QY 1556 sValAerTyThrProArgGluSerSerLeuAlaAerValPheGlnThrGlnValSerAla 1576
DB 4891 GATGCGCTTATCCACCAAGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4950
QY 1576 pProAerSerLeuAlaValAlaAerSerSerCySArgLeuThrTyThrGluLeuAerA 1596
DB 4951 GCGCGATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5010
QY 1596 gGlnSerAerPLeuAlaGlyLysLysLysLysLysLysLysLysLysLysLysLys 1616
DB 5011 CGAGGCGCAACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5070
QY 1616 LAlaValPheAlaProArgSerCySgGlnThrLysLysLysLysLysLysLysLys 1636
DB 5071 GGGTGTGGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5130
QY 1636 aAerLeuAlaTyThrLeuProLeuAerValArgSerProSerAlaArgVal----- 1652
DB 5131 AGGGGCGCTTACGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5190
QY 1653 -----GlnAerPLeuSerGlyLeuSerG1 1661
DB 5191 CGAGACAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5250
QY 1661 YProThrLysLys-----LeuLLeGlnHisAerThrAla----- 1672
DB 5251 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5310
QY 1673 -----ProProAerLLeuGlnValThrAerValGluPheValArgLys 1688
DB 5311 CGCAGAAAGCTTACCGCTTACGCTC----- 5335
QY 1688 pAlaLeuAerAerSerAerAlaAerGlyPheGluValLLeuHisAerSerThrLysP 1708
DB 5336 -----GATCGCGATCATCC 5349
QY 1708 oSerAlaThrSerLeuAlaTyThrValLeuTyThrThrSerGlySerThrLysArgProL 1728
DB 5350 C-----GCCATGTCATCTACCTGACCTGACCTGACCTGACCTGACCTGACCTGAC 5394
QY 1728 YAlaMetLLeuHisArgValLLeuLeuArgThrValThrSerGlyCysLys---ProAs 1747
DB 5395 GCTGACGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5454
QY 1747 nTyProSerGluThrArgMetAlaHisMetAlaThrLLeuAerPheAerGlyLysTy 1767
DB 5455 TATCGCGCGCGAGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5514
QY 1767 rGluLysTySerAlaLeuLeuPheGlyArgThrLeuValCySValAerTyMetThrTh 1787
DB 5515 GAGCTGTACCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5574
QY 1787 rLeuAerAlaArgAlaLeuLysAerValPhePheArgGlnHisValAerAlaLysSer 1807
DB 5575 CAAGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5634
QY 1807 sValThrSerSerGlnAerValProLeuArgValProArgArgLeuSerArgThrL 1827
DB 5635 GACACCGCTGAC----- 5647
QY 1827 uMetPhePhePheLeuValValThrPheSerThrAlaProAerAlaLeuAerAlaGln 1847
DB 5648 -----TGGCGATGCTGCTGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCG 5697
QY 1847 YLeuTyGlnGlyValGlnCyS----- 1854
DB 5698 GGTATACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5757
QY 1855 -----TyAerGlyTyGlyProThrGluAerGlyValMetSerThrLysTyPr 1871

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Db 5758 AGGGCATGTTGGAACTTACGAGCCGACCCAAACCATCTGTCGGGTATCGAGAA 5817
Qy 1871 oileapserThrcluserPheilleaenglyValProileglyArgalaleuamense 1891
Db 5818 GGTACCGACGACGCCAGGTGTGGTGGCAAGCCGATCGGC-----AATAC 5865
Qy 1891 rglValATyValValAAspProglugInleuValGlyTleGlyValMetGlyGlu 1911
Db 5866 CACTTCCAGCTCTCGACCCCGCAGTTTCGACGCGGTCCGCTGGCGCTGAGCGCCGAACT 5925
Qy 1911 uValValIThrGlyAAspGlyLeuValAArgGlyTyTyrSerAAspLys---AlaleuAspGluAs 1930
Db 5926 GTTCACTGGCGGCGATGCTGCGCGCGCTTACCTTAAGCGCCAGCGCTGACCGCCGA 5985
Qy 1930 natrPheVal-----HisIleThrValAsnAspGlnThrValValaTy 1945
Db 5986 GCGCTTCATCCCAACCCGACGCGCCAC-----GGCGCGCTGA 6024
Qy 1945 rArgThrGlyAAspArgValAArgTyTArgTleGlyAAspGlyLeuIleGluPhePheGlyAr 1965
Db 6025 TCCGACCGGACGCTGCTGCGCTACCCG---GACGATGCTGCTGAGATGAGGCGCG 6081
Qy 1965 gmetAAspThrGlyPheValIleAArgGlyAAspArgTleGlySerAlaGluIleGlyValAla 1985
Db 6082 CATCGACACCAAGTTGAAGATTCGCGGTTCGCGATCGAGTTGGCGGAGATCGAGCGCAG 6141
Qy 1985 aLeuLeuArgAAspSerSerValAArgAAspAlaAlaValIleuGlnGlnAsnGluAAspG 2005
Db 6142 CCGGACGGGCTTGGTGGGTGGGTGGCGGAAGTGGCGGTATC----- 6181
Qy 2005 naIAspGluIleuGlyPheValValAlaAAspHisAAspHisSerGluAAsnAspLysG 2025
Db 6181 ----- 6181
Qy 2025 yGlnSerAlaAsnGlnValGluGlyTTrpGlnAAspHisPheGluSerGlyMetTyTyrSerAs 2045
Db 6182 -----GACGTGACGGG----- 6193
Qy 2045 pIleGlyGluIleAAspProserThrIleGlySerAAspPheGlyTTrpThrSerMetTy 2065
Db 6194 -----CCGCTGGCGACGACCTGCGGATATTCGCGCTGA 6231
Qy 2065 rAAspGlySerGlnIleAAspPheAAspGluMetHisGluTTrpLeuGlyGluThrThrArgTh 2085
Db 6232 CGATGCCAGCGCTGCTGACGCGTGA----- 6256
Qy 2085 rLeuHisAAspAAsnAArgSerLeuGlyAAsnValIleuGluIleGlyThrGlySerGlyMetI 2105
Db 6256 ----- 6256
Qy 2105 eLeuPheAAsnLeuAAspSerAArgLeuGluSerTyTValGlyLeuGluPProserAArgSerAl 2125
Db 6256 ----- 6256
Qy 2125 aaIAlaAAspValAAsnLysAlaThrGluSerIleProSerLeuAlaGlyLysAlaLysVa 2145
Db 6256 ----- 6256
Qy 2145 lGlnValGlyThrAlaThrAAspIleGlyGlnValAAspAAspLeuHisProAAspLeuValVa 2165
Db 6256 ----- 6256
Qy 2165 lLeuAAsnSerValIleGlnITyTyrPheProSerSerGlyTyTyrLeuAlaGluIleAlaAAspTh 2185
Db 6257 -----GCCAGGTTCCGGAAC 6273
Qy 2185 rLeuIleHisLeuProAAsnValGlnAArgTlePhePheGlyAAspValAArgSerGlnAlaTh 2205
Db 6274 CCTG----- 6277
Qy 2205 rAAspGlnHisPheLeuAlaAlaAArgAlaIleHisThrLeuGlyLysAAsnAlaThrLysAs 2225
Db 6277 ----- 6277

Qy 2225 pAAspValAArgGlnLysMetAlaGluLeuGluAAspMetGluGluLeuLeuValGluTr 2245
Db 6277 ----- 6277
Qy 2245 oAlaPhePheThrSerLeuLysAAspAArgPheProGlyLeuValGlnHisValGluIleLe 2265
Db 6277 ----- 6277
Qy 2265 uProLysAAsnMetGluAlaValAAsnGluLeuSerAlaTyTArgTyTAlaAlaValAlaHis 2285
Db 6278 -----CGCTGGCATCGAAGGCCA 6297
Qy 2285 eValAArgGlySerLeuGlyAAspGluLeuValLeuProValGluLysAAspAAspTrpLeAs 2305
Db 6298 CCGA----- 6301
Qy 2305 pPheGlnAlaAAsnGlnLeuAAsnGlnLysSerLeuGlyAAspLeuLeuLysSerSerAAspAl 2325
Db 6302 -----TTGAAGTCG----- 6310
Qy 2325 aaAlaIleMetAlaValSerLysIleProPheGluIleThrAlaPheGluAArgGlnValVa 2345
Db 6310 ----- 6310
Qy 2345 lAlaSerLeuAAsnSerAAsnIleAAspGluTTrpGlnLeuSerThrIleAArgSerSerAlaG 2365
Db 6310 ----- 6310
Qy 2365 uGlyAAspSerSerLeuSerValProAAspIlePheAArgIleAlaGlyGluAlaGlyPheAr 2385
Db 6310 ----- 6310
Qy 2385 gValGluValSerSerAlaAArgGlnITrPserGlnAAsnGlyAlaLeuAAspAlaValPheHis 2405
Db 6310 ----- 6310
Qy 2405 sHisCysCysSerGlnGlyAArgThrLeuValAAsnPheProThrAAspHisIleLeuAArgG 2425
Db 6310 ----- 6310
Qy 2425 ySerAAspLeuLeuThrAAsnAArgProLeuGlnAArgLeuGlnAAsnAArgAlaIleG 2445
Db 6310 ----- 6310
Qy 2445 uValAArgGluAArgLeuAAspSerLeuLeuProSerTyTyrMetIleProSerAAsnIleValVa 2465
Db 6311 -----ATGCCGAGCTCATGTGTCGACCCGACCTGGTGT 6345
Qy 2465 lLeuAAspLysMetProLeuAAsnAlaAAsnGlyLysValAAspAArgLysGluLeuSerAArgAr 2485
Db 6346 CATTCCACGCGATCCGCTGACCCCAACGCGCAAGCTCGAACGCGCGCTGCG----- 6400
Qy 2485 gAlaLysValValAProLysGlnGlnIThrAlaAlaAProLeuProIThrPheProIleSerG 2505
Db 6401 -GGCGCTGACCTTGGCGCGCCGCGCCGCTGACCAAGCGCCGACGCGCGCTGACGA 6459
Qy 2505 uValGluValIleLeuCysGluGluLysAlaThrGluValAAspGlyMetLysValAAspIleTh 2525
Db 6460 AGCGCTGGCGCGCATCTGGCGCGCATGTGCTGAAGTCT-----GGCGAGTTGGCTGAG 6513
Qy 2525 rAAspHisPhePheAAsnLeuGlyGlyHisSerLeuLeuAlaThrLysLeuIleSerAArgI 2545
Db 6514 CGACAGCTTCTCGAAGTGGGTGGCATTCCTTGTCTGCGCGTCCGCAATGATGTTGGCGCGCT 6573
Qy 2545 eAAspGlnAArgLeuLysValAArgIleThrValLysAAspValAAspAAspIleAAspAlaIleAl 2565
Db 6574 GCGCCAGCACTGCGCGTGGAGTGGCGCTGCGCTGCTTTCGAGGCGCCGACGACCTGCGC 6633
Qy 2565 aAAspLeuAlaSer-----ValIleAArgGlnGlyLeuGlnGlnProValSerAAspG 2584
Db 6634 GGGCTTCCCGACGCGGCTGGCGGCTGCGACGAGCGGCTGCGACCTGCGC----- 6682

QY 2584 yGInGlyInAspArgSerAlaHisMetAlaProArgThrGluThrGluAlaIleLeuCy 2604
 Db 6683 -----GCATCGCTGTGTGCTCCAGCGGAGAG----- 6709
 QY 2604 sAaRgLuPheAlaValLeuGlyPheGlnValGlyIleThrAspAsnPheAspLe 2624
 Db 6709 ----- 6709
 QY 2624 uGlyGlyHisSerLeuMetAlaThrIleValLeuAlaValArgIleGlyHisArgLeuAspTh 2644
 Db 6709 ----- 6709
 QY 2644 rThrValSerValIleAspValPheAsnHisProValLeuPheGlnLeuAlaIleAlaLe 2664
 Db 6709 ----- 6709
 QY 2664 uAaRAsnLeuValGlnSerIleThrAsnGluIleValGlyGlyArgGluMetAlaGluTy 2684
 Db 6709 ----- 6709
 QY 2684 rSerProPheGlnLeuLeuPheThrGluAspProGluGluPheMetAlaSerGluIleTy 2704
 Db 6710 -----CCCTGCGCTGTGTGTGCTCCAGCAAGCTCAATGGGTACTGTGG----- 6754
 QY 2704 sProGlnLeuGluLeuGlnGluIleIleGlnAspIleTyxProSerThrGlnMetGlnTy 2724
 Db 6755 -----CAACTGGAGCGCGAGCGCGCTTACAAATGCGCGCGCTTGCACCTTGCACCGCG 6810
 QY 2724 sAlaPheLeuPheAsnHisThrThrAlaArgProArgProValProPheTyIleAs 2744
 Db 6811 GGCGCTG----- 6817
 QY 2744 pHeProSerThrSerGluProAspAlaAlaGlyLeuIleValIleValIleValIleValI 2764
 Db 6818 -----GATGTGCGCGCGCTGTGTGCTCCAGCGCGCTTGTCAAGCGCTTGT 6855
 QY 2764 lAsnHisLeuAspIlePheArgThrValPheAlaGluAlaSerGlyLeuTyArgIleVal 2784
 Db 6856 GGCAAGCGCAAGAAAGCTGTGTGCTCCAGCTTGTGTGCTGCAAGCGCGCGCGCTGTG 6915
 QY 2784 lValLeu-----SerValLeu-----AspLeuProIleGlnValIleG 2797
 Db 6916 GATTCAAGCGCGCGAGCGAGGTGCTGCTGCGCGAGCGAGGTGCTGCTGCTGCTGCTG 6975
 QY 2797 uThrGluAspAsnIleAsnThrAlaThrAsnGluPheLeuAspIleValIleValIle 2817
 Db 6976 ATTGCAGCGCAAGCTC-----GAGCAATTGCGCGCTGTGAACC 7011
 QY 2817 oValArgLeu-----GlyHisProLeuIleArgPheThrIleIleLeu-----GlnThrIle 2835
 Db 7012 CTTCGACTGTGTGCAAGCGCGCTGATCCGCTGTGACTTGTGCGCTTGTGAGCGCGCG 7071
 QY 2835 rMetArgValIleMetArgIleSerHisAlaLeuTyArgPoleuSerLeuGlnHisVal 2855
 Db 7072 GCATGTCTGTGTATGAACCTGCAACATCATCAGCATGCGGTGTGCTGCTGCTGCTGCT 7131
 QY 2855 lValArgLeuLeuHisMetLeuTy-----AsnGlyArgSerLeuLeuProP 2871
 Db 7132 GGTCAACGAGCTGTGTGCTGTATCCAGCGCTATCGTATGCGAGCGCGCTGTGCTGCTG 7191
 QY 2871 oHisGlnPheSerArgTyMetGlnTyThrAlaAspGlyArgGluSerGlyHisGlyPh 2891
 Db 7192 CGGCGCTGCGCTGCAATACCGCACTACGCGCTTGTGAGCGCGCA----- 7237
 QY 2891 eTPArgAspValIleGlnAsnThr----- 2899
 Db 7238 -TGGCTGAGAGCGAGCGAGCGAGCGAGCTGCGCTACTGGAGAGCAAGTTGGCGG 7236
 QY 2900 -----PromethrIleLeuSerAspArgThrValValAspGlyAsnAspAlaThrCy 2917
 Db 7297 TGAACAGCGCGGTGTGTGAATTGTGCAACCTACCGCGCGCGAGCGCAAGCGCGCG 7356
 QY 2917 sLysAlaLeuHisLeuSerIleValAlaAsnIlePro-----SerGlnValLeuArgGlySe 2936

Db 7257 TGGCGGC-----CAATTGAGCTGTGCGCTGAGCGCGCGCTGTGCTGAGCACTCAGCGCGCA 7413
 QY 2936 rSerAsnIle-----IleThrGlnAlaThrValPheAsnAlaAlaCysAlaLeuValIle 2954
 Db 7414 GGCGCGAGCGCGAGCGCGCTTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7473
 QY 2954 uSerArgGluSerAspSerIleAspValValPheGlyArgIleValSerGlyArgGlnI 2974
 Db 7474 TCATCGTTACTTCACCTACGCCGAGC-----CCGCTGCG 7509
 QY 2974 lLeuProVal-----GlyTyArgAspIleValGlyProCysThrAs 2998
 Db 7510 CGTCCGCTGCGCGCAATGCGAGCGCGCGAGCAAGAGGGGTGTGCGCTTGTGCTGCTGCT 7569
 QY 2988 nAlaValProValArgAla-----HisIleGluSerSerAspTyArgAsnGlnLeuHis 3006
 Db 7570 TACCAGTGCACAAAGCGCGAGTTTCACTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 7626
 QY 3006 sAaPileGlnAspGlnTyThrLeuLeuSerLeuProHisGluThrIleGlyPheSerAspLe 3026
 Db 7627 CCAGTCCGCGCAAGCGCGCTGTGATGCCAGCGCGCTTCAAGCACTGCGCTTCAAGCTT 7686
 QY 3026 uTyxArgAsnCysThrAspTrpProGluAlaIleThrAsnPheSerCysCysIleThrTy 3046
 Db 7687 GGTGCGCGCTGTGAA-----CCGAGCGCATCTTCAACCAAAACCGCTGTCCAGGT 7740
 QY 3046 rHisAsnPheGluTyHisProGluSerGlnPheGluGlnArgValGluMetGlyVal 3066
 Db 7741 G--ATGTTCAACCAAGCG 7794
 QY 3066 lLeuThrIlePheValAsnIleGluMetAspGluProLeuTyArgPheAlaIleAlaG 3086
 Db 7795 GCAGATGAGCGCGTGTGCTGAGCGAGGTGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 7854
 QY 3086 yGluValGluProAspGlyAlaGlyLeuTyValThrValIleAlaIleAsnThrGlnLeuPh 3106
 Db 7855 CGCGAGCAAGCGCGAGCGCGAGTGAAGCGCGCTTACTTCC-----GCCAGCGAGCTGA 7908
 QY 3106 eGlyArgIleArgValGlu-----HisLeuLeuGluGluValIle 3119
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 QY 3119 rLys 3120
 Db 7969 TCGC 7972
 Db 7969 TCGC 7972
 RESULT 7
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 : Sequence 7449, Application US/10282122A
 : Publication No. US20040029129A1
 : GENERAL INFORMATION:
 : APPLICANT: Wang, Hiansu
 : APPLICANT: Zamudio, Carlos
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 : APPLICANT: Yamamoto, Robert
 : APPLICANT: Forsyth, R.
 : APPLICANT: Xu, H.
 : TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
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PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2001-02-16
Remainder of prior application data removed - See File Wrapper or PALM.
NUMBER OF SEQ. ID NOS: 74614
SOFTWARE: PatentIn version 3.1
SEQ. ID NO: 7449
LENGTH: 15450
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-7449

Alignment Scores:

Pred. No.:	2,75e-148	Length:	15450
Score:	1867.50	Matches:	846
Percent Similarity:	41.22%	Conservative:	521
Best Local Similarity:	25.51%	Mismatches:	1328
Query Match:	11.58%	Indels:	624
		Gaps:	135

US-09-482-788-2 (1-3129) x US-10-282-122A-7449 (1-15450)

QY 16 ThProAlaSerPheCysSerHISGLYAspSerProLeu---AenSerSerTyGluGln 34
DB 4573 ACCGCGTCGCACTTC-----CCGCTGGCCGGGCTTTCCACAGCCAG 4614
QY 35 LeuPheHisLeuTyGlyLeuAspSerSerArgIleGluAlaIleLysProCysThrPro 54
DB 4615 CTGCGTAATTG---TCCTTGATCTCGATTGGGGGACACTCTATCCGTTGTCCCG 4671
QY 55 PheGlnLeuAspMetIleAspCysAsnAlaLeuAspLysGlnSerAlaIleGlyHisAla 74
DB 4672 ATCCAG-----CAGGCGCATGCTTTCACAGT 4698
QY 75 ValTyAspValProThrAsp-----IleAsp 83
DB 4699 CTTCATGGAACGGAAGCGACTATGTACACCACTGGCCATGATCGCGCATTTGGAC 4758
QY 84 IleSerArgPheAlaLeuAlaTPrLysGluIleValAsnGlnThrProAlaLeuArgAla 103
DB 4759 CCGGATCGCTTCGCGGACGCTGGCAGGCCACCTCATGCCCATGAGATCGTCCG--- 4815
QY 104 PheAlaPheThrSerAspSerGlyLysThrSerGlnValIleLeuLysAspSerPhe--- 122
DB 4816 -----AGCGATTCTCTGGAAAGACGCGTGCCT 4845
QY 123 -----ValPhe-SerTrpMetCysTrpSerSerSerSerProAspG1 137
DB 4846 CAGCCGTCGACAGGTGATTCAGACGAGCCTGAGCTCGCGCTGGCCCGCCAGGC 4905
QY 137 uValValArgAsp-----GluAlaAlaAlaAlaAspGlyPr 150
DB 4906 AGTGATCGGACAGCGAGCGAGGCTGAGCGGACCGGTTTCACCGCGCAGGCGG 4965
QY 150 oArgCysAsnArgPheValLeuLeuGluAspMetGlnThrLysCysGlnLeuValTr 170
DB 4966 CCGTTGCGACGC---TTGGTGTGGTG---CCGCTGGCAATGGGAGTGACCTCATCTA 5021
QY 170 pThrPheSerHisAlaLeuValAspValThrPheGlnGlnArgValLeuSerArgValPh 190
DB 5022 TACTATACCAACATCTGTATGATGGCTGAGGACAGCCCACTGCTCGCGAGGTA 5081

QY 190 eAlaAlaTyLeuHisGluLys-----AspThrHisArgProGluThrPr 205
DB 5082 GCAGCGCTATCGGGGACAGAGGTACCGCTACCGTTGGCGCTTACCGGACATACCG 5141
QY 205 o-----GluSerSerAspAlaThrAspThrAspSerGlnSerValSerAlaSerMe 223
DB 5142 TTGGTTGACAGCGCGGATCGAAGCGACCGAGTCC----- 5178
QY 223 tSerCysGluAspAsnAlaValSerAlaThrHisPheTrpGlnThrHisLeuAsnAspLe 243
DB 5179 -----TTTGGCGGATCGCTGGCTCCCT 5204
QY 243 uAsn-----AlaSerValPheProHisLeuSerAspHis 254
DB 5205 GGAATGCGCACAGCTGGCGCGCGGAGGAGGAGGACAGCAGCTGGCAGAGTACGA 5264
QY 254 vLeuMetValProAsnProThrThrThrAlaGlnHisArgIleThrPheProLeuSerG1 274
DB 5265 TCTGGCGGAATCGAATCGGACGACCGCGCAA---CTGGCGTCTTCCCGCAAGGCTCA 5321
QY 274 pLysAlaLeuSerAspSerAlaIleCysArgThrAlaLeuSerIleLeuLeuSerArgTy 294
DB 5322 GAAGTCACCGCTAACAACCTTGGTG---CAAGCGCTGGCGCGCTCTCTGACAGCGCA 5378
QY 294 rThrHisSerAspArgLysAlaLeuPheGlyAlaValThr-----GluGlnSerLeuPr 311
DB 5379 CTGCGGCGAGAGACAGTATCGCTTGGCGCGCGCGGACCGGCGGAGCTGCGC 5438
QY 311 oPheAspLysHisTyLeuAlaAspArgLysThrGlnThrValAlaProLeuArgValHis 331
DB 5439 AGGCATCGAGCGCGAATC-----GATCTGTATTCATATACCTCGCGTATTCGCCGC 5492
QY 331 vCysGlnSerAspAsnLeuArgHisAspAspValMetAspAlaIleSerSerTyAspAspAr 351
DB 5493 GCGGACGCCACAGACAGCGCTCGGAGCTACCTGCAGGGATACAGCGCTCAACCTGCG 5552
QY 351 gLeuGlyHisLeuAlaProPheGlyLeuArgAspIle---ArgAsnThrGlyAspAsnG1 370
DB 5553 GCTGCGGAAACAGACATACGCTCTGTACGACATCCAGCGCTGGCGCGGATGCGCG 5612
QY 370 ySerAlaAlaCysAspPheGlnThrValLeuLeuValThrAspGlySerHisValAsnAs 390
DB 5613 CGAGCGCTGTTCGAT-----AGCATCTGGTGTTCGAAACACTTCCCGTGGCGCA 5663
QY 390 nGlyIleAsn-----GlyPheLeuGlnGlnIleThrGlnSerSerHisAspMetPr 407
DB 5664 GCGCTCGCGCAGAGCTCCCGCGATCTGAGATCTGCAGCTTCCAGCCAGACAGAGAG-- 5721
QY 407 oCysAsnAspArgAlaLeuLeuLeuHisCysGlnMetGluSerSerGlyAlaLeuLeuVa 427
DB 5722 ---ACCAACTACCCCTGACGCTGGATGTACCTCGGAGAGCGGCTGAGCTGACGTA 5777
QY 427 lAlaTyL-----TyAspHisAsnValIleAspSerLeuGlnThrThrArgLeuLeuG1 445
DB 5778 CGTCTATCGCGCGCGGATTTGAGACGAGCGGACATCGCCGAATGAGCCT--- 5829
QY 445 nGlnPheGlyHisLeuIleLysCysLeuGlnSerProLeuAspLeu-----SerSerMe 463
DB 5830 -----CATCTGTGATCTGCTGCAGCGGAGTGGCGGACACCCCTCAGGACAGCCT 5879
QY 463 tAlaGluValAsnLeuMetThrGluTyAspArgAlaGlu---IleGluSerTrpAspSe 482
DB 5880 GGGCGAGCTGGCGCTCTCTGCACCGCGGAGAACCCGAGAGGCGCTCGGATTTGGAGCG 5939
QY 482 rGlnProLeuGluValGlnAspThrLeuLeuHisHisGluMetLeuLysAlaValSerHis 502
DB 5940 A---CCGCTGAG---GCGCTGCGCGCGGCGCGGCTGCGGCGGCTTCCCGCA 5987
QY 502 s-----SerProThrTyAspThrAlaIleGlnAlaIleTrpAspGlyAspTrpThrTy 518
DB 5988 TCAGGACAGCGTGGCGCTGAGCGATCGCGCTGTATGCGGAGGAGATATCTACGTA 6047

QY 518 rsergltleuaspasnaValserArgleuAlaValhle1leuysertleuylleuAr 538
 Db 6048 TCGCGAACTGGATATGGCGCCGAGCGCTGCGCGCTGCGCGCGCGCGCGCTG-- 6105
 QY 538 galaglnAla1lelleProValTyrPhegluylserTyrVal1leAlaserMe 558
 Db 6106 -GCCGGGAAAGCGCTGGCGATCGCTGCGCGCGCTGCGCGCTGCGCGCTG 6164
 QY 558 tleuAlaValleuylserTyrAsna1Aphethrleu1leaspProAsnaProAl 578
 Db 6165 GCTGGGTATCTCAAGCGCGCGCGCGCGCGCTGCGCGCTGCGCGCTGCGCGA 6224
 QY 578 aArgThrAlaGlnValValThrGlnThrArgAlaThrValAla1leuthrserTyrleuH1 598
 Db 6225 GCGCCCTGGCTATATGTGGCGACAGCGCGCGCGCTGCTGATCTGC----- 6273
 QY 598 aArgGlnThrValGlnlyleuValGlyArgCysValValValAspaAsp1leu1leuG1 618
 Db 6274 -CAGAAACCTGCGAGCGCGCTGCGCGCGCGCGCGAGGTGAGCGCGCTGCGCTGA 6332
 QY 618 nserValser-----AlaserAspaPheSerSerleuthrlys-----SerGlnAs 634
 Db 6333 GACCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAC 6392
 QY 634 pleuAlaTyrVal1lePheThrserGlyserThrGlyAspProlysgly1leu1leu1 654
 Db 6393 GCTGGCTTATCTATATCGTCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCTG 6452
 QY 654 uhlAsArgAlaPheSerSerCysAla1leu1lyspheglYAlaserleu1lyleAsnaSerAs 674
 Db 6453 CCAGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 6512
 QY 674 pThrAlaAla1leu1leu1PheglYThrhlAsAlaPheglYAlaCysleu1leu1leu1 694
 Db 6513 CGACTCGCACTCACTGCTTCCCTCGATCGATTCGATGCGCGCGCGCGCGCGCTG 6572
 QY 694 rThrleu1leAsnaGlyGlyCysValCys1leProserAspaAspaArgMetAsnaSer-- 713
 Db 6573 ACCTGCTGCTGCGAGACCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6629
 QY 714 ----leProserPhe1leAsnaGlyTyrAsnaValAsnTyrMetMetAlaThrProserTyr 732
 Db 6630 ACATCTGCGCGATGAGGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCTG 6689
 QY 732 rMetGlyThrPheSerProglu-----AspValProglYleuAlaThrle 747
 Db 6690 TCTTTCAGCAACAGCGCGAGGTTCGCGCGCGCGCGCGCGCGCGCGCGCTG 6749
 QY 747 uValleuValGlyGlnGlnMetserSerValAsnaAla1leThrAlaProlysleuG1 767
 Db 6750 TATCTCTGCGCGAGACCTGCGAGCGCGCGCGCTGTAACCGAGCGCGCTGCGCTGA 6809
 QY 767 nleu----leuAsnaGlyTyrGlyGlnserGlnserSerSer1leCysPheAlaserAsnaMe 786
 Db 6810 AGCTGCTTCAAGCGCTCAAGCTCCACCGAGCGCGGTATCATCTCGCTGCGCTGCGCTG 6869
 QY 786 tSerThrGlnProAsnaSer-----MetGlyArgAlaValGlyAla1leH1serTyrPva 803
 Db 6870 TCGGAGCGCAAGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 6929
 QY 803 l1leAspProAsnaAsp1leAsnaArgleuValPro1leGlyAlaValGlyGlnleuVal11 823
 Db 6930 CATACTGAGACCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 6986
 QY 823 eglu1serProglY1le1leAspArgTyr1leValProProProProglY1leu1lyserProph 843
 Db 6987 CGCGCGCGAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7046
 QY 843 ePheThrAsp1leProserTyrTyrProAlaAsnThrPheProAspGlyAla1lyleu1ly 863
 Db 7047 CGTGGCGGATCGCTTCTCA-----GTTTGGCGCGAGCGCGCTGTA 7085
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Db 7086 TCGCACCGGAGACTGCGCGCTTATCGCGCTGACGCGGTCAAGGTATATCTCGCGCGCG 7145
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 Db 7146 CGATCAGCAATATMAATCCGTGCTTCCGATCGAGATCGGGAATCGAAGCAACT 7205
 QY 903 uArgGlnGlnMetProAspaPheuthr1leVal1leGlnAla1leThrlyAspSer--G1 922
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 QY 922 nserAlaAsnserThrSerleu1leAlaPheleu1leGlySerSerTyrPheglYAsnaR 942
 Db 7251 TGGCGTCGAGTCCGCTGCTGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 7290
 QY 942 gProserAspaAla1lelleuAspH1AspaAlaThrlyAla1leAsn1leu1lyleuG1 962
 Db 7291 ----CGTGAAGCT---ATGCGGGGTAGAGACTTTCGCGAGACTGCGACCTGCTGGC 7343
 QY 962 uGlnValleuProArgH1ser1leProserPheTyr1leCysMetleuGlu1leuProAr 982
 Db 7344 CGGACGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 7403
 QY 982 gThrAlaThrGlyLyv1leAspaArgArgleuArg1leu1leu1lyAsp1leu1leuAs 1002
 Db 7404 GAAAGCGCAACGCGAGCTGATGCAAGCGCTG----- 7437
 QY 1002 pLyvGlnThrGlnGlyAla1leValGlnGlnAlaProAlaPro1leProValPheAlaAs 1022
 Db 7438 -CCGAAGTGCAGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 7496
 QY 1022 pThrAlaAla1leu1leu1H1ser1leTyrPva1leGlnserleuGly1leAspProAlaThrVa 1042
 Db 7497 ACCTTGC-----GTGCGAGCATCTGAGAGCGCTGCTGCTGCTGCTGCTGCTG 7544
 QY 1042 laenValGlyAla1leThrPhePheglu1leu1lyGlyAsnser1leThrAla1leu1lyMetVa 1062
 Db 7545 CGCGCGGAGACACTTCTTCAACTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTG 7604
 QY 1062 laenMetAlaArg--SerValGlyMetAsp1leu1lyValserAsn1leTyrGlnH1sPr 1081
 Db 7605 CTCGCGCTGCGCGAGCAAGCTGAGCTGAGCTGACCTTCCGATCTGTTTCAGCGCGC 7664
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 Db 7665 GGTCTGCGAGACTTGCCTGCTTCCCTGAGTCCAGCGCGCGCGCGCGCTGCTGCT 7724
 QY 1097 rThrleu1leProlysSerThrH1sglnGlyProValGlnGlnserTyrserGlnGlyAr 1117
 Db 7725 GCAAAATATTCGCCGA---CTGCCAGAGCTGCTTTC-----TGCATCTCAGCAAG 7775
 QY 1117 gLeuTyrPheleuAspGlnleuAspValGlyserleuTyrTyrleu1leProTyrAlaVa 1137
 Db 7776 CATGTGCTTCTGGAACCTGAGCGCTGAACCGCGCGCTTATCATCTCCCGAGCGTACT 7835
 QY 1137 lArgMetArgGlyProValAsnValAspaAla1leu1laArgAla1leu1leu1Glu1 1157
 Db 7836 GCAAGTGCAGTCTGCTGAGCAAGCGCGGTGACAGCGCGCTTGCATTTGCTGCTGCT 7895
 QY 1157 nArgH1sglnThrleuArgThrThrPhegluAspGlnAspGlyValGlyValGln1leVa 1177
 Db 7896 GCGCGAGACACTTGGCGACCGCGCTTCCAGAGGTGAGAGGTGAGCGCGCGCGAGAT 7955
 QY 1177 lH1sglyLyvleu1leu1leu1leu1leu1leu1leu1leu1leu1leu1leu1 1196
 Db 7956 CTTGGCGAATATCCGTTGCGCATTTCTGCGAGATTCGCGCGCGCGCGCGAGCAAGCAAC 8015
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Dh	8076	GCTCGCGGTGGTGTGCTGCGGGCGGTGGCGGAGGAGCATGTGTTGGTCATCACCGCA	8135
Qy	1236	SHIStlelleSerAerpglyTPSerlleaBvalleuArgArbLeuBngInleuTy	1256
Dh	8136	CCAAATATCTGTCGCGACGGTGTGTGCATGCACAGTGTGTCGACAACTGCTCCAGCGCTA	8195
Qy	1256	rSerAlaAlaLeuLyAaBserLyAaBProLeuSerAlaLeuThrProLeuProilegI	1276
Dh	8196	TGCGCGCGCGCGCGCGCGCAACA-----CCAGCGTGGCGCCATTGACGGTGA	8246
Qy	1276	nTySerAaBpheaAluTyTrgInLyAaBpGlnPheIleGluIngu-----LyBgI	1294
Dh	8247	GTACGCGCGATATGCTGCTGCGCATCGCGCTGGCTGGACAGCGCGCGAGCGCGCGCA	8306
Qy	1294	nLeuBsnTyTrpLyvLyvGlnLeuLyAaBserSerProLa---LyvIleProThra	1313
Dh	8307	GCTGGATTAATCGCGGTGAGCGCGCTGGCGCGGACAGCGCGGTCTCTGTAACGCGCGCGA	8366
Qy	1313	pPheaAlaArProAlaLeuLeuSerGlyAaBpAlaGlyvAInHsValThrlleAaBpG	1333
Dh	8367	CGGAGTGGCT	8426
Qy	1333	yGlyLeuTyTrgInSerlleuArgAlaPheCyAaBngInHsAnthrThrSerPheaAla	1353
Dh	8427	GTCAATTATCGGAGAGAGCTGCTGGCTGGCGCGCGGAGGGGTGTCACCCCGTCAATCT	8486
Qy	1353	lLeuLeuAlaAlaPheaArgAlaAlaHsTyArgLeuThraAlaValaAlaAlI	1373
Dh	8487	TCTATTGGCGCTCGTTCCAGTGTCTGTTGAAACGCTATACCGGAGCGGACATGCGCGT	8546
Qy	1373	egLyThrProIleAlaAaArgAaAaArgProGlnLeuGlnAaPrlleIleGlyCyvPhea	1393
Dh	8547	CGGGGTACTTATCGCAACCGCAACCGCGCGAGGTCAAGCGCGCTGATCGGCTTCTGT	8606
Qy	1393	lAaAnthrGlnCyvAaEArgIleAeInleAaBpHsHsAaBpThrPheGlyThrlleuIleA	1413
Dh	8607	CAATATCCAGGTGCTGCTGGCTGGCAAGTGAATGCTGGCTGCTGGCGCATCTACTGG	8666
Qy	1413	ngInValLyvAlaThrThrThraAlaAlaPheGluAaBngInAaPrlleProPheGluArgva	1433
Dh	8667	CCGCGTGGCGAGGCGCGCTGGCGCGAGCGCAAGCGCACAGGATGTCGCTTCAGACAAAT	8726
Qy	1433	lValSerAlaLeuGlnProGlySerAaBpLeuSerSerThrProLeuAlaGlnLeuI	1453
Dh	8727	GGTGGATGCTTCGACGCC---GAACGAATCTCAGCACAGCCCGTGTTCACAGTAT	8783
Qy	1453	ePheaAlaValHsSerGlnLyvAaBpLeuGlyAaBpLeuPheGlnGlyLeuGlnSerVa	1473
Dh	8784	GTATATACCAACAGAC-----GGGAGCGCGAGAGATGCCCAAGTCAATGTTT	8831
Qy	1473	lProValProSerLyvAlaTyR-----ThraBpPheaBpMetGluPheHsIle	1489
Dh	8832	GCACATCGAAGATTGCTGCGTGGATGAGTGCAGCGCAAGTTGCATCTTGCCTCGCATAC	8892
Qy	1489	uPheGlnGluThraBpSerLeuLyvGlySerValAaBpAaBpAlaBpGluLeuPheLyvMe	1509
Dh	8892	CTGGGAAACCCCGGACCGGCTTGGGCGCGCGCTGACTTAACCGACCGACCTGTTTCAGGC	8951
Qy	1509	tGluThrAlaGlnAaBpAlaArgValAPhePheGluIleLeuArgAaBngLyLeuGlnSe	1529
Dh	8952	CGGACCGCTCCAGCGCGCGCGCGCGCGCATTTGGAGAACTGCTGCGCGCGCGCATCTGA	9011
Qy	1529	rSerAaBpThrProValSerIleLeuProLeuThraBpGlyIleValThrlleGluTyvle	1549
Dh	9012	CCCCAGGCGACCGTCACTGCTGCCATGCTGCATGCTCCAGAGAGCGTGGCCACTTCT	9071
Qy	1549	uAaBpAlaBpAaBpAlaLyvHsIleValAaBpTyRProAaBpSerSerleuAlaBpAlaPh	1569
Dh	9072	GGAAGGCTGAACCGCACTGCCCGCGAGTAAACCGCTGCACAGCGGCGCGACCGATTGTT	9131
Qy	1569	egInThrGlnValSerAlaTyRProAaBpSerleuAlaValAaBpSerSerCyvAaBpLe	1589
Dh	9132	CGAGAGAGAGGTTCAGCGCAGCGCGACCGCGCGCGCGCTTGCAGCGAGAACGCTT	9191

QY	1589	UTHTYrThrGluLeuAspArgLysSerAspLLeuAlaGlyTrpLeuArgArgSer	1609
Db	9192	GGACTACCGGAGGTGAACCGCGGGGCGAACCGCTGGGCGATGCCCTGATGAGCGCG	9251
QY	1609	rMetProAlaGluThrLeuValAlaValPheAlaProArgSerCysGluThrIleValAl	1629
Db	9252	GGTCGGTGGCGAAGCGCTGGTGGCGGCGCATGAGCGCTTCATGAGATGATGCTGGCG	9311
QY	1629	AspPheArgGlyValLeuIleuValAsnLeuAlaTrpLeuProLeuAspValArgSerProSe	1649
Db	9312	CTGTAGTGGCATCTCAAGGCGCGGCGGCGCTTACGTGGCGAGTGAACCGGAGTACCGCA	9371
QY	1649	rAlaArgValGlnAspLLeuSerGlyLeuSerGlyProThrIleValIleuIleGlyYH	1669
Db	9372	GGAGCGCGAAGCGCTACATGCTGGAGAGACAGCGCGCGTGCAGCGTGGCTGACGACGTGCA	9431
QY	1669	AspThrAlaProProAspLLeuGluValThrAsnValGluPheValArgIleArgAspAl	1689
Db	9432	CTGTAAAGCTCCCTGGCGCGAACGCGTGAAGCGGATGCACTGGACAAAC--GCCGATGC	9488
QY	1689	AlaLeuAsnAspSerAsnAlaAspGlyPheGluValIleGluIleAspSerThrIlePProSe	1709
Db	9489	CTGGCTGGAAACCAATGCCAGAAACAATCCGGAGATGCGA-----CTGAA	9533
QY	1709	rAlaThrSerLeuAlaTrpValLeuTrpThrSerGlySerThrGlyArgProGlyGlyVal	1729
Db	9534	CGGCGAAGATCTTGCCATGTCATCTACATCAACCTCCGCGCTCACACCGGAAACCCAAAGGTGC	9593
QY	1729	IleMetIleGluIleAspValIleIleArgThrValThrSerGlyCysIle-----ProAs	1747
Db	9594	CGCGAACCGCATTCGGCGCTGA--GCACCGCTGTGTGGATGGAGACGAGCGCTTACGCG	9651
QY	1747	nTryProSerGlyThrArgMetAlaHisMetAlaThrIleAlaPheAspGlyAlaSerTrp	1767
Db	9652	CTGGCGCGTCGGCGACACAGCTTGGCAAGAG--ACCGCGTCAAGTTGCACTGTCGGTCTG	9710
QY	1767	rGluIleTrpSerAlaLeuLeuPheGlyArgThrIleValCysValAspTrpMetThrTh	1787
Db	9711	GGAGTCTTCTGGCGCGGTATGATGAGTGGGACCGTTTGATGGTGGCCGCGCGGATGACCA	9770
QY	1787	rLeuAspAlaArgAlaLeuIleuAspValPhePheArgGluHisValAsnIleAlaSerHis	1807
Db	9771	TCCGAGACCCGCGCAAGCTGTGGCGCTGATCAACCCGAAAGGGGTGCACACCTGCACCT	9830
QY	1807	SvalThrSer-----SerSerGlnAspValProLeuArgValProAr	1821
Db	9831	CGTCCCGTCCATGCTGCGAGCGCTTCTGCGAGACGAAAGCGTCC-----	9873
QY	1821	gArgLeuSerArgThrIleuMetPhePheLeuValValThrAspSerThrAlaProAs	1841
Db	9874	----GTCTCTGCGACAGCTGAAAGCATGTTTGACAGCGCGAGGCGCTGTGGCGGA	9929
QY	1841	rAla-----LeuAspAlaGlnGlyLeuTrpGlnGlyValGlnC	1854
Db	9930	CGCCACAGACAGGTGTTCGCCAAGTGGCGCGACGCGCGCTC-----	9972
QY	1854	gTryAsnGlyTrpGlyProThrGluAsnGlyValMetSerThrIleTrpProIleAspSe	1874
Db	9973	-TATTAACCTGTATGGCCCGACGAGCGCGGCATCGACGTACCCACTGG-----AGCTG	10025S
QY	1874	rThrGluSerPheIleAsnGlyValProIleGlyArgAlaLeuAsnAspSerGlyValA	1894
Db	10026	CGTGGAGAGAGGCGAAGACCGGTGCGCATGCGCCGCGCATGCGAACCTGGCGTCTGA	10085S
QY	1894	rValValAspProGluGlnIleuValGlyIleGlyValMetGlyGluLeuValValTh	1914
Db	10086	CATCTCGATGGAGCATCTGGAGCGCGGTGGCGGCGGTGCTCGCGAGACTGACTGGCG	10145S
QY	1914	rGlyAspGlyLeuAlaArgGlyTrpSerAspLys---AlaLeuAspGluAsnArgPheVa	1933
Db	10146	CGGTGGGCGGCTGGCTGTGGCTTACCAACAGCGCTCCGGGCGTCACTGCCGAGGTTTCG	10205S

QY 1933 1-----HislethrvAlaAspArgInthrValIleAlaTyrArgThrGlyAspArgVal 1951
 Db 1206 GCGACGCGCGCTGTGGCTGGGAG-----CGAGATGACCGCACCGCGGACCTGGC 10256
 QY 1951 1AgtTyrArgTllegIYAspGlyLeuIlegIuPhePheGlyArgMetAspThrGlnPhe 1971
 Db 10257 GCGCTACCGC-----GCCATGGGGGTGATCGATACCGCGCGCGATTCACCAACGAGTGAA 10313
 QY 1971 sllleArgGlyAsnArgTllegIuSerAlaGluIlegIuAlaAlaLeuLeuArgAspSerse 1991
 Db 10314 GCTGGCGGCGCTGGCTGATCCAGCTGGCGGAGATGAGCGCGCTGTGTGAGCATCCGTG 10373
 QY 1991 rValArgAspAlaAlaValIleuGlnGlnAsnGlnAspGlnAlaProGluIleuG 2011
 Db 10374 GGTGGCGGAGCGCGCTGTGGCTGGCGGTGACAGCAG-----CAGTTGGTCCG 10421
 QY 2011 yPheValAlaAlaAspHisAspHisSerGluAsnAspArgGlyGlnSerAlaAsnGlnVal 2031
 Db 10422 CTACGTGTGTCTGGAGAGCGAGCGCGGCGGACTGGCGGAGAGCGCTGGCGCGACCTGGC 10481
 QY 2031 lgluGlyTyrGlnAspHisPheGluSerGlyMetTyr----- 2043
 Db 10482 GACAAAGCTGCGCGAATATCATGTGTGCGCGGACGTGGCTGGCGATGCGGCT 10541
 QY 2044 -SerAspIlegIYgluIleAspProSerThrIlegIYSerAspPheGlyTyrThrse 2063
 Db 10542 GAGTCCGAAAGCGCATGATCGCAAGCGCGCTGCCGACCGCAAGCTGTGGGGGCA 10601
 QY 2063 rmetTyrAspGlySerGlnIleAspPheAspGluMetHisGluTyrleuGlyGluThrth 2083
 Db 10602 GACGATGTGTGCGCGGAGATGAGAGCGAGCATGCGCGCGCTGTGGCGGACGT 10661
 QY 2083 rArgThrIleuHisAspAsnArgSerleuGlyAsnValleuGluIlegIYThrGlySerG 2103
 Db 10662 GCTGAAGCTGAGAGGTGGCGCGCGCACCGAACCTTTGCGCTGGT-----GCCGATTC 10718
 QY 2103 ymetIleuPheAsnLeuAspSerArgleuGluSerTyrValGlyleuGluProSerAr 2123
 Db 10719 CATCGTTTCATCCAGGTGTGATCGATCGCGCGC-----GCGGACATCCAG----- 10767
 QY 2123 gSerAlaAlaAlaPheValAsnIlyValatThrGluSerIleProSerleuAlaGlyLysAl 2143
 Db 10768 -----TTCACTCCGAAAGACCTGTTCACAAACAGACCGTCAAGGGGCTGGC 10814
 QY 2143 alysVal-----GlnValGlyThrAlaThrAspIlegIYGlnValAspAsnIleProAs 2162
 Db 10815 GCGAGTGTGCGCGGTAGGGGTGGCGGCAATGAGACAG----- 10854
 QY 2162 pLeuValIleuAsnSerValIlegIYrPheProSerSerGluTyrleuAlaGluI 2182
 Db 10855 -----GGGCTGT 10862
 QY 2182 eAlaAspThrleuIleHisleuProAsnValGlnArgIlePhePheGlyAspValArgse 2202
 Db 10863 GAGCGGAGAGCGGTGTGTGGCG-----TTCCAGCGGTGTGTTC----- 10905
 QY 2202 rGlnAlaThrAsnGluHisPheleuAlaAlaArgAlaIleHisThrleuGlyLysAsnAl 2222
 Db 10905 ----- 10905
 QY 2222 aThrIlyAspAspValArgGluIlyMetAlaGluLeuGluAspMetGluGluIleuLe 2242
 Db 10906 -----GACAGCGGATTCCTCCATCCGACAGCATCGAACCGATTCATTCCT 10949
 QY 2242 uValGluPro-----AlaPhePheThrSerleuIlyAspArgPheProGlyLeuVal 2259
 Db 10950 GTTGAAGCGCGCGAGCGCTGAAATGCGAAGGACACTGGAAGCGGCTTGGAGCGCTGGT 11009
 QY 2259 lgluHisValGluIleuProIlyAsnMetGluAlaValAsnGluLeuSerAlaTyrAr 2279
 Db 11010 TGAACATCACAGCATTTGGCTGTGGCTTC-----CATGAACCGGACCGAACCTG 11060
 QY 2279 gTyrAlaAlaValAlaHisValArgGlySerleuGlyAspGluLeuValleuProValG 2299

Db 11061 GCATGCCGAA-----CATGCCGAGCAAGCTGGGCGGTGGCTGTGGCGTCCGA 11114
 QY 2299 ulYAspAspTyrPleAspPheGlnAlaAsnGlnLeu-----AsnGluLysse 2315
 Db 11115 GCGCG-----GTGACCGGAGCAAGCGTGGAGTGTCTGTGGAGAGATTCGACGCCAG 11165
 QY 2315 rLeu-----GlyAspLeuLeuLysSer-----SerAspAlaAl 2326
 Db 11166 CTTGACCTGCGGAGCGGCGGCGGCTGTGGAGGCTGTGTGGATATGCGGACGCGG 11225
 QY 2326 aIleMetAlaValSerIlyIleProPheGluIleThrAlaPheGluArgGlnValAl 2346
 Db 11226 C-----CAGGCTGTGTGTGTGT 11243
 QY 2346 aSerLeuAsnSerAsnIleAsp-----GluTyrGlnLeu-----Se 2358
 Db 11244 GATCCACCATCTGGTGTGACGCGGCGGTCTGTGGCGGATTCGTGGAGATTTGCAAG 11303
 QY 2358 rThrIleArgSerSerAlaGluGlyAspSerSerLeuSerValProAspIlePheArgI 2378
 Db 11304 GCGTTACACAGACAGCTCCGTGGAGAGCTCG-----CGGCT 11342
 QY 2378 eAlaGlyGluAlaGlyPheArgValGluValSerSerAlaArgGlnTyrSerGlnAsnG 2398
 Db 11343 GCGTGGC-----AGACCAAGCGGCTTGAAGCGCTGGGCG----- 11376
 QY 2398 yAlaLeuAspAlaValaPheHisIleValCysCysSerGlnIlyArgThrleuValAsnPhePr 2418
 Db 11377 -----GGCCGA----- 11382
 QY 2418 oThrAspHisIleuAsnArgIlySer-----AspLe 2428
 Db 11383 -GTAGCGAGCATGCGCGGTGTGTGTGATGATGAAGCGCAATTCAGATTGTGGCGCGAGCT 11441
 QY 2428 uLeuThrAsnArgProLeu-----GlnArgleuGlnAsnArgAr 2441
 Db 11442 GCTGAAGAGCGCGCGCGGCGGAGCTCCGTGGAGCATCCGCAAGCGGCTGTGAGCAGCG 11501
 QY 2441 glleAlaIleGluValArgGluArgleu--ArgSerleuLeuProSerTyrmetIlePr 2460
 Db 11502 TTTCGCTACCTCCGTGCGAGATGCGCTTCGACCGGAGCTTACCGAACGCG----- 11550
 QY 2460 oSerAsnIleValValleuAspIlyMetProLeuAsnAlaAsnGlyLysValAspArgLy 2480
 Db 11551 -----TTGCTGAAGCGAGCGCGGCGGAGCTTACCGAACCGGATTCAGATCT 11597
 QY 2480 sGluLeuSerArgArgAlaLysValValProLysGlnGlnThrAlaAlaProLeuProth 2500
 Db 11598 TCGCTGACCGCGCGCTGGCGGAGTGTCTGCCGTGGAGCGGCGCTCT----- 11646
 QY 2500 rPheProIleSerGluValGluValIleLeuCySGluGluAlaThrGluValPheGlyMe 2520
 Db 11647 -----TCAG 11651
 QY 2520 tLysValAspIleThrAspHisPhePheAsnLeuGlyGlyHisSerleuLeuAlaThrly 2540
 Db 11652 CTTGTACACCTGAGAGCGAT-----GGCGGAGAGAGCTGTTCGCGCATAT 11699
 QY 2540 sLeuIleSerArg-----IleAspGlnArgleuLysValArgIleThrVally 2556
 Db 11700 CGACCTGATCGCACCGGTGGGTTCACACAGATTTCCTCCGCTGGCGCTGAGC----- 11754
 QY 2556 sAspValPheAspHisPheProValPheAlaAspLeuAlaSerValIleArgGlnGlyLeuG 2576
 Db 11755 -----CCGCTC-----GCGGATCTTGGCGAGTCTCCCTGAGCGATCAAGGA 11795
 QY 2576 yLeuGlnGlnProValSerAsp--GlyGlnGlyGlnAspArgSerAlaHisMetAlaPr 2595
 Db 11796 ACAATTGCGGCAATTCGACAAAGGCGCTGGGTATGCTGTGGCTATCTGCGCTGG 11855
 QY 2595 cArgThrGluThrGluAlaIleLeuCySAspArgIlyPheAlaLysValleuGlyPhe----- 2613

Db	11856	A-----	-----GAGGAAAGTCCCGGGTCTGGCGGGCTTGGC	11888
Qy	2614	-GlnValGlyLeuThrAspAsnPhePheAspLeuGlyGlyHisSerLeuMetAlaThrIty	2633	
Db	11889	GCAGCGCGCGGATCTTTCAATTAC-----CTGGGCGAGTTGCGAGCTGATTCAGCA	11942	CGA
Qy	2633	AlaLeuAlaVal-----ArgIleGlyHisArgLeuAspPheThrValIse	2647	
Db	11993	GATGGCTCTGCTGGACCCGCTGGCGAAAGCGGGGGCGAAGATGACCCC-----	11994	
Qy	2647	rValIlyAspValPheAspHisProValLeuPheGlnLeuAlaIleAlaLeuAspValIle	2667	
Db	11995	-----GGGCGTCCGCTGGACAACTG	12014	CTG
Qy	2667	uValGlnSerIyThrAsnGluIleValGlyGlyArgGluMetAlaGluItySerProh	2687	
Db	12015	GCTG---AGTCTCAATGGCCGGGGTTTCCAGCGGTGAATGATGACACTGGAGCTTTCAG	12071	CTG
Qy	2687	eglLeuLeuPheThrGluAspProGluGluPheMetAlaSerGluIleIyAspProIine	2707	
Db	12072	CTCCGAGATGTTCCGCGAGACCGAGTGGCTGGCTGGCCGATGACTATGTGGCTGAGCT	12131	CTG
Qy	2707	u-----	2707	
Db	12132	GACGGCGGTGTCGACTTCTGCTCGATTGGCCACGCGCATGGGCGACGCGCTTCGATTT	12191	CTG
Qy	2708	-----GluLeuGlnGluI	2712	
Db	12192	CCCGCTGGCGGGTGTGACGACGCGCGCTGTGATGCCCTGCGATCGCGTCCGATGAGAG--	12249	CTG
Qy	2712	eIleGlnAspIleItyrProSerThrGlnMetGlnIyAlaPheLeuPheAspHisThrth	2732	
Db	12250	-GTCCAGGACACTTATCGCTGTACCCATGCGACGACGAGGAGTCTGTC--CAATCGCT	12305	CTG
Qy	2732	rAlaArpProArpProPheValProPheItyrIleAspPheProSerThSerGluProAs	2752	
Db	12306	G-----TACGACGACGATCGAGGAGTATCATCATCATGATGGCTGTGA	12350	CTG
Qy	2752	pAlaAlaGlyLeu-----IleIyAlaCysGluSerIyValAsnHisIle	2767	
Db	12351	TGTGTCCGCGCTTCGATCTCCGCGCGCTTCGCGGACCTGGACATGCGCCCTGGACCGGCA	12410	CTG
Qy	2767	uAspIlePheArgThrValPheAlaGluAlaSerGlyGluLeuItyrGlnValValIeuse	2787	
Db	12411	CGCGATCTCTGGCGAGTGGTTCGCG--TGGCAGGGGAGACTGCACGAG-----	12456	
Qy	2787	rCysLeuAspLeuProIleGlnValIleGlu-----ThrGluAs	2800	
Db	12457	-----CCCTTCGAGATCGTCTATCGACAGCGCCAGTGGCTGCTGGCGGAA	12503	CTG
Qy	2800	pAsnIleAsnThrAlaThrAsnGlu-----PheLeuAspGluPheAlaIyAspGluBr	2817	
Db	12504	GACCTGACCGACGGCGGAGATCGGAGCGCGCGCTGCGCGCTGGCTGGCGGCGAGCG	12563	CTG
Qy	2817	oValArg-----LeuGlyHisProLeuIleArgPheThrIleIleIyAspGlnth	2833	
Db	12564	CGAACCGCGGTTTGAATCGACGCGCTGGCGCACTGTTGCGGCTGTTGGTGAAGCTCC	12623	CTG
Qy	2833	rIyAs---SerMetArgValIleMetArgIleSerHisAlaLeuItyrAspGluIyAspSerIe	2852	
Db	12624	CGAAGGTGAGCATCACTGATCTTACACCCATCATCATCATCTCTGGACGAGTGAAGCA	12683	CTG
Qy	2852	uGlnHisValAlaArgIyLeuHisMetLeuItyrAsnGluIyArgSerIyLeuProhI	2872	
Db	12684	TGCCAGATGCTGTACGCGAGCGTGTGAGTCTTACCGCGAGCGCTCG-----CCGGA	12734	CTG
Qy	2872	sgIlnPhe-----SerArgItyrMetGlnItyrThrAla-----AspGluArgGlu	2886	
Db	12735	GCAGTCTCGGAGTGGCGGCTTATACGACTACATGCGCTGGTTGACGCGACGACGCGCG	12794	CTG
Qy	2886	uSerGluHisIyIyPheTrpArgAspValIleGlnAsnThrProMetThrIleIyAspSerAs	2906	
Db	12795	AGCTACCGAGCATTTGGCGCGAG-----CAGATCGCGCTTCTGGACGA	12839	CTG

QY	2906	pAsPThc---ValValAspGly-----AaaAspAlaThrCyluYaaI	2919
Dd	12840	GCCGACCGCATTTGGTCTTCAGGCACATGGCTCACGCCGGAATGCAChTCGGCCAAAGCGGTCCG	12899
QY	2919	aLeuHieLseuSerLySaeIleValAanIleProserGlnValLeuArg-----GlySerSe	2937
Dd	12900	AGAACCACTCGTGAGGTGGTAGCCGAACCGGTACTCGCGCGGCTTCGGGATTTCGGCCCGCG	12959
QY	2937	rAmIIlelleThrGlnAlaThrValPheasnIalAaCYsAlaLeuValLeuSerArgGI	2957
Dd	12960	CCACCAAGTCACTTCATATACCCTTGCCAGGCGGGCTGGCGGCTGCTCTCCAACGCTTA	13019
QY	2957	uSerAspSerLySaeIleValPheGlyArgIleValIsargIlyArgGlnGly---LeuPr	2976
Dd	13020	TACCGACAACAACACCGGTGTCTTCGGCGCCACCGTCTCGGCGCGCCCTCCGAGATCTGCC	13079
QY	2976	O---ValGluTyrgInaAspIleValGlyProCyvrhAsnAlaAvalProValArgAlaHI	2995
Dd	13080	GGGTGTGAGAACAG-----GTCCGGGTGTGTTCAATCAATACCTTCGCGTGGTGGTAAAC	13133
QY	2995	sIlE---GluSerSerAspTyrrasnGlnLeuLeuHISaapIleGlnAspGlnTyrlLeuE	3014
Dd	13134	GCTGGCTCCACAGATGACCTTCGACGAACTGCTGCAAGGCGCTGCAACGGCAACACTGGC	13193
QY	3014	uSerLeuProHISgluThrIleGlyPheSerAspLeuLyArgAasnCyethrAspTrpr	3034
Dd	13194	GTTCCGGGGAACAGGAGCACACGCGCTCTGTTCCAGCTGCAGCGC-----TGS--	13239
QY	3034	oGluAlaIleThrAnPheSerCyScySileThrTYrHisasn-----PheGluTy	3051
Dd	13240	-----GCGGGGTTCGGCGCGGACAGCGCGTTCGACAACTGTTGTGTTCGAAA	13289
QY	3051	rHisProGluSerGlnPheGluGlnIlnArgValGluMetGlyValLeuThrLyPheVa	3071
Dd	13290	CTACCCGATGGACGAGGTGCTCGAAGCGTCTCCGCTGAGAGGGrv-----CGTTTCGG	13343
QY	3071	IaSnIleGluMetAspGluProLeu---TYrAspLeuAlaIleAla	3085
Dd	13344	TGCCGTAGCGATGCACGAGCAGAACATATCCGCTGCGCTGGC	13389
RESULT 8			
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# Publication No. US20040029129A1			
# GENERAL INFORMATION:			
# APPLICANT: Wang, Liangsu			
# APPLICANT: Zamudio, Carlos			
# APPLICANT: Malone, Cheryl			
# APPLICANT: Haselbeck, Robert			
# APPLICANT: Ohlsen, Karl			
# APPLICANT: Zvekind, Judith			
# APPLICANT: Wall, Daniel			
# APPLICANT: Trawick, John			
# APPLICANT: Carr, Grant			
# APPLICANT: Yamamoto, Robert			
# APPLICANT: Forsyth, R.			
# APPLICANT: Xu, H.			
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# FILE REFERENCE: EPIITA.034A			
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Dh 13579 CCGGAGCAGACT---GTGGACGTGCTGTTTCCGATCCGCGAGGGCGGTCCGCCATC 13635
Qy 559 LeuAlaValLeuYsSerGlyAsnAlaPheThrLeuIleAspProAsnAspProProAla 578
Dh 13636 CTGGCGGTGCTCAAGACGGGGGGGGCTTACTGCTCCCATTCACCCGTGCGCCCGCAGACC 13695
Qy 579 ArgThrAlaGlnValValThrGlnThrArgAlaThrValAlaLeuThrSerLeuLeuHis 598
Dh 13696 CGCGTCAGATTCAATGCTCGCGCAGACCGCAACCGATCCGCGCGTCACACCC--- 13746
Qy 599 ArgGlnThrValGlnYsLeuValGlyArgCysValVal-----ValAsnAspGlu 615
Dh 13747 GCGGAGGTGGCGGCGCGCTGCGCGCGCGCGCTGACCGCTGTCAGAGTCGACGATCCG 13806
Qy 616 LeuLeuGlnSerValSerAlaSerAspAspPheSerSerLeuThrYsSerGlnAspLeu 635
Dh 13807 GGCATCATACCTCG-----CCGACACACCGCGCTGCCCGTCCCGACCGGACGACATC 13860
Qy 636 AlaTyrValIlePheThrSerGlySerThrGlyAsnProIyGlyIleMetIleGlnHis 655
Dh 13861 GCGTACCTGATCTACACTCCGCGCACACCGGTGCGCCCAAGCGCTTGGCGTCACTCAC 13920
Qy 656 ArgAlaPheSerSerCysAlaLeuYsPheGlyAlaSerLeu-----GlyIleAsn 672
Dh 13921 CACACACGTGACCCAGCTGCTGCTGCTGACGCGCGCGCTGCCCGCGCGGGGTGTGG 13980
Qy 673 SerAspThrArgAlaLeuGlnPheGlyThrHisAlaPheGlyAlaCysLeuLeuGlnIle 692
Dh 13981 TCCGATATCTACATCGCTG-----GCTTTCACGCTGCTGCTGCGTGGAGATC 14025
Qy 693 MetThrThrLeuIleAsnGlyGlyCysValCysIleProSerAspAspArgMetAsn 712
Dh 14026 TTCGGCGCGCTGCGCGCGCGGACGCGTGGTGTG----- 14061
Qy 713 SerIleProSerPheIleAsnArg-----Tyr 721
Dh 14062 ---ATGCGCCAGCGCGCGCGCTGACCGCACGACCTGCACGACGCGCTGATCGCCGG 14118
Qy 722 AsnValAsnThrMetMetAlaThrProSerTyrMetGlyThrPheSerProGluAspVal 741
Dh 14119 CACGTACCGTGCACCCAAACCCCGTCCCGCTGCGCATGCTCTCCCGCAGGGGTG 14178
Qy 742 ProGlyLeuAlaThrLeuValIleGlyGlnIleMetSerSerSerValAsnAlaIle 761
Dh 14179 GAGTCGCTG---TCGCTGTGCTGCGCGGAGGCGCTGCCCGCGAGGTGTGACCAA 14235
Qy 762 TrpAlaProIyLeuGlnLeuLeuAsnGlyTyrGlyGlnSerGlyIleAsnSerIleCys 781
Dh 14236 TGGGCGCGCGGACGCGGTGATGCTACGCGCTACGCGCCGACCGAA---ACCAGCATGTGC 14292
Qy 782 PheAlaSerAsnMetSerThrGluProAsnAsnMetGlyArgAlaVal----- 797
Dh 14293 GTGAGC-----ATCAGCGCGCCCGCTGACCGCGGGATGTGGCATACCGCCGATCGGG 14343
Qy 798 -----GlyAlaHisSerTyrIleValIleAspProAsnAspIleAsnArgLeuVal 813
Dh 14344 TCGCGCGTGCATGGGCGCGCGCTGTCTGCTGCTGAC-----GAATCGCTGCGCGCGGTG 14397
Qy 814 ProIleGlyAlaValIleGlyLeuValIleGlnSerProGlyIleAlaAspAspTyrIle 833
Dh 14398 CCGCGCGCGTGTGGCGGAACTTACGCTGCGCGGATCCGCTGCGCGGACGAGGTATCTC 14457
Qy 834 ValProProProGluYsSerProPhePheThrAspIleProSerTyrIleProAla 853
Dh 14458 GCGCGCGCGCTC---CTTGACCGCGCGCGCG---TTCTGCTGCGTCCCGTTCGCGCGCGCCACAGC 14514
Qy 854 AsnThrPheProAspGlyAlaValYsLeuTyrArgThrGlyAspLeuAlaArgTyrAlaSer 873
Dh 14515 -----GCGCGGATGTATCGACCGCGGACCTGTGGCGGTGCGGTGCCGCC 14566
Qy 874 AspGlySerIleValCysLeuGlyArgIleAspSerGlnValYsIleArgGlyGlnArg 893
Dh 14557 GACGGGAGCTGTGACTACTTGGCGCGGCGCGACGACGAGCATGCTACGCGGCTTACCGC 14616

Qy 894 ValGlnLeuGlyAlaIleGlnThrHisLeuArgGlnIleMetProAspAspLeuThrIle 913
Dh 14617 ATCGAGCTGGCGGATATCCAGCGCGCGCTGCGCGCTGACCGGGGTGAGCAGCGCGCTC 14676
Qy 914 ValValGlnAlaThrIyAspSerGlnSerAlaAsnSerThrSerLeuIleAlaPheLeu 933
Dh 14677 GTGCTC-----GCCCGGAGGACAAATCCCGGGGACAAAGCGGTGTGGCTGCTACATC 14727
Qy 934 IleGlySerSerTyrPheGlyAsnArgProSerAspAlaHisIleLeuAspHisAspAla 953
Dh 14728 ACCGGCACCGCC-----GACCGCGCGGAGCGC----- 14754
Qy 954 ThrYsAlaIleAsnIleYsLeuGlnGlnValLeuProArgHisSerIleProSerPhe 973
Dh 14755 -----CGCGCGCGCTGTGGCGAGCGGCTGCGCGCTGACATATGTCGCCCGCGCC 14802
Qy 974 TyrIleCysMetLeuGlnLeuProArgThrAlaThrGlyYsAlaIleAspArgAlaGlu 993
Dh 14803 GTCTGGGCTCGACCGCAATCCGTTGACCCCGCAAGAAACTCGACCGCGCGCGCTG 14862
Qy 994 ArgIleMetGlyYsAspIleLeuAspYsGlnThrGlnIyAlaIleValGlnIleAla 1013
Dh 14862 ----- 14862
Qy 1014 ProAlaProIleProValPheAla-----AspThrAla 1024
Dh 14863 -----CCGCGACCCGATCGCGCGCGCGGTGATGACCGCGCCCGCACAGACCCACCGAG 14916
Qy 1025 AlaYsLeuHisSerIleTyrValGlnSerLeuGlyYsIleAspProAlaThrValAsnVal 1044
Dh 14917 GAGATCTGCGCGGATCTACGCGCGGAGTGTGGGTGTGAG-----CGGCTGCGCGCTC 14970
Qy 1045 GlyAlaThrPhePheGlnLeuGlyYsAsnSerIleThrAlaIleYsMetValAsnMet 1064
Dh 14971 GAGACTCTCTTTCATCTGCGCGCGGAGACAGATCTGCGCATGCGCGCTGATCGCGCC 15030
Qy 1065 AlaArg---SerValGlyMetAspLeuYsValSerAsnIleTyrGlnHisProThrLeu 1083
Dh 15031 GTCAACCGCGCGCTGAACCGCGGACCTGCGCGACCGTGTTCAGAGCGCGCACCGTGC 15090
Qy 1084 AlaGlyYsSerAlaValValYsGlyAspProLeuSerTyrThrLeuIleProYsSer 1103
Dh 15091 GCGCGCTACCGCGCGGATC---GGGAGGCGCGAGC---GACTCGACCGCTGTGACG 15144
Qy 1104 ThrIleGlnIyPro-----ValGlnGlnSerTyrSerGlnIyArgLeuTyrPheLeu 1121
Dh 15145 GCGGTGAGCGCGCGCGGTGTGCGCGCTGCTGCGCGCAACCGCGCTGTGCTCTG 15204
Qy 1122 AspGlnLeuAspValGlySerLeuTyrIleProTyrAlaValArgMetArgIly 1141
Dh 15205 GATCAATTCAGAGGCGCGCTGACCGCGGTTTACATGAGCGCGCGCTGCGGTGACGCGC 15264
Qy 1142 ProValAsnValAspAlaLeuArgAlaLeuAlaIleGlnGlnAlaGlnThr 1161
Dh 15265 CCGCTGACACCGCGCGCTGCGCGCGCTGCGCGACCTGTGCGCGCGCGACGAGAGC 15324
Qy 1162 LeuArgThrThrPheGlnAspGlnAspGlyValGlyValGlnIleVal-----HisGlu 1179
Dh 15325 CTGGGACCTGTTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 15384
Qy 1180 YsLeuSerGlnIleMetYsValIleAspLeuCysGlySerAspLeuAspProPhe--- 1198
Dh 15385 CCGGCGGACTTGGGTGGAGGTCGTGTCAGCGCAGGCGGTGTCGGGAGCAACATGAGC 15444
Qy 1199 GluValLeuAsnGlnGlnGlnThrThrProPheAsnLeuSerSerGlnAlaGlyTyrArg 1218
Dh 15445 GAGCGCATCGCGCGCACCGCGCGCTACACCTTGCACCTTGCAGCCCGCAATCCGCTGCGC 15504
Qy 1219 AlaThrLeuAspArgLeuGlyGluAspAspHisIleLeuThrIleValMetHisIle 1238
Dh 15505 GCAAGCTTTTCTGCTTCACGACGACCGGACGATGTGTGTCGCGTGTGACACCATC 15564

QY	1239	ILSESRPGIYTPSRPILEAPVALLEUADYGRSPLEUENGLINLEUYRSEALA	1255
Db	15565	GCGCGGACGCGCATGTCATCAACCCCGGTGGTGTATCTCGGTGGCGGCTTAGCC--	15622
QY	1259	ALALEUYSAPSERILYASAPPROLEUSERALALEUTHRPROLEUPROILEGINYRSE	1278
Db	15622	-----CGGGGGTGGCGGGGACAGCCCGGGGCTGGAGCGCGGTGGACGATCACTC	15677
QY	1279	ASPPHEALALYSTIRGINLYSAPRGINPHEILEGLINGLU-----	1292
Db	15676	GACTACACGCGTGTGGACGCGCGCAATTCGGATGATCCACGATCCCGGACGCGCATC	15733
QY	1293	---LYEGLINLEUENINRYTRPLYLYLYGLINLEUYSAPSERSEPRQALALYS-----	1309
Db	15736	GCGCGCCAGCGCTGACCTTAGCGAGAGCGCGCTGGCC--GGCATGCCAGCGGCTGGCG	15799
QY	1310	ILEPROTHIRAPHEALATARGPROALALEULEUSERGLYASRALAGLYCYVALINISVAL	1329
Db	15793	TCGCGCCACCGAC-----CGGCCCTATCCGCTGTGGCCGACACAGCGGGGCGGACGGTGTG	15844
QY	1330	THRIILEAP-----GLYGLINLEUYRGLINSEIRLEUARGALAPHECYSAENGLIHISASN	1347
Db	15847	GAATCAGACTGGCGCGCGGAGCTGCACAGAGAAATCGGACATCGGACATGCGCGCGGACAAAC	15900
QY	1348	THIRSEIRPHEVALVALLEULEUALALAPHEARGALALAHISRYARAGLEUTHRALA	1367
Db	15907	GCCACCGAGCTTCAAGTAGATTCAGACGCGGCTTGACCGGTGCTGGCCAAAGCTTGCGGCC	15966
QY	1368	VALGLINAPRALVALILEGLYTHPROILEALAHENARGAHNARGPROGLINLEUGLNASP	1387
Db	15967	AATCCGATGCGGGGCGGGGCTTCCGATCCGGGGGGCGCGCCACCGCGGCGCTGAGAC	16022
QY	1388	ILEILEGLCYSPHEVALAENTHRGINCYSEIRTRGLEASNILLEAPRHSNISAPRTHR	1407
Db	16027	CTGGTCGGGTCTCTTCGTCACACACCTGATGCTGGGTGAGACGCGCGCGGAGATCCGACG	16088
QY	1408	PHEGLYTHREULILEANGINVALLYALATHRTHRTHRALALAPHEGLINANGULNASP	1427
Db	16087	TTCCACCGAGCTGCGCGCGCGGTCCGACCGCGAGCTTGAGGCTTTCAGACACAGAT	16144
QY	1428	ILEPROPHEGLIARGVALVALISERALEUENINPROGLYSEIRARGAPLEUSERSETHR	1447
Db	16147	GTGCGGCTTCAGAGCTGCTGTGGAGCGGCTCAACCG--ACCAGACCTCACCAATCAC	16202
QY	1448	PROLEUALAGINLEULE-----PHEALVALINISERGINLYSAPLEU	1462
Db	16204	CCGCTGGTGAAGGTAGTACGTGACCTGGACAGAACTTCCCGGGGACAGACCGGCGCGGCC	16266
QY	1463	GLYARGPHELYSPHEGINGLYLEUGINUSERVALPROVALPROSERLYALATYRTHR--	1481
Db	16264	GCGGGGCTGTCCCTCGCGGATGTGAAATACCGCCGATCCGCTGACACCCACACCGCG	16322
QY	1482	ARGPHEAPMETGLUPHEHISLEUPHEGLN-----GLUTHRAPSER	1495
Db	16324	CGGATGCACTGACCTTCTCCGTGGCGAAGCGCTGAGCGAGACGGCGGAAACCGGGCGGG	16388
QY	1496	LEULYSEIRSEVALAENPHEALAAPGLINLEUPHELYSEMETGLUTHRALVALISVAL	1515
Db	16384	ATCGCGCGGACAGTGGAAATTCGACACGAGCTGTTCACCGGACAGCATTCAGACGCTG	16444
QY	1516	VALARGVALPHEPHEGLIILELEUARGHANGILEUGINSEIRSEARGTHRPROVALSER	1535
Db	16444	ATCGCGGCGGCTGCGCGCGGTGCTGAGAGCGATGACCGCGGACCGGACAAATCGTGTTCG	16500
QY	1536	ILELEUPROLEUTHIRAPGLYILEVALTHIRLEULN-----LYSLEUASPVAL	1551
Db	16504	TCGGTGGACCTGCTCGAC-----GAGGCGGAGACAGCGCCGCTTGACACCC	16564
QY	1552	LEUENVALLYSHISVAL-----ASPTYRPROARGINUSERSEIRLEUALAASPVAL	1568
Db	16549	CTGGGCAACCGGGGCGGTGACCGGACCTCCGCGCGGTTCGATTCCTCCCAACACTT	16600
QY	1569	PHEGLINTHRGINVALSERALATYRPROHAPSERLEUALVALVALAASPSERSECYARG	1588

Db	1660	TTCCCGCAGCAGCGCCCGCAGCCCGCAGCCGCTCCGCTGCTCTCGCGCGCGCGCG	1666
Oy	1589	LeuThrTyrrThrgIuleuAspArgGlnSerAspIleLeuAlaGlyTrpLeuArg--Arg	1607
Db	16669	ATGACCTACCGGGAGCTGCAGCAGAGCGCCGCAACCGGTGGCGGCACCTGCGCGTGG	16722
Oy	1608	ArgSerMetProAlaGluThrLeuValAlaValPheAlaProArgSerCysGluThrIle	16277
Db	16729	GGGGCGCGCCCGGAGCACCCGTTGCGACTGCTGTTTTC--CGGTGGCCGAGCGCATC	16788
Oy	1628	ValAlaPhePheGlyValIleuValAsnLeuAlaTrpLeuProLeuAspValArgSer	16477
Db	16786	GTCGCGATCCTCGGGGGTCTCAAGTCCGGGGCGGCGCTACTGCGCATGCACCGCGCTG	16847
Oy	1648	ProSerAlaArgValGlnAspIleLeuSerGlyLeuSerGlyProThrIleValLeuIle	16677
Db	16846	CCGGGCGAGCGGATCGGGTTCATCTGCGCGAC--CGCCGCGCGTGGTCGCATGAC	16907
Oy	1668	GlyHisAspThrAlaPro-----ProAspIleGluValThrAsnValGlu	16827
Db	16903	ACCGCCAGCTGGGGCGCGCGCTGCACGCCGACGACGACGCGCATGTCGACGTGCAC	16966
Oy	1683	PheValArgIleArgAspAlaLeuAsnAspSerAsnAlaAspGlyPheGluValIleGlu	17027
Db	16963	GACCCCGGATCGAGCGCGCGCCCTCAAGCGC-----	16997
Oy	1703	HisAspSerThrIleProSerAlaThrSerIleuAlaTrpValLeuTyrrThrSerGlySer	17227
Db	16996	-----CTGCCGCGCGCGGGGCGGACGACGATCGCTACCTAGCTACACTCGCGGACCC	17047
Oy	1723	ThrGlyArgProGlyGlyValMetIleGluHisArgValIleIleArgThrValThrSer	17427
Db	17050	ACCGCGCTGCCAAGGCGCTTGGCGGTGAGCCACGCTAAGCGCGCCAGTTGCTTACGAGC	17107
Oy	1743	GlyCysIleProAsnTyrrProSerGluThrArgMetAlaHisMetAlaThrIleAlaPhe	17627
Db	17110	GAG-----TCGGGGGCTGCCCGCGAGGGCGTGTGTGCGAGTGGCATTCGCTGGCTTC	17167
Oy	1763	AspGlyAlaSerTyrrGluIleTyrrSerAlaLeuLeuPheGlyArgThrLeuValCysVal	17827
Db	17164	GAGCGTGCGGTGGAGATCTTCTGGCGCCAGCTGACGCGGGCGGGCTGTGTGTATC	17227
Oy	1783	AspTyrrMetThrThrLeuAspAlaArgAlaLeuLysAspValPhePheArgGluHisVal	18027
Db	17224	CCCGAATCCGTGGCCCTTCCACCGAAGACCTTGACGCGCTGCTATTAACCGAACAGTTC	17287
Oy	1803	AsnAlaIaIaSerHisValThrSerSerSerGlnAspValProLeuArgValProArgArg	18227
Db	17284	AGCGTCTCAACCGACCCCGTGGCGGGCGGCGCCCTGTCA-----CCCGAAGGC	17337
Oy	1823	LeuSerArgThrLeuMetPhePhePheLeuValValThrAspSerThrAlaProAspAla	18427
Db	17335	CTCGAGAGAC-----CTCAACCTGGTGTGTGGCCGCGCAGGCGTGGCGAGCGAG	17387
Oy	1843	LeuAspAlaGlnGlyLeuTyrrGlnGlyValGlnCysTyrrAsnGlyTyrrGlyProThrGlu	18627
Db	17383	CTG---GTGCAACGCTGGGCGCGCGGGCGGACGTATCAACGCTTACGCGCCACCGAG	17437
Oy	1663	AsnGlyValMetSerThrTrpIleTyrrProIleAspSerThr-----GluSerPheIle	18797
Db	17440	-----GCCACGCTGTACGCGCGCATCGCGCGCGCGCTGCGGCGCGGAGCGCTG	17487
Oy	1880	AsnGlyValProIleGlyArgAlaLeuAsnAsnSerGlyAlaTyrrValAlaAspProGlu	18997
Db	17488	GCTGTGTGTGCGGATCGCTCCCGCGTCCCGGCGCGGGCGGGCGGTTCGTGTGTGAAGAATGC	17547
Oy	1900	GlnGlnLeuValGlyIleGlyValMetGlyGlyLeuValValThrGlyAspGlyLeuAla	19197
Db	17548	CTGCGCCCGGCGCGCGGTGTGTGTGTGGAGACTTATGTCCGCGCGCGCGGGGTGCTCC	17607
Oy	1920	ArgGlyTyrrSerAspLys--AlaLeuAspGluAsnArgPheValHisIleThrValAsn	19387

Db 17608 TCGCGCTATTGGCGGCGCGGCTGACCGCGCTCCGCGCTTCCGCTCGG 17667
Qy 1939 AspGlnThrValIysAlaIleArgThrGlyAspArgValArgIleGlyAspGly 1958
Db 17668 GCGCCCGCGCGCGCGGAGTATCCGCGCGACCTGGTGGCTGGCGCC---GGCGACGGC 17724
Qy 1959 LeuIleGlnPheGlyArgMetAspThrGlnPheIleValIleArgIleAsnArgIleGlu 1978
Db 17725 CAATGAGTATCTGGCGCGCGCTGACGACAGGTCAAGATCCGCGCTCCCATCTGAA 17784
Qy 1979 SerAlaGlnIleGlnIleAlaIleLeuLeuArgAspSerSerValArgAspAlaIleVal 1998
Db 17785 CTCGGGAGTGGCGCGCGCTGGCTGGGTGACCGGTGACCGAGCGGTGGTGGTGC 17844
Qy 1999 LeuGlnGlnAsnGlnAspGlnAlaProGlnIleLeuGlnPheValIleAlaAspHisAsp 2018
Db 17845 GCGCGGAGGACCGCGCGCGCGGACAGCGCTGGTCCGCTACATCACC----- 17892
Qy 2019 HisSerGlnAsnAspIleValGlnSerAlaAsnGlnValGlnGlyTrpGlnAspHisPhe 2038
Db 17892 ----- 17892
Qy 2039 GluSerGlyMetIleAspAspIleGlyGlnIleAspProSerThrIleGlySerAspPhe 2058
Db 17893 -----GGCACCGCGGACCGCGCGCGCGCGGTGGCGCGC----- 17922
Qy 2059 LysGlyTrpThrSerMetIleAspGlySerGlnIleAspPheAspGluMetHisGluTrp 2078
Db 17922 ----- 17922
Qy 2079 LeuGlnGlnThrThrArgThrLeuHisAspAsnArgSerLeuGlnValLeuGlnIle 2098
Db 17922 ----- 17922
Qy 2099 GlyThrGlySerGlyMetIleLeuPheAsnLeuAspSerArgLeuGlnIleGlyValGly 2118
Db 17923 -----GCGCTGGCGGACCGCGCGCGCGCGCTGCATC----- 17952
Qy 2119 LeuGlnProSerArgSerAlaAlaAlaPheValAsnIleValArgIleGlnIlePro-- 2137
Db 17953 -----GTCCGCGCGCGCGCTGCTC-----ACGCTCGACGGAATCCGCTTG 17991
Qy 2138 SerLeuAlaGlyValAlaIleValGlnValGlyThrAlaThrAspIleGlyGlnValAsp 2157
Db 17992 ACCCGCAACGGAACCTCGACACCGCGCGCTGCCCGACCGCAATCTCCGACGCGGAC 18051
Qy 2158 AspLeuHis---ProAspLeuValIleLeuAsnSerValIleGlnIleTrpPheProSerSer 2176
Db 18052 CGGTATCGCGCGCGCGAC-----AACCGCTGC-----GAG 18081
Qy 2177 GluTrpLeuAlaGlnIleAlaAspThrLeuIleHisLeuProAsnValGlnArgIle-- 2195
Db 18082 GAAATCTGGCGCGGACTATGCGCGACAGTGTCTG-----GGCGTGGACGGGTGGG 18132
Qy 2196 -----PhePhe-----GlyAspValArgSerGlnAlaThrAsnGlnHis 2208
Db 18133 GTCGACGACTCGTTCTTCGACTGGCGCGGAC-----AGCATCTCTCGATGCAAGTGG 18186
Qy 2209 PheLeuAlaIleArgAlaIleHisIleThrLeuGlyIleValAsnAlaThrIleAsp-- 2227
Db 18187 GTACACCGCGCGCGCGCGCGCGCTGGTGCAG-----ACCGCGCAATCTTGTGTC 18240
Qy 2228 ArgGlnIleMetAlaGlnIleGlnIleAspMetGlnGlnIleLeuLeuValGlnProAlaPhe 2247
Db 18241 GACGACAGCGGTGGCGCGGTGGCGCGGAGTGGCGGACGCGGACGCGCGC--- 18297
Qy 2248 PheThrSerLeuIleAspArgPheProGlyLeuValGlnHisValGlnIleLeuProLys 2267
Db 18297 ----- 18297
Qy 2268 AsnMetGlnIleAlaIleAsnIleuSerAla-----TyrArgTrpAlaIleValVal 2284
Db 18298 GCGGACGAGGATGTGGCGAGATCACCGGACCGCGGATCATCGCTGGCTGGACGAGCTG 18357

Qy 2285 HisValArgIleSerLeuGlnAspGlnLeuValLeuProValGlnIleAspAspTrpIle 2304
Db 18358 GAAGCGCGCGCGCGC----- 18372
Qy 2305 AspPheGlnAlaAsnGlnIleuAsnGlnIleuSerLeuGlyAspLeuLeuIleuSerSerAsp 2324
Db 18373 -----CAAGTCATGATTCACCAAGGCCATCTG----- 18402
Qy 2325 AlaAlaIleMetAlaValSerIleProPheGlnIleThrAlaPheGlnArgIleVal 2344
Db 18403 -----GTCCGCGCGCGCGCGCGGTGAC-----GAGCGCGACGTG 18438
Qy 2345 ValIleSerLeuAsnSerAsnIleAspGlu-----TrpGlnLeuSerThrIleArg 2361
Db 18439 GTACAGGTGTGACGCGCGCTGTGACCGGACCGCATCTCGCGCTGGCGCTGACGCGC 18498
Qy 2362 SerSerAlaGlnIleuAspSerSerIleuSerValProAspIlePheArgIle---AlaGly 2380
Db 18499 GACGACGCCACCGCGAGTGTGCTGCAGAGTCCGAGCCGCGGTGGTGGACGCGCGC 18558
Qy 2381 -----GluAlaGlyPheArg 2385
Db 18559 GCCTGCTGATGCGGTGACAGACTGTCCGACCGCGCGCTCATCGAGCGCGGTGGCG 18618
Qy 2386 ValGlu-----ValSerSerAlaArgIleTrpSerGln---AsnGlyAlaLeu 2400
Db 18619 CTGAACCGCGCGCGCGCGGTGATCTCAGCGCGGTGGCGGACCGCACCGCGGACGTG 18678
Qy 2401 AspAlaValPheHisIleCysSerGlnGly-----ArgThrLeu----- 2414
Db 18679 GTGTGATTCATCCACCACTGCGCGCTGACAGGTGTCTATGGGAAATCTGTCTGCAGAC 18738
Qy 2415 ValAsnPhePro---ThrAspHisHis-----LeuArgIleSerAsp 2427
Db 18739 TTGAACATGCGCGCGCGGACGACATCAAGCGCGGACCGGTGGCTTACCGCGCGCGCG 18798
Qy 2428 LeuLeuThrAsnArgProLeuGlnArgLeuGlnAsnArgIleAlaIleGlnValArg 2447
Db 18799 ACCTCGTTCGCGCGGTGGCGGTGACCGGCTGGCGGACCGCACCGCGGACGTTGGCG 18858
Qy 2448 GluArgLeuArgSerIleuAspProSerIleProSerAsnIle----- 2463
Db 18859 GACCGGAGC---CGGCGCTGGACGCGGTGGCGGACCGCGCGCGCGCTGCCGCGTGG 18917
Qy 2464 -----ValIleLeuAspIleMetProLeuAsnAlaAsnGlyIleValAsp 2478
Db 18918 TCCCGACGTGACACTTGGCTCCCGCGCGGACCTCTGACCGGACTGGACACCGAAAC 18977
Qy 2479 ArgIleGlnLeuSerArg---ArgAlaIleValIleProLysGlnIleThrAlaIlePro 2497
Db 18978 CACCGCATCTCTGCTGAGGTGGCGCGGACGATTCACCGCGGCTGGCGAGACATCTCT 19037
Qy 2498 -LeuProThrPheProIleSerGlnValGlnValIleLeuValGlnIle-----AlaThr 2515
Db 19038 GCTGATCGCTTGGCTGGCG-----TGGCGGAGTTTGGCGGAC 19079
Qy 2515 rGlnValPheGlyMetIleValAspIleThrAspHisPheAsnLeuGly----- 2532
Db 19080 CCGCGGACGCGGATCGGACATCGAGGCGGAC-----GGCGGCGGCA 19127
Qy 2533 -----GlyHisSerLeuLeuAlaThrIleValIleSerArgIleAspGlnArgLeuIle 2550
Db 19128 GGAATGGGCGCGGACATCGACTGTCCACACCGGTGGCTGTTCACCAACAAATGACC 19187
Qy 2550 eValArgIleThrVal-----LysAspValPheAspHisPheProValPhe 2564
Db 19188 GTTCGCTTACCGTGGCGCGCTGTGATGGGCGAGGTGTGGCGGCGCGCGGAGACT 19247
Qy 2564 eAlaAspLeuAlaSerValIleArgGlnIleLeu-----GlyLeuGlnIleProValSerAs 2583
Db 19248 GGGGACATCTTCAAGCGCGGACGAAACATCTCCGCTGCGCTCCGACCGCGGTAGCTA 19307

QY 2583 pgljnglmglnaspargseralahlsmetalaproargthrgluthrglualalle 2603
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 QY 2603 ucysarggluphnealalyvalleuglypneginvalglytlethraspasmphene 2623
 DB 19356 cccggcgatcgaggttaactactctgggcccagggcgccgacgaatgacccgcca 19415
 QY 2623 pleu-----glylyhiserleumetalathrlyseuvalvalargilegly-- 2639
 DB 19416 catgtggccggcccgacccggacggcgctgagacggcaccggcgccgacatccccat 19475
 QY 2640 -----hisargleuaspthrthralyservalysaspvalpneaspisprova 2656
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 DB 19536 gctggcagccgacacgtgacgtggcgccctgagacgtgacgtgacgtgacgtgacgt 19595
 QY 2672 rhangluile-----valgi 2677
 DB 19596 gagccggctggtgctccagacgctgacccgacatctgacgacgtgacgacgacgacg 19655
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 DB 19656 cggcgtagacggcgctgacacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgt 19692
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 DB 19693 -----accagacacacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgt 19745
 QY 2717 rproserthnglmetglunlysalphleupheaphisethrthralarg---proar 2736
 DB 19746 gggcgtagacggcgctgacgaggtgctgctgttccacggacacacgacgacgacgacg 19805
 QY 2736 gprophevalprophethrlyleaspheproserthsergluprophalialaglyle 2756
 DB 19806 cgaactctatggcgggcgacgtgacacgtgacgtgacgtgacgtgacgtgacgtgacgt 19865
 QY 2756 uilelysalacyserleuvalenhisleuaspilaeaphargthralphealgi 2776
 DB 19866 gggcgtagacggcgctgacgaggtgctgacgtgacgtgacgtgacgtgacgtgacgt 19925
 QY 2776 ualasergljleuethrglunvalvalleusercysleuaspheproileglnalil 2796
 DB 19926 cggctgacgacgacggcgctgacacgtgacgtgacgtgacgtgacgtgacgtgacgt 19985
 QY 2796 egluthr-----gluaspheanilleanthralathrasnglupheleuaspglupheal 2814
 DB 19986 cgaactgacgacgacgacgacgacgtgacgtgacgtgacgtgacgtgacgtgacgtgac 20036
 QY 2814 alysgluprovalargleuglyhis--proleuileargpethrthralelys--gl 2832
 DB 20037 cggcgtagacggcgctgacacgtgacgtgacgtgacgtgacgtgacgtgacgtgacgt 20096
 QY 2832 nthrlysermetargvalillemetharglieserhisalaleuethrarglyleuserle 2852
 DB 20097 gacccgacggcgacgtgctgctgacacacacacacacacacacacacacacacacac 20156
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 DB 20157 gccgactctgttggcgagatcttccggcgcttactacggctgacggcttccggcgccgc 20216
 QY 2872 scglupheserarglyrmetglintythrthralasp--glyargglusercylhisglph 2891
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 QY 2891 etrpargaspvalillegln-----asnthrprometthrilleuserasphartha 2909
 DB 20277 gggcgtagacggcgctgctgacacacacacacacacacacacacacacacacacacac 20336
 QY 2909 lvalaspgljleuaspalathrcyslysalaleuhsleuserlyleilvalenilepr 2929

DB 20337 cgaactcgggccgacacagctc-----gagacgttaccctcgcc 20375
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 DB 20376 cggcgtagacggcgctgacacacacacacacacacacacacacacacacacacac 20435
 QY 2944 rvalpneaspalalacyasalaleuvalleuserargluseraspherysalpvala 2964
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 DB 20496 cttcgac 20555
 QY 2984 yprocythrthralavalprovalargliallglileuseraseraspherythn--gl 3003
 DB 20556 cgtgctgac 20615
 QY 3003 pleuethisaspilleglnaprglntyleuethrleuethrprohileglnthrlleglyph 3023
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 DB 20868 cgaatgac 20927
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 RESULT 9
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QY 558 MetLeuAlaValLeuYsSerGlyAsnAlaPheThrLeuIleAspProAsnAspPro 577
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 QY 598 HisArgGlnThrValGlnLysLeuValGlyArgCys---ValValAlaAspArgLysLeu 616
 DB 1678 -----ACGAGTTGCTGGCGCAGTTGCCGATTCTCTGCACAGTTGACAG 1722
 QY 617 LeuGlnSerValSerAlaSerAspAspPheSer-----SerLeuThrLys 631
 DB 1723 CTGGATCTGGCGGATCGCTAGTGGCTACAGACCCGAAACCCGATCAACGACCTCG 1782
 QY 632 SerGlnAspLeuAlaTyrValIlePheThrSerGlySerThrGlyAspProLysGlyIle 651
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 QY 666 GlyAlaSerLeuGlyIleAsnSerAspThrArgAlaLeuGlnPheGlyThrHisAlaPhe 685
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 DB 1945 GACTTCTCGGTGGAGATTTCGCGCGCTGCTGACGCTGACGCTGATATGCTG 2004
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 DB 2065 ACGGTCTTACACAGACGCCATCCGCTTCAAGCAATTGATGCGCGCTTGTGATTC 2124
 QY 739 GlnAspValProGlyLeuAlaThrLeuValLeuValGlyGlnIleMetSerSerSerVal 758
 DB 2125 ACTTGGTGTATTCGCTGGAACAATATCTTGGCGCGAAGCGCTGACGCTTGCAGC 2184
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 DB 2305 CCGGACGACCGCATTTGGCGAGGATTTGGGACCTGTGATGACGTGACGCGCAT 2364
 QY 809 IleAsnArgLeuValProIleGlyAlaValGlyLeuValIleGlnSerProGlyIle 828
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 QY 829 AlaArgAspTyr-----IleValProProProPro 838
 DB 2422 GCGCGGGTTATCACAACCGCGCTGACCTACGCGCTGACGCGCTTGTGCA 2472
 QY 839 GlnLysSerProPhePheThrAspIleProSerTrpTyrProAlaAsnThrPheProAsp 858
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 QY 998 LysAspIleLeuAspLysGlnThrGlnGlyAlaIleValGlnGlnAlaProAlaProIle 1017
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 QY 1018 ProValPheAlaAspThrAlaAlaLysLeuHisSerIleTrpValGlnSerLeuGlyIle 1037
 DB 2896 -----GCGCAGCTGGAAGAAGATTGCGCTGCTGAGCGCGCTCAAGTTC 2946
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 DB 3109 AAAAATGCGAAAGTATCATGACCTGACGAATTCATTAATCCTGCA-GGCATCTCAA 3167
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 QY 1167 GlnAspGlnAspGlyValGlyValGlnIleValHisGlnLysLeuSerGlnGlnMetLys 1186

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DB 3588 GTTATGATCAATGGCGCTGGCGCGGAAACGGTGGAAAGCAT-----GTTATGCGAAAGTA 3641
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DB 3642 CACGGCGCTTTCATGCAATGAGCGCGCTGTGGCGGCTACGAGCGCTTGAATCATAGC 3701
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QY 1246 AspValLeuAryAaspLeuAengInLeuTySerAalaLeuValAaspSerLeuAasp 1265
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QY 1286 Asp-----GlnHeliLeuGlnGluGlnLysGlnLeuAenTyTTPryLysGlnLeuLys 1303
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QY 1304 AspSerSerPro--AlaTyIleProThrAaspPheAalaArgProAalaLeuLeuSerGly 1322
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DB 4512 CTGGCTGCTCGCTGACCTAGCGCACCGACTGTTTCAACCGCAACCATGAGCGCATG 4571
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DB 4932 GCGCGGCGCGCTACGCTGCGCTGACCCGATTAACCGAGATGCGCTTACGCTTCTG 4991
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DB 5310 GAGATTTTCGCGCGCTGTCAGCGGTCGAGCTGCTGATCGCTGCTGCGGAGTAAAC 5369
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DB 5430 AGCGCATCGCGCTTCAAGCAATGATGCGGCTGCTGATTCGCT-----GTGCGG 5483
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DB 5484 ATGTGCTTACAAAGATCATCTTC-----GGCGGC 5513
QY 1841 AepAalaLeuAaspAalaGlnGlyLeuTy-----GlnGlyVal 1852
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1873 AspSerThrGluSerPheIleAsnGlyValProIleGlyArgAlaLeuAsnSerGly 1892
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Qy 2152 AspIleGlyGlnValAspAspLeuHisAspAspLeuValValLeuAsnSerValIleGln 2171
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Qy 2272 ValAsnGluLeuSerAlaTyrArgTyrAlaAlaValAlaHisValArgGlySerLeuGly 2291
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Qy 2432 ArgProLeuGlnArgLeuGlnAsnArgGlyIleAlaIleGluValArgGluArgLeuArg 2451
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Db 6471 GACGGCGCAGCTTCATCAAGCGCGACCGGACAGCGCGCTGGCTGTTCAGCGCAG 6530
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Qy 2703 IleLysProGlnLeuGlnGlnGlnIleIleGlnAspIleTyrProSerThrGlnMet 2722
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Qy 2723 GlnLysAlaPheLeuPheAspHisThrThrAlaArgProArgProPheValIleProPheTyr 2742
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Qy 2763 LeuValAsnHisLeuAspIlePheArgThrValPheAlaGlnLysSerGlyGlnLeuTyr 2782
Db 6648 CTGATGCGCGCGTCACGAACCTCGCGCAGCACTTCGCGCAGCAGGCGGCAACAGCGCGTG 6707
Qy 2783 GlnValValLeuSer-----CysLeuAspLeuProIleGlnValIleGlnThrGlnAsp 2800
Db 6708 CAGATCATTCATGCGCGCGCTGACCTGACCTGACCTGTAATCCGTCGCGCGCGGCGAG 6767
Qy 2801 AsnIleAsnThrIleThrAsnGlnPheLeuAspGluPheAlaLysGluProValArgLeu 2820
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Qy 2839 IleMetArgIleSerHisAlaLeuTyrAspGlyLeuSerLeuGlnHisValIleArgLys 2858
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Qy 2859 LeuHisMetLeuTyrAsnGlyArgSer-----LeuLeuPro-----Pro 2871
Db 6936 CTGGTGCGCTGTACGAAGCTACAGCCAGGCGCGAGGTCGCTGCTGCAACTGGAC 6995
Qy 2872 HisGlnPheSerArgTyrMetGlnTyrThrAlaAspGlyArgGlnSerGlyHis----- 2889
Db 6996 ATGCACTAGCCCACTATGCGCTGTGGCAACGCACTGATGACGCCGCGTGAAGCAGGCA 7055
Qy 2890 -----GlyPheTyrArgAspValIle---GlnAsnThrProMetThrIleLeuSer 2905
Db 7056 CGGCAACTGGCGATCTGAAGACAGCAATGGGCGACAGACAGCGCATTCGAGGCTGCT 7115
Qy 2906 AspAsp-----ThrValValAspGlyAsnAspAlaThrCysValValAlaLeuHisLeu 2922
Db 7116 GCCGATCATTCAGCCCGCTGTCGCAAGCAGCTCGGTCGCGCGCTGCGGTCGAACTG 7175
Qy 2923 Ser---LysIleValAsnIleProSerGlnValLeuArgLysSerAsnIleIleThr 2941
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RESULT 10
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; Sequence 1, Application US/09976059
; Patent No. US20020164747A1
; GENERAL INFORMATION:
; APPLICANT: Farnet, Chris
; APPLICANT: Zazopoulos, Emmanuel
; APPLICANT: Stafla, Alfredo
; TITLE OF INVENTION: Genes and Proteins for Biosynthesis of Ramoplanin
; FILE REFERENCE: 3019-PCR
; CURRENT APPLICATION NUMBER: US/09/976,059
; CURRENT FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 88421
; TYPE: DNA
; ORGANISM: Actinoplanes sp.
; FEATURE:
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; OTHER INFORMATION: ORF 1; positive strandedness
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; OTHER INFORMATION: ORF 2; positive strandedness
; NAME/KEY: misc_feature
; LOCATION: (4038)..(5048)
; OTHER INFORMATION: ORF 3; positive strandedness
; NAME/KEY: misc_feature
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	OTHER INFORMATION: ORF 32; positive strandedness	
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	LOCATION: (87494)..(88420)	
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	US-09-976-059-1	
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Score:	1824.50	Matches: 852
Percent Similarity:	39.45%	Conservative: 466
Best Local Similarity:	25.50%	Mismatches: 1251
Query Match:	11.31%	Indels: 777
DB:	9	Gaps: 125
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Oy	106 PheThSerApSergLyUvTrHserGlnVal-----lLeuLyAspSer	121
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Oy	141 pglAlaAlaAlaAlaAlaAlaSerGlyPro-----ArgCyAsnArgPheValIeuDe	158
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Dd	29255 GGCGCGCGCTGAGTGTCCGCGGAGAGACACGAGCTATTTCGCGAGTTGCTCGCGA	29314
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Dd	29315 CGTCACC-----	29321
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Oy	218 lSerValValSerMetSer-CyGlnUasp-----AsnAlaValSerAlaThrHisPheT	236
Dd	29369 CCGGCGCGCTCAGAGTCTCGCTCGCGCTCGCGAGGCGCGCGCTCGCGCTCGCGAGGT	29428
Oy	236 TrpGlnThrHiSleuAsnArpLeuAsnAlaSerValPheProHisleuSerArpHisleuM	256
Dd	29429 GGCGCGGACACTCGCGCTCAGCGCG-GCCACCGCTTTC--CACCTGGCC-----	29474
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Dd	29474 -----	29474
Oy	276 lAeuSerArpSerAlaIleCyAArgThrAlaIeuSerIleIeuIeuSerArgTYUthrN	296
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Db 29563 CCGAAGCCGGTCCG-----GGCTGTCTATCAACAGCTGC 29598
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Db 29599 CGGTGGCGGCTG-----CGACTGAACGGCAGAGGTGGGGAGCGCGTGAACG 29646
Qy 347 eTyrAerAerAerGlyLeuGlnHisLeu-----AlaProPheGlyLeuArg 362
Db 29647 CCGTGGCGGACAGATGCGGAGCTGATGCGGACGACGACGCGCGCTGCGTGC 29706
Qy 362 sp1LeuArgAunThrGlyAerAunGlySerAlaAlaCyAerPheGlnThrValLeuLeu 382
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Qy 382 alThrAerGlySerHisValAunAunGlyLleAunGlyPheLeuGlnAl1leThrGln 402
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Qy 402 eTsrHisPheMetProCyAerAunAunArgAlaLeuLeuLeuHisCyGlnMetGlnSers 422
Db 29818 TGGTGCACCGCGACACGACCAATATCCGCTGTGTGTC-----TCCGTCGACGACG 29868
Qy 422 eTsrGlyAlaLeuLeu-----ValAlaTyrTyrAerHisAunVal1leA 436
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Qy 456 eTsrProLeuAerLeuSerSerMetAlaGlyValAunMetThrGlyTyrAerArgAlaG 476
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Qy 476 lueGln-----SerThrAunSerGlnProLeuGlnValGlnAerThrLeu 492
Db 30025 AGATTCGACAGCGGCTGTTCAACGCTGGAACGACAGCAGCTCGCGCTGATGAGTGCCTG 30084
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Db 30595 TGTGTTCATGCGCGCGACGCTTGTGATGCGCTGTGATGATGATGATGATGATGATGATG 30654
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Db 31162 CTGACACAGCGGCGCTGCTGATTTGCGCGGCGGCGCGATGATGATGATGATGATGATGATG 31221
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QY 1412 leAsnGlnValaIglYalathrThrAlaAlaPheGlnleuGlnAspIleProPheGln 1432
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QY 1432 rglValaIserAlaLeuGlnProGlySerArgAspLeuSerThrProleuAlaGln 1452
|||
Db 32743 AACTCGTGAAGACCTTGCACCC---ACCGCTCTCTGCGCGGACCCCTTTCAGG 32799
QY 1452 eulIlePheAlaValaHIsSer---GlnYsAspLeuGlyArgPheIysPheGlnGlyLeu 1471
|||
Db 32800 TCAATGATGACCTTGCAGAGCGCTCGCGGAGCAAGACCGCTGGCTCGCGGCTGC 32859
QY 1471 IuSerValProAlaPro-----SerIlyAlaTyThrArgPheAspMetClnPhe 1488
|||
Db 32860 GGGTCAACGACCTCCGCGCGGAGACACCCCAAGGTGAGACTGCACTGACCTGTC 32919
QY 1488 IeLeuPheGlnGlnIuThrAspSerleuIlyserValaenPheAlaAspGlnleuPhe 1508
|||
Db 32920 ACAAGTGGCGGCGCGGAGAGGATGACGCCAGCTCTGGCGCGCGGACCTTTCG 32979
QY 1508 yMetClnThrValaIgluaenValaValaArgValPhePheGlnIleLeuArgAsnGlyLeu 1528
|||
Db 32980 AGCAGAGACGCTGCGCGCTGCGCGAC-----CGTGTGCTCGAACCCTGGAAG 33030
QY 1528 IuSerSerArgThrProValaSerIleleuProleuThrAspGlyIleValaThrleuGln 1548
|||
Db 33031 CCAATGGCGGCGCGCGGACGAC-----ValIyHIsValaAspTy 1560
QY 1548 yLeuAspValleuAsn-----ValIyHIsValaAspTy 1560
|||
Db 33064 GATCGAGGTGCTGTGCGCGGAGCGGAGCTGCGCGCTGCTGAGAGTGAACGACGCG 33123
QY 1560 roArg-----GluSerSerleuAlaAspValPheGlnThrGlnValaSerAlaTy 1577
|||
Db 33124 CTGCTCGGTGTGAGTGTCTGCTGCGCGGCTGCTTTCGCGGACAGTGGCGGCTGCC 33183
QY 1577 roAspSerleuAlaValaIAspSerSerCyArgleuThrTyThrGlnleuAspArg 1597
|||
Db 33184 CCGACCGGCTGCGCGTGTGCGGAGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 33243
QY 1597 IuSerAspIleleuAlaGlyTrPleuArgArgSerMetProAlaGlnThrleuVala 1617
|||
Db 33244 GGTGCGATGTGTGTGCGCGGAGCTGTGCGCGGCGGTGTGAGTGTGAGTGTGCGGTTG 33303
QY 1617 laValaPheAlaProArgSerCyGlnThrIleValaAlaPhePheGlnValaIleuYsAla 1637
|||
Db 33304 TGGTGGCGTGGAGCGGTCTCCGAGGTGTCTCCGCGTGTGGCGGTGGCGGAGGCGG 33363
QY 1637 snleuAlaTyrlleuProleuAspValaArgSerProSerAlaArgValaGlnAspIleu 1657
|||
Db 33364 GGGCGGCTGTGTTCGCTGATTTGCGTGGCGGAGCGGCGGTGTGATGCGGTGTG 33423
QY 1657 eArgIly-----LeuSerGlyProThrIleVala 1666
|||
Db 33424 CGGACTGGCGCGCGGATTCGCTGCTGACCGCGGAGACCGGCTGATCGGTCTGT 33483
QY 1666 eu-----IleGlnHIsAspThrAlaProProAspIleGlnValaThrAsnValaGlnPhe 1684

Db 33484 CCGCGCGCTGGCGGGGATTCCGCGCTC----- 33512
Qy 1684 aAlaArgIleAaGAPAlaLeuAaAspSerAaAlaAspGlyPheGluValIleGluHisA 1704
Db 33513 -----GTCCTCCGGGACCTTGACCGCGGATCCGGCGCTGTGTG----- 33551
Qy 1704 spSerThrIlyProSerAlaThrSerLeuAlaIlyValLeuIlyThrSerGlySerThg 1724
Db 33552 --CCGGCGCGGTCCGGGTCCGGGTCCGGGTCTACCGCATGTACACTCGGGTTCACCG 33609
Qy 1724 IyAArgProIlyGlyValMetIleGluHisArgValIleIleAArgThrValThrSerIlyC 1744
Db 33610 GTCGGCGCAAGGAGTGTGTGACCAACCAACCACTCGGATTGTGCGACCAACGAT 33669
Qy 1744 YalIleProAenIyProSerGluThrArgMetAlaHisMetAlaThrIleAlaPheAsp 1764
Db 33670 GTTGGGGTCCGACCCG-----CGGGTCTTTTCCACGCGCCCGACGCTTCGACG 33720
Qy 1764 IyAlaSerIyGlyIleIyThrSerAlaLeuLeuPheGlyArgThrLeuValCysValAspT 1784
Db 33721 CGTCTGTATGATTTGGGTGCGCTTTGTAATGGCGGACGCTGCTG--GTGGCTC 33777
Qy 1784 yMetThrThrLeuAaPAlaArgAlaLeuIyAspValPhePheAArgGluHisValAsnA 1804
Db 33778 CGCGCGCACACATCGACGCAACGCTTTGAGGACCTG--ATCGCGCGCATGATGTA 33834
Qy 1804 laAlaSerHisValIThrSerSerGlnAspValProLeuArgValProArgArgLeuS 1824
Db 33835 CGACAGTGCATGTGACCGCGGC-----TTGT 33861
Qy 1824 exArgThrIleu-----MetPhePhePheLeuValIThrAspSerThrAlaProAspA 1842
Db 33862 TGGCGGAGTGCACCGCTGCTTCGCGGCGCTGACCGAGTCTCACGGGCGGGATG 33921
Qy 1842 laLeuAaPAlaGlnGlyLeuIyGln-----GlyValGlnCysIyA 1856
Db 33922 CGGTGTCCGCGGAGCGGCTGCGCGCTCAAGACGGGAATCCGGGTCTCGGGTCCGCG 33981
Qy 1856 smGlyIyArgIyProThrGluAaAsnIyValMetSerThrIleIyProIleAspSerThg 1876
Db 33982 AGCTGTAAGCGCGGACCGAGGTGACCTTGTGCGGACGACATCTCTGAT----- 34034
Qy 1876 lAspPheIleAaGlnIyValProIleGlyArgAlaLeuAaAsnSerGlyValAlyVal 1896
Db 34035 -----GACGGGTGCGCATCGGCGCGCTGACCAACCGCGGTCTACGCTTC 34083
Qy 1896 alAspProGluGlnGlnLeuValGlyIleGlyValMetGlyGluLeuValIThrGlyA 1916
Db 34084 TCAGACGACCTCTCGCGCGCGCTCCGACAGGTGTGTGGGAGACTGTATGTGCGCGGT 34143
Qy 1916 spGlyLeuAlaArgGlyIyThrSerAsp---LysAlaLeuAaPAlaAsnArgPheValHisI 1935
Db 34144 CGGCTCTGGCGCGGCTTATGCGGACATGCCCGGGTGTGACCGGACGATTCCTCCCG 34203
Qy 1935 leThrValAaAspGlnThrValIyAlaIyArgThrGlyAspArgValArgIyArgI 1955
Db 34204 ACCCATTCACACCGCGGT---CGCTCTACCGCACGGGTGATCTGTGCGGGT---G 34257
Qy 1955 leGlyAspGlyLeuIleGluPhePheGlyArgMetAspThrGlnPheIyValIleArgGlyA 1975
Db 34258 CCGACGATGTGTGCTGCTGCTTCTGCGGCGCGGATGATCAGGTAAATTCGTGGCT 34317
Qy 1975 smArgIleGluSerAlaGluIleGluAlaIleLeuAaAspSerSerValArgAspA 1995
Db 34318 ATCGGGGTGAGCGCGGAGGATTAAGCGGTCTGCTCAACACCGGACGCTCCGACG 34377
Qy 1995 laAlaValValLeuGlnGlnAaAsnGluAaPAlaProGluIleLeuGlyPheValValA 2015
Db 34378 TACAGATGTGTCTCGCGGAGGACCCCAAGGCGACAGCGCTGTGCTGCTCAAGCTCTC 34436
Qy 2015 laAspHisAspHisSerGluAaAspIyGlyGlnSerAlaAsnGlnValGlnGlyIyTrp- 2034

Db 34437 -----GGCGGAGATGTCGAGCGGTATG 34458
Qy 2035 --GlnAspHisPheGluSerGlyMetIyThr---SerAspIleGlyGluIleAspProSerT 2053
Db 34459 CGAGAGAGCGGCTTCGGGGCTATAGTTCGCTCGGCTTTGCGAGATTGAGTGCCTGC 34518
Qy 2053 hrIleGlySerAspPheIyGlyIyTrpThrSerMetIyArgGlySerGlnIleAspPheA 2073
Db 34519 CGCTGACCAAGCAACAGAG-----GTCCACCGGCGGCTCTCCGCGCGC 34563
Qy 2073 spGluMetHisGluIyTrpLeuGlyGluThrThrArgThrIleuHisAspAsn-----A 2090
Db 2090 rGserLeuGlyAaValLeuGluIleGlyThr----- 2100
Qy 34624 CCGCGTTCGCGGAGGTGTCTGACCTGGATCGGCTGCTGCAACGACTTCTTGCCC 34683
Db 2101 -----GlySerGlyMetIleLeuPheAaAsnLeuAaAspSerArgLeuGluSerIyValGlyL 2119
Qy 34684 TCGCGCGGCATTCGCTGCTGCTGCTGCTGCTGAGATCTGCGCGCGCAC---GGCG 34740
Db 2119 euGluProSerArgSerAlaAlaIlePheValAsnIyAlaThrGluSerIleProSerI 2139
Qy 34741 TTCACATCTCTCGTTCGGGCGCTCTTC-----GCAACCCCAACCGCGCGCGC 34788
Db 2139 euAlaGlyIyValAlaIyValGlnValGlyIyThrAlaThr---AspIle----- 2153
Qy 34789 TGGCGCGCTCGGG-----GAAACCGCGTCCCGGACGAGCGCGCCCAACCTCA 34836
Db 2154 -----GlyGlnValAspAspLeuHisProAspLeuValIleAaAsnSerValIleG 2171
Qy 34837 TCCCGCAGGCGCGCGCGCCAGAACTGACCCCGACATGCTGCGCTGTCGACTG--- 34892
Db 2171 lntyPheProSerSerGluIyIleuAla----- 2180
Qy 34893 -----ACCGGAGAGAACTGACCACTCGTGGCGCGCGGCTCCGCGCGCGCTC 34941
Db 2181 --GluIleAlaAspThrIleuIleIleLeuProAaValGlnArgIlePhePheGlyAspV 2200
Qy 34942 CCAACATCCGCGGACATCTACCCCTAGCCCGGTGCAAGAGGACATTTCTTCCACACC 35001
Db 2200 alArgSerGlnAla---ThrAsnGluHisPheLeuAlaIleGlnAlaIleHisThrLeuG 2219
Qy 35002 TCATGACCGAGGCGGATGACCAACGAGTCTACCTCTGCGCGGATTCGCGCTCGCG 35061
Db 2219 IyLysAaAsnIleThrIyAspAspValArgGlnIyMetAlaGluLeuGluAspMetGluG 2239
Qy 35062 GCGGT-----C 35067
Db 2239 lntGluLeuLeuValGluProAlaPhePheThrSerLeuIyAspArgPheProGlyLeuV 2259
Qy 35068 CCGAGGTG-----GACGCTTCTCTGGGGCCC 35094
Db 2259 alGluHisValGluIleLeuProLysAaMetGluAlaValAaGluLeuSerAlaIyA 2279
Qy 35095 TGCAGCAGGTG-----GTGGACCGGACGACGATCTATC 35127
Db 2279 rGlyIyAla-----AlaValValHisValArgGlyS 2289
Qy 35128 GACAGGCGCATCGCTGCGACAACTCGGCGAGCGCTTCGACAGGTGTGTGACCGGACGCA 35187
Db 2289 exLeuGlyAspGluLeuValLeuProValGluIyAspAspTrpIleAspPheGlnAlaA 2309
Qy 35188 CCGTGCCTGCGACGAAAGTCAACCC-----G 35214
Db 2309 smGluLeuAaGlnIySerLeuGlyAspLeuLeuIySerSerAspAlaAlaIleMetA 2329
Qy 35215 ACCAGCTGACGCGCGCGGACCGCGCGCGCTCCGCTGCAACGACCCCTGCTCA 35274
Db 2329 laValSerIySilePro----- 2334
Qy 35275 GCGTCCACATCGACCCGAAACCGGAGGCGGCTGCTGCTGCTCCGATGACCAACC 35334

QY 2335 -----PheGluIleThrAlaPheGlu---ArgGlnValAlaAs 2347
DB 35335 TCGTGAGAGACACACACCGCCCTCGACATCTCTCCAGAGATCCGACCATCTCTCCGC 35394
QY 2347 eTleuAsnSerAsn-----IleAspGluTrpGlnL 2357
DB 35395 GCGCAACCGACACCTCCCGCCCGTACCGTTCCGCGACTTCGTGGCCGACGCGCGCC 35454
QY 2357 euserThrIleAspSerSerAlaGlu-----GlyAsp 2367
DB 35455 TCGCGCTCTCCCGCGAGACAGAGGCTACTTCGCGCGCTCTCGGAGAGCTACCG 35514
QY 2368 -----SerSerLeuSerValProAspIlePheArgIleAlaGlyAlaGlyPheA 2385
DB 35515 AGACCAACCGCCCGCTACGCGCTGCGCGACGTACGAAC---GACGGCACCGCATCGGTG 35571
QY 2385 rGValGluVal-SerSerAlaArgGlnTrpSerGlnAsnGlyAlaLeuAspAla----- 2402
DB 35572 GGGCCGAGGTGAGCTCGACGCGCGCTGCGCGCGCGCTGCGGACCTC-GCCCGCGAC 35630
QY 2403 -----ValPheHisIleCysCysSerGlnGlyAlaTrpIleVal 2415
DB 35631 CCGGCGCTACGCCCGGACGAGTCTTCATCTGACCTGCGCGCGCGCTGCGCGCGCTG 35690
QY 2416 AsnPheProThrAspHisIleAspArgGlySerAspLeuThrAsn----- 2431
DB 35691 GCCGA-CCGGAGAGAGCTCTCTTCGACACCGCTCTGTTCAGACGAGTGGCTCCGCGCC 35749
QY 2432 -----ArgProLeuGlnArg-----LeuGlnAsn 2439
DB 35750 CCGCGGAGTCCCGCGCTTCATGAACACCTCGCGCTCGGTAACGCTGTCGCGGAC 35809
QY 2440 ArgArg-IleAlaIle---GluValArgGluArgLeuArgSerLeuLeuProSerTyrrme 2458
DB 35810 CCGCGCGAGGCTCTGGACAGGTGCGCGACCGCTCGCGAGCTAGTGGCGCAC----- 35864
QY 2458 tIleProSerAsnIleValIleuAspIleMetProLeuAsnAlaAsnGlyValAs 2478
DB 35865 -----GAGCACGCGCGCGCTC----- 35879
QY 2478 pArgGlyGluLeuSerArgAlaValProGlyGlnGlnIleAlaProLe 2498
DB 35880 -----GCGTGGCCGACGAGCGCGCGCTGCGC-----GCGGAGCGCGCT 35923
QY 2498 uProThrPheProIleSerGluValGluValIleLeuCysGluGluAlaThrGluValPh 2518
DB 35924 GTTCACG-----TCGTT-GTTCAACTACCGCTATGCGCGCGCGCGCGCACGC 35973
QY 2518 eGlyMetIysValAspIleThrAspHisPhePheAsnLeuGly-----GI 2533
DB 35974 CCGACGATCCGCTGCGCGCGCGCGCGCGCTGCTCCGCTGGAGAACGACACATACCGCG 36033
QY 2533 yHisSerLeuLeuAlaThrIysLeuIleSerArgIleAspGlnArgLeuIysValArgI 2553
DB 36034 TCAC-----CGTGTGATCGACGACGACGACGCGGAT 36066
QY 2553 e-ThrValIysAspValPheAspHisProValPheAlaAsp----- 2566
DB 36067 TCGCGGTACAGGTGACGCTGCGCGCGCGCGCGCGAGGTGCTCGCTGCTCC 36126
QY 2567 -----LeuAlaSerValIleArgGln----- 2573
DB 36127 GCAACACCTGACCCCGCTGCGCGCGCTCGACGCACTCCGAGATCCGCGTGGCCG 36186
QY 2574 -----GlyLeuGlyLeuGlnGlnProValS 2582
DB 36187 AGCTGGCGCCGCGCGCTGCTCCGCGCGCGCGCGCGCGCGGTCTCGTGGCTCC 36246
QY 2582 eTAspGlyGlnGlyAlaAspArgSerAlaHisMetAlaProArgTrpGluThrGluAlaI 2602
DB 36247 CCGCCGCGCGAG---CCGGCGACCGCGCGCGCGCTCGCGCACCGCGCTACGAGAGC 36303

QY 2602 IeLeuCysAspGluPheAlaIysValLeuGlyPhe---GlnValGlyIleThrAspAsn 2621
DB 36304 TGAATCGCACGCGGTACGCCACAGTCTGAGGTGACCGGCTGGCGCGACGACACT 36363
QY 2621 hePheAspLeuGlyGlyHisSerLeuMetAlaThrIysValAlaValArgIleGlyHisA 2641
DB 36364 TCTTCCCGCTGGCGGCACTCGCTCTCGCACCGCGCGGTGCTACCGCGATCGCTCGG 36423
QY 2641 rGLeuAspThrThrIleValSerValIysAspValPheAspHisProValLeuPheGlnLeu 2661
DB 36424 CGCTGGCGGTGAGGTGACCATTCGCGCGCTCTTCAGAGCTCACCGCGACGCTGG 36483
QY 2661 IAlaIleAlaLeuAspAsnLeuValGlnSerIysThrAsnGluIleValGlyIysArgGlu 2681
DB 36484 CCGCGCGCGCTG-----ACCGCGCTCGGACCGCGCGCGG--- 36518
QY 2681 eTAlaGluTrpSerProPheGlnLeuLeuPheThrGluAspProGluGluPheMetAla 2701
DB 36519 -----GTGCAACCGCGCGCG-----AGACACGCGCGGAGCGGATTCGCTGT 36561
QY 2701 eGluIleIysProGlnLeu-----GluLeuGlnGluIleIleGlnAspIleT 2717
DB 36562 CTTTCGCGACGCGCGCTGTGCTGCTGCTGCGCGAGCTGAG----- 36602
QY 2717 yProSerThrGlnMetGlnIysAlaPheLeuPheAspHisIleThrAlaArgProArg 2737
DB 36603 -----GCGACGACGCGCCACCTACAGACACAGACGCGCG----- 36635
QY 2737 roPheValProPheTyrlleAspPheProSerThrSerGluProAspAlaIleGlyLeu 2757
DB 36636 -----CTGCGGCTCTCCGCGCGCTGACCGCGCGCGCTCA 36672
QY 2757 IeIysAlaCysGluSerLeuValAsnHisIleuAspIlePheArgThrValPheAlaGlu 2777
DB 36673 CCGCGGCGCTGACGACGATGATGCGCGCGACGAGGCTGCGCGACGATGATCGCGCG 36732
QY 2777 IAspGlyGluLeuTyrglnValValLeuSerCysIleuAspLeu-----ProIleGln 2795
DB 36733 AGGACGCGCGCGCTGACGATGCTGCTCCCGCGCGAGGACGCGCGCGGTGAGA 36792
QY 2795 aIleGlu---ThrGluAspAsnIleAsnThrAlaThrAsnGluPhe-----L 2810
DB 36793 TCGTGGAGGTGCTCCCGCGAGCTTGGCGCGCGCTGCGACGAGTGGCGCGTTACCGCT 36852
QY 2810 eAspArgIlePheAlaIysGluProValArgLeuGlyHisProLeuIleArgPheThrIle 2830
DB 36853 TCGACCTGCGCGCGAGATACGATCGCGCG-----CGCTGATCGCGTGGCGCG 36906
QY 2830 IeIysGlnThrIysSerMetArgValIleMetArgIleSerHisAlaIleuTyrrAspGly 2850
DB 36907 CCGACACGTC-----CTGCTCTGTGATTCACACATTCGACACGACGAGAT 36954
QY 2850 euserLeuGlnHisValIysValIysIleuHisMetLeuTyrrAsnGlyArg-----SerL 2868
DB 36955 GGTGATGAGCGCGCTGCGCGCGACCTCGCGCGCTACGAGCGCGCGCTGCGCGCG 37014
QY 2868 euleuPro-----ProHisGlnPheSerArgTyrrMetGlnTyrr----- 2881
DB 37015 GGGCACGCGCTGGAGCGCGCTCGCTCGATGACGCGCATCGCGCTGCGAGGAG 37074
QY 2882 -----AlaAspGly-----ArgGluSerGlyHisGlyPheTyrrA 2893
DB 37075 AGTTGCTGGCGCGCGCGGTGACCGGAGAGCTGCGCGAGCGCGAGCTGCGCTACGCG 37134
QY 2893 rAspValIleGlnAsnThrProMetThrIle-----LeuSerAspAspT 2908
DB 37135 GCGACACCTGCGCGCGGATCGCGCGGAGATCCCGCTTCGCGCGACCGCTTCCGCGCG 37194
QY 2908 hrValIysAsp-----GlyAsnAspAlaThrCysIysValIleuHisLeuSerTyrrIle 2926
DB 37195 CCGTGGCTTGCACCGCGCGCGGAGTGGCG-----A 37227
QY 2926 aIleuIleProSerGlnValIleuArgGlySerSerAsn-----IleIleThrGlnAlaT 2944

[illegible]

Alignment Scores:	
Pred. No.:	1.11e-138
Score:	1804.50
	Length: 9025608
	Matches: 842

Percent Similarity:	35.12%	Conservative:	516
Best Local Similarity:	21.77%	Mismatches:	1242
Query Match:	11.19%	Indels:	1269
DB:	15	Gaps:	137

Qy	7	ValAspGlyArgGlnAspLeuProPheThrProAlaSerPheCysSerHisGlyAspSer	26
Db	4514414	GTGACACACCGGGCCCGACAGTCCGCCCGCTCCGGGACAC-----GGGACCTC	4514367
Qy	27	ProLeuAsnSerSerTyrGluGlnLeuPheHisLeuTyrGluLeuAspSerSerArgIle	46
Db	4514366	CCCCCTCTCTCCGGTCCAGCCCGCCCTGTGGTCTTCGACCGGAGCACCCCGGACGCC	4514307
Qy	47	GlnAlaIleLeuProCysThrProPheGlnLeuAspMetIleAspCysAsnAlaLeuAsp	66
Db	4514306	GAGTGGGTCGCCCG-----	4514292
Qy	67	LeuGlnSerAlaIleGlnHisAlaValTyrAspValProThrAspIleAspIleSerArg	86
Db	4514291	-----CTCTTCCTCGCGCTCCGGGTTCCCTGACCGCGGAC	4514253
Qy	87	PheAlaLeuAlaTyrPheGluIleValAsnGlnThrProAlaLeuArgAlaPheAlaPhe	106
Db	4514252	GTGGCGCGGCGCTCGACGGCGCTCGCCCGCGACAGCCGTGGCCACC--CGCTAC	4514196
Qy	107	ThrSerAspSerGlyTyrThrSerGlnValIleLeuLysAspSerPheValPheSerTyr	126
Db	4514195	GTGCACACAGGCGCGGACCGCGGCACATATC-----	4514163
Qy	127	MetCysTyrPheSerSerSerSerPro-----AspGlu	137
Db	4514162	-----GACGCGCCGGGCGCGGACCGTCGAGCTGCGCGTCGAGAC	4514121
Qy	138	ValValArgAspGlnAlaAlaAla-----Ala	146
Db	4514120	ACCGCCCGGACCGGGGTGGCCGCTTCGGGCGACAGTTCAGCGGGCTTGACCTC	4514061
Qy	147	AlaSerGlyProArgCysAsnArgPheValLeuLeuGlnAspMetGlnThrLysLysCys	166
Db	4514060	GCCCGGGGCCCGCTGTGGCC-----GCCCTGTGGCCCGGGGCGCGGAGAACCAT	4514007
Qy	167	GlnLeuValTyrPhePheSerHisAlaLeuValAsp-----ValThrPheGlnGln	183
Db	4514006	GTCTCTCTTCGACGATGATCATCATCACTCGCACGGCTGTGTGACGGTATCTTGGAA	4513947
Qy	184	ArgValLeuSerArgValPheAlaAlaTyrLysHisGlnLysAspThrHisArgProGlu	203
Db	4513946	CGGAGCTGGCGGACGTGTGGCGCGGACCGGGCGCGCGCGGACCTGCCGAA	4513887
Qy	204	ThrPro-----GluSerSerAspAlaThrAspThrAsp	214
Db	4513886	CTGCCCTTCACGACGACGACGCTCTCGGAGGGGTGCCCGCTCACGAGCGCGCTC	4513827
Qy	215	SerGlnSerValSerValValSerMetSerCysGlnAspAsnAlaValSerAlaThrHis	234
Db	4513826	GTGCAGGGC-----GAGCTAACCCAC	4513806
Qy	235	PheTyrGlnThrHisIleuAsnAspLeuAsnAlaSerValPheProHisLeuSerAspHis	254
Db	4513805	---TGGCGCGCGCGCTCGACGCGATCGCCCGCTCGACCTGCCCC-----GCCGACAC	4513755
Qy	255	LeuMetValProAsnProThrThrThrAlaGlnHisArgIleThrPhePro-----	271
Db	4513754	-----CCCGCGCGGCGGTGCTGATCCGCGCGCGCGCTGACCTGTCGGCTC	4513704
Qy	272	-----LeuSerGlnLysAlaLeuSerAsnSerAla-----	281
Db	4513703	GCCCGCGAACCTCGCGCTCAACATGACGAGTGGCGCGGACCGACCGGCGCACCCGCTC	4513644
Qy	282	---IleCysArgThrAlaLeuSerIleLeuLeuSerArgTyrThrHisSerAspGlnAla	300

QY 946 a-----HisIleuAspH1sAAspAlaThrLeuAlaIleAsnIleuSle 961
Db 4511658 CGCGCGCGCGCTGCCCGCCAGCTCCGCGCCACTGCGCGCGACGC----- 4511616
QY 961 uGUGInValLeuProArgHisSerIleProSerPheTyrIleCysMetLeuGluLeuP 981
Db 4511615 -----CTGCCAGATACATGATCCGGACCTTCACCGCGCTTCACACGATCCC 4511566
QY 981 oATGThrAlaThrGlyLeuIleAspArgArgLeuArgIleMetGlyLeuAspIleLe 1001
Db 4511565 GGTCAAGCGCAAGCGCAAGGTTCGACCGAGCGCTCCGCGCGCGGAGCGACCGCGCA 4511506
QY 1001 uAAspLysGlnThrGlnGlyAlaIleValGlnGlnAlaProAlaProIleProValPheAl 1021
Db 4511505 CGACGAGAGC-----CATGTGCGCACCGAC-----CG 4511479
QY 1021 aAAspThrAlaAlaLysLeuHisSerIleTyrValGlnSerLeuGlyIleAspProAlaTh 1041
Db 4511478 CCGCGTCGAGAGAGCGCTCCGCGAGATCTGACCGCACTGCTCGGC----- 4511433
QY 1041 rValAsnValGlyAla-----ThrPheGluLeuGlyGlyAsnSerIleThrAlaAl 1059
Db 4511432 -GTCCAGCGCGGACACACACAACTTCTTCACATGCGCGCAATTCCATCTCGCGAT 4511374
QY 1059 eLysMetVal--AsnMetAlaArgSerValGlyMetAspLeuLysValSerAsnIleTy 1078
Db 4511373 CCGCGCTGATCTCCCACTCCAGCGACGAGTTGAGATGACTTCGCGGTCCGACGCGCTT 4511314
QY 1078 rGlnHisProThrLeuAlaGlyIleSerAlaValValLysGly----- 1092
Db 4511313 CGAGGACCGACAGGTCCGCGTATCGCGCACCGCTCGA--GAGCGGTCACCGCCAGA 4511255
QY 1092 ----- 1092
Db 4511254 TCGCGCGCTCTCCGACGCGGACCTCTCGACAGCGGCGCGACCGACACACACACC 4511195
QY 1092 ----- 1092
Db 4511194 TCACGACAAACCGACGCTGAGAGGACGACGAGATGAGACCGGGGAAATGAGAAACC 4511135
QY 1093 -----ApproLeuSerTyrThrLeu----- 1099
Db 4511134 CGTCTCTCGGAGCACTGATGCCAGCGGCTCCGCGGAACTGTGCGCGCGCTCTCGC 4511075
QY 1100 -----IleProLysSerThrHisGluGlyPr 1108
Db 4511074 GGGCGCGCGACGCGCGCCACCGCGCGCGGACATCCCGCGCGCGACCGGAGCGGCC 4511015
QY 1108 oValGlnGlnSerTyrSerGlnGlyArgLeuTyrPheLeuAspGlnLeuAspValGlySe 1128
Db 4511014 GCTGCCGCTGTCGACGCGGACGAGATGTGGTCTTCAGCGCGCTGAGCGCGGACG 4510955
QY 1128 rLeuTyrTyrLeuIleProTyrAlaValArgMetArgGlyProValAsnValAspAlaLe 1148
Db 4510954 CCGCGAATACCTGCTGCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4510895
QY 1148 uATGArgAlaLeuAlaIleLeuGlnArgHisGlnThrLeuArgThrThrPheGluAs 1168
Db 4510894 CGACAGAGCTGGGACACAACTGCTGAGCGGCGGACGAGATCTGCGACCGCGTACGCGCT 4510835
QY 1168 rGlnAspGlyValGlyAlaGlnIleValHisGluLysLeuSerGlnLysMetLysValI 1188
Db 4510834 GAGCGGCGAGAGCGCTCCAGATCATCATGAC-----GCGCGCGCGCGCTGCGCT 4510784
QY 1188 eAAspLeuCysGlyY--SerAspLeuAspProPheGluValLeu--AsnGlnGlnGlnTh 1206
Db 4510783 GAGCGGCTCGGCGCGCGGACGACGAGGCTCGCGCGCTGTCGAGGCGGCTGCGC 4510724
QY 1206 rThrProPheAsnLysSerSerGlnAlaGlyTyrArgAlaThrLeuLeuArgGlyG 1226
Db 4510723 CCGCGGCTTGACCTCGCGCGGACGCTGCGCGGCGGCGGCTGATCCGCGCTCGCGCA 4510664
QY 1226 uAAspAspHisIleLeuThrIleValMetHisIleIleSerAspGlyTyrSerIleAs 1246

Db 4510663 CGAGGACAGCTCTCGCGGTGTCTTCCACCACTACCTCTGCGACGCTGCTCACCGG 4510604
QY 1246 rValIleuArgArgAspLeuAsnGlnLeuTyrSerAlaAlaLeuLysAspSerLysAspPr 1266
Db 4510603 CGTCTTCGACAGAACTACGCCCTGTACAGGGC----- 4510567
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QY 1286 rGlnPheIleGluGln-----GluLysGlnLeuAsnTyrThrLysGlnLeuLysAs 1304
Db 4510510 CGAGCTGACCGGAGAGTCTCTCAACGTCACTTCGACACTGAGAGCGCGGTGCGGA 4510451
QY 1304 pSerSerProAlaLysIleProThrAspPheAlaAspProAlaLeuLysSerGlyAspAl 1324
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QY 1324 aGlyCysValHisValThrIleAspGlyLeuTyrGlnSerLeuArgHisCysAs 1344
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QY 1344 nGlnHisAsnThrThrSerPheValValLeuLeuAlaAlaPheArgAlaAlaHisTyrAr 1364
Db 4510330 CGCGGACGACGACCGCGCTGATGCTGCTTCGCGCGCTTACAGAGCTGTCGCGCG 4510271
QY 1364 gLeuThrAlaValAlaGluAspAlaValIleGlyThrProIleAlaAsnArgAsnArgProG 1384
Db 4510270 CACACCGCGCGCGCGGACATGCCCGCTGCGACCGCGCTGCGCGCGCGCGCGCGCG 4510211
QY 1384 uLeuGluAspHisIleGlyCysPheValAsnThrGlnCysMetArgIleAsnIleAspHis 1404
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QY 1404 sHisAspThrPheGlyThrLeuIleAsnGlnValValAlaThrThrAlaAlaPheG 1424
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QY 1424 uAsnGluAspIleProPheGluArgValValSerAlaLeuGlnProGlySerArgAspLe 1444
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QY 1444 uSerSerThrProLeuAlaGlnLeuIlePheAlaValHisSerGlnLysAspLeuGlyAr 1464
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QY 1464 gPheLysPheGlnGlyLeuGluSerValProValProSerLysAla---TyrThrArgPr 1483
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QY 1483 eAspMetGluPheHisLeuPheGlnGlnThrAsp---SerLeuLysGlySerValAspPr 1502
Db 4509916 CGACCTGACCTCCAAATACGTAGAGGCGGAGCGGCTGTCGCGGCGGACCTGAGGTA 4509857
QY 1502 eAlaAspGlyLeuPheLysMetGluThrValGluAsnValAlaArgValPhePheGluI 1522
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QY 1522 eLeuArgAsnGlyLeuGlnSerSerArgThrProValSerIleLeuProLeuThrAsp 1542
Db 4509805 GCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4509746
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QY 1562 uSerSerLeuAlaAspValPheGlnThrGlnValSerAlaTyrProAspSerLeuAlaVa 1582
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QY 1582 lValAspSerSerCysArgLeuThrTyrGlnLysAspArgGlnSerAspIleLeuAl 1602

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 QY 1602 AGTCTPLeuArgArgArgSerMetProAlaGluThrLeuValAlaValPheAlaProAr 1622
 Db 4509565 CACGCCCTGATGCGAAGGGGGTCCGCCGAGAGCGCTGCGGGCTGAGCTGAGCG 4509506
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 QY 1662 oThrTrileValLeuTrileGluHisAspThrAlaProProAspTrileGluValThrAsnValG 1682
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 QY 1682 uPheValArgTrileArgAspAlaLeuAsnAspSerAsnAlaAspGlyPheGluValTrileG 1702
 Db 4509340 GCTGCTGCTCTC-----GACACGAGCGCGCGGACCTGGCGCGC 4509302
 QY 1702 uHisAspSerThrLysPro-----SerAlaThrSerLeuAlaTryleuTrile 1718
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 QY 1718 rThrSerGlySerThrGlyArgProGlyGlyValMetTrileGluHisArgValTrileAr 1738
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 QY 1807 sValThrSerSerSerGlnAspValProLeuArgValProArgTrileuSerArgTrile 1827
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 QY 1904 yTrileGlyValMetGlyGluLeuValValThrGlyAspGlyLeuAlaArgGlyTrileSerAs 1924
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 QY 2003 -----GluAspGlnAla----- 2006
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 QY 2007 -----ProGluTrileu-----GlyP 2012
 Db 4508323 CGGACGCTGCTGCTCCACTGGCGCGCGCTGCGCGGATACATGATCCCGCGCGTT 4508264
 QY 2012 eValValAlaAsp-----HisAspHisSerGluAsnAspLys----- 2024
 Db 4508263 GGTGCGCTTCGAGCGGCTGCTGCTGCTGACCAACAGCGCATGTCGACAGCGCGCTGCC 4508204
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 Db 4508184 -CTGCGGCGCGCGGACAGCTGCTGCGCGCGCGGACCGTGCAGAGAGAGAGTCCCGAGT 4508126
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 QY 2080 yGlu----- 2081
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 QY 2082 -ThrTrileArgThrLeuHisAspAsnArgSerLeuGlyAsnValLeuGluTrileGlyThrG 2101
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 QY 2101 ySer----- 2102
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 QY 2102 ----- 2102
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 QY 2103 -GlyMetTrileu-----PheAsnLeuAspSe 2111
 Db 4507825 CGGATGCTGTGAGATGTCTCAACGACGAGAGACCGGACCGGACCGGACCGGACCTTC 4507766
 QY 2111 r-----ArgLeuGluSerTrileValGlyLeuGluProSerArgSerAlaAlaPhe 2128
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 QY 2128 eVal-----AsnLysAlaThrGluSerTrileProSerLeuAlaGly----- 2141
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 QY 2142 -----LysAlaLysValGlnValGly----- 2148
 Db 4507645 CTTGCAATGCTGTCAACACGAGCGGAGATGCGGTGCGGCGGACCTGACTCCCT 4507586
 QY 2149 -----ThrAlaThrAspTrileGlyGlnVa 2156
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CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 33665
LENGTH: 10296
TYPE: DNA
ORGANISM: Pseudomonas syringae
US-10-282-122A-33665

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Alignment Scores:
Pred. No.: 3,06e-140 Length: 10296
Score: 1770.50 Matches: 732
Percent Similarity: 36.28% Conservative: 463
Best Local Similarity: 22.22% Mismatches: 1052
Query Match: 10.98% Indels: 1047
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US-09-482-788-2 (1-3129) x US-10-282-122A-33665 (1-10296)

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QY 84 ILeSerArpPheAlaLeuAlaTTrpLyGluIleValaGlnThrProAlaLeuAla 103
DB 187 ATCTTGAGCGCAGCCT-----AATGCCATCATCAGCGGCGTAAAGCGCTACGACC 240
QY 104 PheAlaPheThrSerArpSerGlyLyThrSerGlnValIleLeuLyAerSerPheVal 123
DB 241 ---TCATTTTCCTGGTAAAGATCTACCGTCGACAGTGAATCAGCGCGCGCTG 297
QY 124 Phe-----SerTrpMetCyeTrpSerSerSerSerSerProAerGluVal 138
DB 298 CTGATAGCGCTGTAAACTGGCGCGCTCTTGAACGAACTCACCTGCAACAGTTC 357
QY 139 ValArgAerGluAlaAla-----AlaAla 146
DB 358 ATGATGATAGAGCGCGCAGCCCTTGACCTGACGAGCGACACACATGATCCGCGCACA 417
QY 147 AlaSerGlyProArgCysAerAerPheValIleLeuGlnAerMetGlnThrLyAerCys 166
DB 418 GCCATCGAAGTCAAGCGCGCGTGAAGCATGCTCTGCTG----- 453
QY 167 GlnLeuValTrpThrPheSerHisAlaLeuValAerValThrPheGlnAerValLeu 186
DB 454 -----CTGACCTGATCATATGCTTGCAGATGCTGCTGCATAGCGTGTCTG 504
QY 187 SerArgValPheAlaAlaLyLyGlnIleAerThrHisAerProGluThrProGlu 206
DB 505 GACGAATCTAGTGGCTTACAGCGCGAGCTG----- 537
QY 207 SerSerAerAlaThrAerThrAerSerGlnSerValSerValAerMetSerCys--- 225

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DB 538 AACGGCTAGCCSCTGACCTTCAAGCGCTTGAATACATATGCSGACATGAGCGCTGTGG 597
QY 226 -----GluAerAlaValSerAlaThrHisPheTrpGlnThrHis 239
DB 598 CAAGGGAATGCTGCGAAGAGTCTGCAACACAGCTGATTTATGGAGATCGAC 657
QY 240 LeuAerAerPheAlaSerValPheProHisLeuSerAerHisLeuMetValProAer 259
DB 658 CTCAGGATGCG---CCAGCGTTCTTGAATGCTGCGCGAGCGG-----CCCCG 705
QY 260 ProThrThrThr-----AlaGlnHisArgIleThrPhe----- 270
DB 706 CCGTCAAGACTGCAATGCGGGGTAAACCGGGTCACTTCACTTCCCGCGCACTCGGA 765
QY 271 -----ProLeuSerGlnLy-----AlaLeuSerAerAlaIleCys 283
DB 766 GCGCAATCCGAGAACTCAACCCCAACGCAATGATGACGCTTGTCAAGACGCTGATGT 825
QY 284 ArgThrAlaLeuSerIleLeuLeuSerArgTrpThrHisAerAerGluAlaPheGly 303
DB 826 -----GCTTCAATAGCTGTGCTGCGCTTGAAGCAATGACCGCATCTGTATCGGG 879
QY 304 -----AlaValThrGlnAerLeuProPheAerHis 315
DB 880 TATCCGCTGCGCAATGCGCGCTGCGCAATGCAACCGCGTGTCTTCTGTCAC 939
QY 316 TyrLeuAla-----AerGlyThrTrpGlnThrValAlaProLeuAerValHis 331
DB 940 ACCCTGCTGCTGCGCACTGATGACAGCAACAGCATGCTTCCGCTTATCGCAACAG 999
QY 332 CysGlnSerAerAerAerAerAerAerAerAerAerAerAerAerAerAerAerAer 351
DB 1000 ACCCAATGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1041
QY 352 LeuGlyHisLeuAlaProPhe-----GlyLeuAerAerIleAerAerThr 366
DB 1042 -----CCGTTGCAAGACTGCTGAGCGCTTACCGCTGCGCGAGAGCTG 1086
QY 367 GYAspAerGlySerAlaAlaCysAerPheGlnThrValLeuLeu----- 381
DB 1087 -----AACCACTCGCGCTC-----TTTCAAGCTGCTGCTTCTTCTTCAACAGAC 1134
QY 382 ValThrAerGlySerHisValaAerAerGlyIleAerGlyPheLeuGlnIleThrGlu 401
DB 1135 CTGGCGGAGACTGACGCTGACGTGAGCAACCTCGCGCAGCTGAGCAAGTGGCGG 1194
QY 402 SerSerHisPheMetProCysAerAerAerAerAerAerAerAerAerAerAerAer 421
DB 1195 TTCTCGAAGTT-----GACCTGCTCTGGAATGAACACTCGCGCAACACAC 1242
QY 422 SerGlyAlaLeuLeu-----ValAlaTrpTyrAerHisAerValIleAerSerLeu 438
DB 1243 CTGGAGAGCTTCTTCAAGTACCGGACCGCGCTTATGACAGCGCAACATGTAACGATG 1302
QY 439 GlnThrThrArgLeuLeuGlnIlePheGlyHisLeuIleCysLeuGlnIleProLeu 458
DB 1303 AGT-----GGCTATATGCTGATATTAATGCAATCATGCTG 1338
QY 459 -----AerLeuSerMetAlaGluValAerLeuMetThrGluTrpAerAerAerGlu 476
DB 1339 GTGACACCACTCCCGTATCGCGGACCTGGAATTTTGGCCCTGACGAGAACGCTGTCC 1398
QY 477 IleGluSerTrpAerSerGlnProLeuGluVal-----GlnAerThrLeuIleHis 494
DB 1399 CGACTGCGACCGGACCGGACCGCTGCCACAGCTGATGATCAATGCTGCGACAGAT 1458
QY 495 GlnMetLeuAerAlaValSerHisAerProThrLyThrAlaIleGlnAlaTrpAerGly 514
DB 1459 CTGATTCTGACCAAGCGCGGCGGACCGCTGAGCGGCACTGATTTCTGCGCGGCGAG 1518
QY 515 AspTrpThrTyrSerGlnLeuAerAerAerAerAerAerAerAerAerAerAerAerAer 534

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Db	5536	ATTGGCAAGCGCTGTTCAACTCCAGATGTACGTTCTTCGACGCGCACTGTCAACCGGTT	5595
Qy	1904	GIyILleGIyValMeGIyGIuLeuValValThrGIyAerGIyLeuAlaAArgGIyTyrSer	1923
Db	5596	CCGGTCGGCGGTACAGAGTGATCTTAACTGCTGGCGCTTCACCTTGGCGCGCTGTACGG	5655
Qy	1924	AerYyValA---LeuAerGIuAenAArgPheValHisIleThValAenAerGIuThVal	1942
Db	5656	GAGCGTCCCGATATCATCTGCCGAACGTTTCGTT-----CCCAATCCCAACGCTC	5706
Qy	1943	-----LyValATyArgThrGIyAerAArgValArgTyArgIleGIyAerGIy	1958
Db	5707	TCCGCGGGCGCGCTGATGTACAAAGCCGCGTATGTCGGCGCTAT-----CTTCCGTATGGA	5763
Qy	1959	LeuILleGIuPhePheGIyATgMetAerThrGIuPheIyValAArgGIyAenAArgIleGIu	1978
Db	5764	AATATTCAGATATCTGGGGCGCGTCCGACCATGAGTCAAGATTCGCGCTTCAGATGAG	5823
Qy	1979	SerAlaGIuIleGIuAlaLeuLeuAArgAerSerSerValAArgAerAlaValVal	1998
Db	5824	CTGGCCCGAGGTGCAACAGCACTATAGGCCACGAAGAACGGTGGCAAGCGCGCGCATG	5883
Qy	1999	LeuGIuGIuAenGIuAerGIuAlAerGIuIleLeuGIyPheValAlaAerPheAer	2018
Db	5884	GTCCGGGAAGACCGTCCAGCGGCTGAADAAGCTGGTGGTTATCTGAGTC-----	5931
Qy	2019	HisSerGIuAenAerLyGIuGIuSerAlAenGIuValGIuGIyTTPGIuAerPhe	2038
Db	5931	-----	5931
Qy	2039	GIuSerGIuMetYrSerAerPheIleGIyGIuIleAerProSerThrIleGIySerAerPhe	2058
Db	5931	-----	5931
Qy	2059	LyAerGIyTTPThrSerMetYrAerGIySerGIuIleAerPheAerGIuMetHisIleTTP	2078
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Qy	2079	LeuGIyGIuThrThrArgThrLeuHisAerAArgSerIleuGIyAenValLeuGIuIle	2098
Db	5931	-----	5931
Qy	2099	GIyThrGIySerGIuMetIleLeuPheAenLeuAerSerAArgLeuGIuSerTyValGIy	2118
Db	5931	-----	5931
Qy	2119	LeuGIuProSerAArgSerAlaAlaAerPheValAenLyAlaThrGIuSerIleProSer	2138
Db	5931	-----	5931
Qy	2139	LeuAlaGIyValAlyValGIuValGIyThrAlaThrAerPheIleGIyGIuValAAspAer	2158
Db	5931	-----	5931
Qy	2159	LeuHisProAerPheValValLeuAenSerValIleGIuTyTrPheProSerSerGIuTy	2178
Db	5931	-----	5931
Qy	2179	LeuAlaGIuIleAlaAerThrLeuIleHisAerProAenValGIuAArgIlePhePheGIy	2198
Db	5931	-----	5931
Qy	2199	AerValAArgSerGIuAlaThrAAsnGIuHisPhePheLeuAlaAArgAlaIleHisThrLeu	2218
Db	5931	-----	5931
Qy	2219	GIyLyAAsnAlaThrLyAerAerValAArgGIuLyMetAlaGIuLeuGIuAerMetGIu	2238
Db	5931	-----	5931

QY	2239	GlutIuLeuLeuValIGluProAlaPhePheThrSerLeuLysAspArgPheProGlyLeu	2258
Db	5931	-----	5931
QY	2259	ValGluHisValGluIleLeuProLysAsnMetGluAlaValAsnGluLeuSerAlaTyr	2278
Db	5931	-----	5931
QY	2279	ArgTyrAlaAlaValAlaHisValArgGlySerLeuGlyAspGluLeuValLeuProVal	2298
Db	5931	-----	5931
QY	2299	GluLysAspAspTyrPileAspPheGlnAlaAsnGlnLeuAsnGlnLysSerLeuGlyAsp	2318
Db	5931	-----	5931
QY	2319	LeuLeuLysSerSerAspAlaAlaIleMetAlaValSerLysIleProPheGluIleThr	2338
Db	5931	-----	5931
QY	2339	AlaPheGluArgGlnValAlaAlaSerLeuAsnSerAsnIleAspGluTyrPnLeuSer	2358
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Db	5932	-----GCCAAAAGCGACTGCGCTGAACATC-----	5958
QY	2379	AlaGluGlyAlaGlyPheArgValGluValSerSerAlaArgGlnTyrPserGlnAsnGly	2398
Db	5958	-----	5958
QY	2399	AlaLeuAspAlaValAlaPheHisIleGlyCysSerGlnGlyArgThrLeuValAsnPhePro	2418
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QY	2419	ThrAspHisHisLeuArgGlySerAspLeuLeuThrAsnArgProLeuGlnArgLeuGln	2438
Db	5958	-----	5958
QY	2439	AsnArgAlaGluIleAlaIleGluValAlaArgGluArgLeuArgSerLeuLeuProSerTyrMet	2458
Db	5959	-----GTGGACATCAAGGACATCTGGCAGCAGCAAGCGCTGCCGATTACATG	6003
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Db	6004	GTGGCGACACCACTTCGTATCTCTGGCCAGCCCTGGACCCCAAGTGGGAAAGTGCAC	6053
QY	2479	ArgLysGluLeuSerArgArgAlaLysValAlaProLysGlnGlnThrAlaAlaProLeu	2498
Db	6064	AAAGCC-----	6065
QY	2499	ProThrPheProLieserGluValGluValIleLeuCysGluGluAlaThrGluValPhe	2518
Db	6069	-----	6069
QY	2519	GlyMetLysValAspPileThrAspHisPhePheAsnLeuGlyGluHisSerLeuLeuAla	2538
Db	6069	-----	6068
QY	2539	ThrLysLeuLieserArgIleAspGlnArgLeuLysValAlaArgIleThrValLysAspVal	2558
Db	6069	-----	6069
QY	2559	PheAspHisProValPheAlaAspLeuAlaSerValIleArgGlnGlyLeuGln	2578
Db	6070	-----TTCGTGCCG-----	6078
QY	2579	GlnProValSerAspGlyGlnGlyGlnAspArgSerAlaHisMetAlaProArgThrGlu	2598
Db	6079	CAGCGGAAACGACACACAC-----GAAATCATATGTTGGCCCCCGAGAGCGAC	6129

QY 2599 ThrGlnAlaIleuCyAaerGluPheAlaIyValIeuGlyPhe---GlnValIyIle 2617
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 QY 2618 ThrAspAsnIlePhePheArgGlyGlyHisSerIleuMetAlaThrIySleAlaIValArg 2637
 Db 6190 ACCGATACCTCTTGCAGACTGTGGGCACTTTGTCTGCACATCAGTGTGTTTCCGCT 6249
 QY 2638 IleGlyHisArgIleuAspThrThrValSerValIyAspValPheAsnIleProValIle 2657
 Db 6250 ATTGGCAACAGCGATGTGCATATGCGCTGGCAACCTGTTGAAGCCGCAACATC 6309
 QY 2658 PheGlnIleu-----AlaIleAlaIleuAspAsnIleValGln 2669
 Db 6310 GAACAAATGTCTCGCCGCTGAGCACAAGCCGCGTATGACCTGTGACGATCATCTGCC 6369
 QY 2670 SerIyThrAsnGluIleValIyGlyArgGluMetIleAlaIyIySerProPheGlnIleu 2689
 Db 6370 ACCAACCAGCGC-----TCCGGCATGAAGTCTGCTCTATGCGCCAAAGCGTCTG 6420
 QY 2690 LeuPheThrGluAsp---ProGluGluPheMetAlaSerGluIleIyProGlnIleuGlu 2708
 Db 6421 TTCTTCTGATGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 6480
 QY 2709 LeuGlnGluIleIleGlnAspIleIyIyProSerThrGlnMetGlnIyValIlePheIleuPhe 2728
 Db 6481 CTG----- 6483
 QY 2729 AspHisThrThrAlaArgProArgProPheValIleProPheIyIleAspPheProSerThr 2748
 Db 6483 ----- 6483
 QY 2749 SerGluProAspAlaIleGlyIleuIleIyValIeCys---GlnSerIleuValAsnHisIleu 2767
 Db 6484 AAGGCGCGCTGAAGAAAGCGGCTGTGACGATGCTGACGATGCTGATGCTGATGCTGAC 6543
 QY 2768 AspIlePheArgThrValPheAla---GlnAlaSerGluIleuIyIyGlnIleValIle 2785
 Db 6544 GAACCCCTGCGCAGCATTCGCTTGCAGGAGACGCGGAGTGTGAGTGTGAGTGTGATCAT 6603
 QY 2786 -----LeuSerCylAspAspIleuProIleGlnValIleGluIleIyIleGlu 2799
 Db 6604 CCCCCGAGCTCGATACGCTGATCTCTGATTTGCGC-----CATACCGCT 6651
 QY 2800 AspAsnIleAsnThrAlaThrAsnGluPheIleuAspGlu-----PheAlaIy 2815
 Db 6652 CAGCCGCTGCGGCTGGAAGAAAGCGTATGCGATGCTGATGCTGATGCTGATGCTGATG 6711
 QY 2816 GluProValArgIleuGlyHisProIleuIleArgPheThrIleIleIyGlnIleIySer 2835
 Db 6712 GAAGACC-----GGTCCCTGCTGAGTCTCTGCTGCGAGTGTGCGGAGCAG 6759
 QY 2836 MetArgValIleMet---ArgIleSerHisAlaIleuIyAspArgIyIleuSerIleuGlnHis 2854
 Db 6760 CACCAATATCTGCTTTACCGGATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 6819
 QY 2855 ValValArgIyIleuHisMetIyIyAsnGly-----ArgSerIleuIy 2869
 Db 6820 CTACCGCGAGATCATGCGGCTTACCAAGCGTTTGCACAGACGAGCATCATCGCTTG 6879
 QY 2870 ProProHisGlnPheSerArgIyIyMetGlnIyThrAlaAspArgIyIyGlu----- 2886
 Db 6880 CCGCTCTGGAATC---CAGTACAGCGATCATCGCTTGTGCGAGCTGTGATCAAGGCC 6936
 QY 2887 -----SerGlyHisGlyPheThrArgAspValIleGlnAsnThrProMet 2901
 Db 6937 CCAAGCGTTTTCAGCGAGGCTGCTGCTGCTGCGCAGCAGCGATCATCGAGCCTGCC 6996
 QY 2902 ThrIle---LeuSerAspAsp-----ThrValIleAspArgIyIyAsp 2914
 Db 6997 CGGCTGAGGCTGCGAGCAGCAGCGCGCTGCGCGATTCAGACGCTTACAGGCTGAGGCC 7056
 QY 2915 AlaThrCylAspAlaIleuHis-----LeuSerIyIleValIleAsnIlePro 2929

Db 7057 GTTACC-----CATACATGCGCCCCAACCTGTCCAGAGATCGATCATCTTG 7104
 QY 2930 SerGlnValIleuArgIyIySerAsnIleIleThrGlnAlaThrValPheAlaIVal 2949
 Db 7105 AGCCAAAGCTTG---GGGATGACACCGCTTATGATGATGCTGCTGCTGCTGCTGCTG 7152
 QY 2950 CysAlaIleuValIleuSerArgIyIySerAspSerIyAspValIlePheGlyArgIyIleVal 2969
 Db 7153 ---AGTCTGCTGAGCGCGGACAGCGGCGACGCGATGATGCTGCGGAGCGCCATC 7209
 QY 2970 SerGlyArgGlnIleuProValIyIyGluIleAspIleValIyIyProCysIleIyAspAla 2989
 Db 7210 GCCAACCGGACCCGAAACCGAGTGTGAA-----CCCTGATGAGCTGTGCTGCAACAG 7263
 QY 2990 ValProValArgAlaHisIleGluSer---AspIyAsnGlnIleuHisAspIle 3008
 Db 7264 CTGGACCTGCGCAGCAGCATTTGAAGGACACCCGATGCTGCGCATTTATTCGAACAGCTC 7233
 QY 3009 GlnAspGlnIyIleuSerIleuProIleGluIleIyIleIyPheSer----- 3024
 Db 7324 AGGAACACCACTCGCGCTTATGCGCCACCAAGACTGCGGTTGCAAAAAGTGTGAA 7283
 QY 3025 -----AspIleuIyAspGlyIyIleIyAspIyIyProGluAlaIleIyIyAspSerCys 3042
 Db 7384 GCGCTGATACGCTCGGACGATGATGCTGCA-----CTGTTCCAGCTG 7431
 QY 3043 CysIleThrIyIleAspPheGluIyIyIleProGluSer-----GlnPheGluGlnIle 3060
 Db 7432 ATGTTTGTCTACAGAACAGCGGCGCGGACCTGTAATAATTCGAGCGTGCAGTCCG 7491
 QY 7492 ATCTTCGATCGGAGCACACAG-----GCCAAATTC 7524
 Db 3061 ArgValGluMetGlyValIleuThrIyPheValAsnIleGluMetAspGluProIleuIy 3080
 QY 3081 AspIleuAlaIleAlaGlyIleuIyIyProAspGlyIyIyIleuIyIyValIleIle 3100
 Db 7525 GACTTGAGCTG-----GAGCTGAGCGCCGACGCTGCGAGGCTGATGATGATGAGTGGAA 7578
 QY 3101 AlaIyThrGlnIleuPheGlyArgIyIyValIleIyIle 3114
 Db 7579 TACAACCTGCGACCTGTTTCAGCGCAGCAGCATTTGAAGCGCTG 7620

RESULT 13
 US-10-282-122A-33846
 : Sequence 33846, Application US/10282122A
 : Publication No. US20040029129A1
 : GENERAL INFORMATION:
 : APPLICANT: Wang, Liangsu
 : APPLICANT: Zamudio, Carlos
 : APPLICANT: Malone, Cheryl
 : APPLICANT: Haselbeck, Robert
 : APPLICANT: Ohlsen, Karl
 : APPLICANT: Zyskind, Judith
 : APPLICANT: Wall, Daniel
 : APPLICANT: Trawick, John
 : APPLICANT: Carr, Grant
 : APPLICANT: Yamamoto, Robert
 : APPLICANT: Foreyth, R.
 : TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 : FILE REFERENCE: ELITRA.034A
 : CURRENT APPLICATION NUMBER: US/10/282,122A
 : CURRENT FILING DATE: 2003-02-20
 : PRIOR APPLICATION NUMBER: 60/191,078
 : PRIOR FILING DATE: 2000-03-21
 : PRIOR APPLICATION NUMBER: 60/206,848
 : PRIOR FILING DATE: 2000-05-23
 : PRIOR APPLICATION NUMBER: 60/207,727
 : PRIOR FILING DATE: 2000-05-26
 : PRIOR APPLICATION NUMBER: 60/230,335
 : PRIOR FILING DATE: 2000-09-06
 : PRIOR APPLICATION NUMBER: 60/230,347

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; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33846
; LENGTH: 6288
; TYPE: DNA
; ORGANISM: Pseudomonas syringae
; US-10-282-122A-33846

Alignment Scores:
Pred. No.: 5.57e-139      Length: 6288
Score: 1752.00           Matches: 591
Percent Similarity: 44.30%      Conservative: 338
Best Local Similarity: 28.18%      Mismatches: 849
Query Match: 10.86%           Indels: 321
DB: 16                      Gaps: 65

US-09-482-788-2 (1-3129) x US-10-282-122A-33846 (1-6288)
QY 39 TYRGILeuaspserArgIleGluAlaIleLysPro-----CysThrProPhe 55
DB 161 TAGGGCTGGCTGTTCC---ATGAGGCGATATAGCAGGAGGAGGCTGTCATCTG 217
QY 56 GlnLeuaspMetIleaspCysasnAlaLeuaspLysGlnSerAlaIleGlyHisAlaVal 75
DB 218 TCGATATCA-----GACTCGCATCTGTCGATTTTCAGACTACG 256
QY 76 TyrAspValProThrAspIleaspIleSerArgPheAlaLeuAlaTyrLysGluIleVal 95
DB 257 TTGACAGTGTGCGAGCGAG---CGCTGGAATACCTTCAAC 292
QY 96 AsnGlnThrProAlaLeuArgAla-----PheAlaPheThrSerAspSer 110
DB 293 AATCATTTTCCGACCGTTCATCCCTTGGAAGGCATCTTTGGAGAGTCGACGCTGTAC 352
QY 111 GlyLysThrSerGlnValIleLeu-----LysAspSerPheValPheSerTrpMet-- 127
DB 353 GGTGCAATGCATCCCATCTACTGCTGGGCGGTCGCATCTTTGTCATGATGCGG 412
QY 128 -----CysTrpSerSer 131
DB 413 CAGGGGTAAAGCTGTTCTGCGATGAGTGAAGAAAGCTCAATATTGTGGCGGGCA 472
QY 132 SerSerSerProAspGlu-----ValValArgAspGluAlaAla 144
DB 473 TCGACGACGCTC-GAGGAAGCCCTTCTTACAGACACTTCTGTATCAAGACAAAGCCTAT 531
QY 145 AlaAlaAlaSerGlyProArgCysAsnArgPheValIleuLeuGluAspMetGlnThrLys 164
DB 532 CTGAGTTGCTGCGG-CCTGAGCGCGGACGAGGCGTTTGGCGGAAACGCTATACACA--- 587
QY 165 LysCysGlnLeuValTyrThrPheSerHisAlaLeuValAspValThrPheGlnGlnArg 184
DB 587 ----- 587
QY 185 ValLeuSerArgValPheAlaAlaTyrLysHisGluLysAspThrHisArgProGluThr 204
DB 587 ----- 587
QY 205 ProGluSerSerAspAlaThrAspThrAspSerGlnSerValSerValIleSerMetSer 224
DB 588 -----ACTGCGCGCACCTCTGCTGACAGTGTCCGCGCATCA 623

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QY 225 CysGlu-AspAsnAlaValSerAlaThrHisPheTrpGlnThrHisLeuAsnAspLeu-- 243
DB 624 TGCCTGGGTTTCATGTGCAAGAGCGGCTATATTCGTCGACGATTAAGGTCGCTGT 683
QY 244 -AsnAlaSerValPheProHisIleuSerAspHisIleuMetValProAsnProThrThr 263
DB 684 CAATGCCCTGTGCT-----GCCGTTC 704
QY 263 rAlaGlnHisArgIleThrPheProLeuSerGlnLysAlaLeuSerAsnSerAlaIleCys 283
DB 705 CACCGAGCAT-----GACCTTCTCTCTGCGGATATT 737
QY 283 sArgThrAlaLeuSerIleLeuLeuSerArgTyrThrHisSerAspGluAlaLeuPheG1 303
DB 738 CTTCGCCCGCTGAGCGGCTATTTTACCGTTGCGATGCTGAGAGGTCATCATCGG 797
QY 303 yAlaValThrGluHisLeuProPheAspLysHisTyrLeuAla----- 318
DB 798 C-----ATGCCCTGTCATAACCGCAGCAGCGCTGTGCAAAAAAGAC 839
QY 319 -AspGlyThrTyrGlnThrValAlaProLeuArgValHisCysGlnSerLysLeuArgAl 338
DB 840 GATCGGATGTGTTTCTTCCGTTATTCGATGCGGCGTACCGGTCACCCATGCTGCTCT 899
QY 338 aserAspValMetAspAlaIleSerSerTyrAspAspArg----- 351
DB 900 GCTCGAATTGATGGCATATGCGCCGCGCAATTCGACGCTGTACCCCATAGCATTT 959
QY 352 -----LeuGlyHisIleuAlaProPheGlyLeuArg 361
DB 960 TCCAAATCGGAACTGAATGCGCCCTCAATATTGGCATTTCCAGCGCAAGCATCTT 1019
QY 361 gAspIleArgAsnThrGlyAspAsnGlySerAlaAlaCysAspPheGlnThrValLeuLe 381
DB 1020 CGATATCAGCTTTCATTCGAAAATTGACGG-----GACTTT- 1059
QY 381 uValThrAspGlySerHisValAsnAsnGlyIleAsnGlyPheLeuGlnGlnIleThrG1 401
DB 1060 -ATCTTTGGCGGCTCCCTCGG-----CAGCGCATCAGAT 1094
QY 401 uSerSerHisPheMetProCysAsnAsnArgAlaLeuLeuLeuHisCysGlnMetGluSe 421
DB 1095 GTACAGCGGCTTC-----GATCAGACGCCACT 1121
QY 421 rSerGlyAlaLeuLeuValAlaTyrTyrAspHisAsnValIle----- 435
DB 1122 CTCAATCGCTATCTGCGATTACTTCAACGATGACATTGTGTTGACTTTAACTTCAA 1181
QY 436 -----AspSerLeuGlnThrThrArgLeuLeuGlnGlnPheGlnGlyHis 449
DB 1182 TGTGACCTGTTTGGCCAGACGAAATTGAA-----CGAATTCGGAGCCGCTTACGCT 1235
QY 449 sLeuIleLysCysLeuGlnSerProLeuAspLeuSerSerMetAlaGluValAsnLeuMe 469
DB 1236 GCTCTCGTAAG---TTGGTTCCCGCTATAGTCAACACGATTAAGCAGCTTGCGCTGAT 1292
QY 469 cThrGluTyrAspArgAlaGluIle---GluSerTrpAsnSer-----GlnProLeuG1 486
DB 1293 GGGCGAAACCGACGCGCGGCAAGGCTCTGCGAGTTCAACGAAACATAGAGCATTTGCA 1352
QY 486 uValGlnAspThrLeuIleHisIleGluMetLeuLysValValSerHisSerProThrLys 506
DB 1353 G---CAGGATCTATTGCTCATGACGCTTTTTCGAACACGACGAGCGACGCTCAAGC 1409
QY 506 sThrAlaIleGlnAlaIleTrpAspGlyAspTrpThrTyrSerGlyLeuAspAsnValSerSe 526
DB 1410 GCTTGACACTGTGTGGCGGACGAGGTGTGACTTACGCGGACCTCAAGACGACCAAG 1469
QY 526 rArgLeuAlaValHisIleLysSerLeuGlyLeuArgAlaGlnGlnAlaIleIleProVa 546
DB 1470 CCAAGTGGCTCATGTCTTGTCTGTCATGCGGCAATTGTTGCCAGACGCGC---GTGGGAT 1526

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Db 3519 TGTGCTGCTGTTGACCATGCACCATCGTATCGATGCTGTCGATGGGCACTTTTGAC 3578
Qy 1249 gATgAspLeuAenGlnLeuTyrSerAlaAlaLeuLysAspSerLysAspProLeuSerAl 1269
Db 3579 GCGCGAGTTGGAGCGCTCTACCGGAGCGGTTCGCAAGATGAGGACGCGC----- 3630
Qy 1269 aLeuThrProLeuProIleGlnTyrSerAspPheAlaLysTrpGlnLysAspGlnPheAl 1289
Db 3631 -TTGCGCGCGCTTGTATTGATACGCGGACCTACGCAATGTGGCAACGAACTGGTTGAG 3689
Qy 1289 egluGln-----GlnLysGlnLeuLysnTyrTrpLysGlnLeuLysAspSerPr 1307
Db 3690 CGCGGAGATTCACACAGCAAGCACTTACTGCGGACGCGCTCTGCTCAT---GCGCC 3746
Qy 1307 oAla-----LysIleProThrAspPheAlaArgProAlaLeuLeuSerLysAspAlaG 1325
Db 3747 GGCATTGCTGATGTTCGCGCTACCGCTGATCGTCCGCAACAGGACTATACGGGTGC 3806
Qy 1325 yCyValHisValThrIleAspGlnLeuLysTrpGlnSerLeuArgAlaPheCyAsnGln 1345
Db 3807 GTCCGTAAGCTGTGCTGCTGATGCGACCGTGCAGCAATGACCTCAAGACGTGAGTGGCG 3866
Qy 1345 whIsanThrThrSerPheValIleLeuLeuAlaAlaPheArgAlaAlaHisTyrArgLe 1365
Db 3867 GCACGGCACCACTCTTTTCATGACACTACGCGCGGCTGGCAACGGTATTGAGTCTTT 3926
Qy 1365 uThrAlaValGlnAspAlaValIleGlnThrProIleAlaAsnArgAsnArgProGlnLe 1385
Db 3927 GTACGGGACAGATGAGGTGTATCGGTTCGCGGTGCGAACCGGATGACCGCGAGGT 3986
Qy 1385 uGlnAspIleIleGlnCyAspValAsnThrGlnCysMetArgIleAsnIleAspHisAl 1405
Db 3987 CGAGGGCCGTGATGGTTTTTTTTCGCAACACCTGCGCTTCCGGTATGTGTACAGCGA 4046
Qy 1405 sAspThrPheGlnThrLeuIleAsnGlnValLysAlaThrThrAlaAlaPheGlnAs 1425
Db 4047 CCGGACGGTGCAGGCACTTGTGAGTGCAGTCAAGGCTTCGACCGTGGCGCGATGAA 4106
Qy 1425 nGlnAspIleProPheGlnArgValIleSerAlaLeuGlnProGlnSerArgAspLeuSe 1445
Db 4107 CCGAGATCTGCTTCGAGGAGGTGTGAGTGTCTCAACCG---GTGGCGACGTTGTC 4163
Qy 1445 rSerThrProLeuAlaGlnLeuIlePheAlaValHisSerGlnLysAspLeuGlnArgPh 1465
Db 4164 CCATACCCCGCTTTCAGGCGGATGCTGTCTGGCAGAAACATG---CCGACGGCGGAAT 4220
Qy 1465 eLysPheGlnGlnLysLeuSerValProValProSerLysAla---TyrThrArgPheAs 1484
Db 4221 CCGGATTCGACGGGCTGGAGCTGACGCTGATTCGATTCGTAAGCAGCACCAAGTACGA 4280
Qy 1484 pMetGlnPheHisLeuPheGlnGlnLysThrAspSerLeuLysGlnSerValAsnPheAlaAs 1504
Db 4281 TGTGTGCTGCACTTGGCGGAGGTAGAGGCGCGATGTGCGTTCGCTGAAATATGGAC 4340
Qy 1504 pGlnLeuPheLysMetGlnThrValGlnAsnValIleArgValPhePheGlnIleLeuArg 1524
Db 4341 GCGGCTTTCGACAGACATACGCGGCAACACTAGTGGCGATTCGAAACGGGTGCTGG 4400
Qy 1524 gAsnGlnLysLeuGlnSerSerArgThrProValSerIleLeuProLeuThrAspGlnLysLe 1544
Db 4401 TCGCAATGTGAGAACGAGCGGCGGAGTTCGAGGCGATCAAGCTTTGGGCGGAACGGA 4460
Qy 1544 lThrLeuGlnLysLeuAspValIleuAsnValLysHisValAspTyrProArgGlnSerSe 1564
Db 4461 ACGCCGCAAGTACTGTTCAGATTCAACGCAACACACAGCGCTTCGCAAGGATTTAT 4520
Qy 1564 rLeuAlaAspValPheGlnThrGlnValSerAlaTyrProAspSerLeuAlaValIleAs 1584
Db 4521 GCTTCATACGCTTTTTCGAAACAGACGAGCGACGACGACCGCGCTTGGCGTGGATG 4580
Qy 1584 pSerSerCyAspGlnLeuThrTyrThrGlnLeuAspArgGlnSerAspIleLeuAlaGlnLys 1604
Db 4581 CCGCGACGAACGAGTGAACGCGCATTCACAAACGCAATATCAGGTTGCTCATGT 4640

Qy 1604 pLeuArgArgSerMetProIleGlnThrLeuValAlaValPheAlaProArgSerCy 1624
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Qy 1624 sGlnThrIleValAlaPhePheGlnValLeuLysAlaAsnLeuAlaTyrLeuProLeuAs 1644
Db 4701 GGAATGTGTGTGGCTTGTGGGATCTGAAGGTGGCGGTGCATATGTGCGCTGGA 4760
Qy 1644 pValArgSerProSerAlaArgValGlnAspIleLeuSerGlnLysSerGlnProThrIle 1664
Db 4761 CCTGTGGTATCCCTGGAGCGGTGTTCATGCTGGAGGAC---AGCGCGCGGTGGC 4817
Qy 1664 eValLeuIleGlnLysHisThrAlaProProAspIleGlnValThrAsnValGlnPheVal 1684
Db 4818 GGTCTGTGTACCGCCGAACCCG-----GACTGTGGGTGGCGGTGGTGC 4865
Qy 1684 lArgIleArgAspAlaLeuAsnAspSerAsnAlaAspGlnPheGlnValIleGlnHisAs 1704
Db 4866 GTGGCGATCCGATGCTGTGATCTGCMAAGCGCAACTGGCGCGCTGAAGCTGACATGA 4925
Qy 1704 pSerThrLysProSerAlaThr-----SerLeuAlaTyrValLeuTyrThrSerGlnSe 1722
Db 4926 TCCGCTGTTCGACGCGTCAAGCAGCAGCACTGGCTTATGTATCTATCTCGGATTC 4985
Qy 1722 rThrGlnArgProLysGlnValMetIleGlnHisArgValIleIle---ArgThrValTh 1741
Db 4986 GACCGGACCGCAAGGCGCTGATGATGACATTTGGCCATTTGTGAACCGCTGTATG 5045
Qy 1741 rSerGlnCyAspIleProAsnTyrProSerGlnThrArgMetAlaHisMetAlaThrIleAl 1761
Db 5046 GCGGACGACCACTATGCGTGAAGTGCAGAACCGCTTCTGCAAGAACACCGTTGCG 5105
Qy 1761 aPheAspGlnLysSerTyrGlnLysThrSerAlaLeuLeuPheGlnLysArgThrLeuValCy 1781
Db 5106 GTTTCAGTGTGCGTCTGGGAGTTTTCCTTCCTGCTGCGCGGTGGCAATGGTGTAT 5165
Qy 1781 sValAspTyrMetThrThrLeuAspAlaArgAlaLeuLysAspValPhePheArgGlnHis 1801
Db 5166 CGCAGCTCCGCGAGCGCATGACGACCCCGAGTATCTGGCGGAGTTATCCGAGCTGGCG 5225
Qy 1801 sValAsnAlaAlaSerHisValThrSerSerSerGlnAspValProLeuArgValProAr 1821
Db 5226 AGTGAAGATTTGCATTTGTATTCCTTCATGTTGCAAGCTTCCTCATGACAGTTGGCCC 5285
Qy 1821 gArgLeuSerArgThrLeuMetPhePhePheLeuValValThrAspSerThrAlaProAs 1841
Db 5286 GCTGCGATGTAGCAATTTGGCGAGGTGTC-----TGTAGCGCGAGGCGTTGCCCTA 5339
Qy 1841 pAlaLeuAspAla-----GlnGlnLysTyrGlnGlnValIleGlnCyAspThrAsnGlnLys 1859
Db 5340 TAGTTTGCAAAAGCACTTCGAGCAACGCTTGGCGCATGTGCATTCGATTAACCTGTATGG 5399
Qy 1859 yProThrGlnLysGlnLysValMetSerThrIleTyrPro---IleAspSerThrLeuSerPh 1878
Db 5400 CCTTACTGAAGCGCGTGTGCAACGTCACTTCTGCACTGGGTGGCGGACCTGACATACGGG 5459
Qy 1878 eIleAsnGlnValProIleGlnArgAlaLeuAsnAsnSerGlnAlaTyrValValAspPr 1898
Db 5460 GATC-----GTGCGGATTTGGCGGCGCGCTGCGCAAAACCGGCTGTATCTGTGGACCC 5513
Qy 1898 oGlnGlnGlnLeuValGlnLysValMetGlnGlnLeuValValThrGlnAspGlnLysLe 1918
Db 5514 GCATATGCAACCGGTCTCCGCTGGCTGGCGGAGATTTTACATCGCGGATATACAGCT 5573
Qy 1918 uAlaArgGlnTyrSerAspLys---AlaLeuAspGlnAsnArgPheValHisIleThrVal 1937
Db 5574 GCGTCCGGCTATTTGAATGTGATGCGTACCGCGGACGATTCGTGAAGACCGTTT 5633
Qy 1937 l---AsnAspGlnThrValLysAlaTyrArgThrGlnLysAspArgValArgTyrArgIleG 1956
Db 5634 CAGTAAACGCCGACGCGCGGATGTATAGAGCGGCGATCTGGGCGTTGG---CTGGC 5690

QY 500 valserhiserprothrlythrlyalleglnalatrpsgllyasprthrlyrser 519
DB 4297 GTGAAAAAACACAGTAATAATGGCGTCTTTTGGTAATAAATCCCTAACGATACAG 4356
QY 520 Gluleuaphanvalserisargleualvalhisilelyserleuglyleualgala 539
DB 4357 CAACGTGACACAGAGCTAATCACTAGCGCTATTACAAAACATAGAGAGTGCAGCA 4416
QY 540 Glnglnalalietleprovaltyrpheglulyserserlystrvalilealsersmetleu 559
DB 4417 GAAACAGAGA---GTAGAAATTGGCTGGATCGCTCTTAGAAATGTAATCTCCCTATT 4473
QY 560 AlaValleulysergllyasnalaphethrleuileasproasaproproalaarg 579
DB 4474 GCAGTTCACAAAGCCGGCGGTGTACGTTCCCTGCAGCCCGGCTATCCCAAGACGCT 4533
QY 580 Thralaglnalvalthrlnthrargalathrvalalaleuthrser----- 595
DB 4534 TTACAGTTTATATCAACAGACTCAAAATCTCAATCTTATTAATCTCAAACTTCCTTATTA 4593
QY 596 -----LyleuHisargluThrValGlnLylVal 606
DB 4594 AACACCTCCCACTATAGAAATAGCATTAATAAACCTTTAAACTCTCTCTGC 4653
QY 607 GlyArgCyvalvalvalaAspAspGluLeuGlnSerValSerAlasAspAspPhe 626
DB 4654 GCCTGCGCGCTGCTGCTGAATAATAATCATCCCACTCATCCAGCAACCGAANAACC 4713
QY 627 SerSerleuthrlyserglinaAspLeuAlaTyrrValilephethrsergllyserthgly 646
DB 4714 AATGATTATATCAACACCCCAATCAACTCGCTACTAATTTACACTCGGTTCAACCGGA 4773
QY 647 AspProlysergllyleuileglnhisargAlaPheSerSerCyvalaleuLylPheGly 666
DB 4774 ACACCCAAAGCGCGCAAAATTTGCACAGAGCTTAAGCAACTTTTAACCGCAATGCC 4833
QY 667 AlaserleuGlyleasnerAspThrArgAlaleuGlnPheGlyThrHisAlaPheGly 686
DB 4834 AAGGACACAGACTCAACAGCAAGATACCTTTACTGTCACACCTAGACCTTTGAT 4893
QY 687 AlaCylleuleuGlnleuethrThrLeuileasnGlyCyvalCys----- 703
DB 4894 ATTGCAGCTTAAAGATTCTTACCTTAATGTCGCTGCTGTTAGCTTATAGTAGAA 4953
QY 704 -----IleProserAspAspArgMetAsnSerIleProserPheIleAsnArgTyr 721
DB 4954 AGGGAAGTCACTCTAGTGAAGAGAGA-----TTAGCAACAGCGATGCACAACT 5004
QY 722 AsnValAsnTrpMetCalaThrProser-----TyrMetGlyThr 735
DB 5005 CAATATCCTTTATGCAAGCAACCCCAAGCACTTGGCGGTACTTTAGCCAGTGTGG 5064
QY 736 PheSerProGluAspValPro-----GlyLeuAlaThrLeuValLleuValGly 751
DB 5065 GAAGGTAAACAGACTGAATAATCTCTGCGCGGCAAGCATTAAGTAACACCTAGCC 5124
QY 752 GluGlnMetSerSerValAsnAlaIleThrAlaProLylLeuGlnLeuLeuAsnGly 771
DB 5125 CAACAAATTAATATCTCTACTCAAGAACTCG-----AACTTA 5163
QY 772 TyrglGlnSerGlnSerSerIleCysPheAlasSerAsnMetSer---ThrGluPro 790
DB 5164 TAGGACCAACAGAAACACCATTTGGTCAGCAGCCCAAAAACCTCATATGATGAACCC 5223
QY 791 AsnAsnMetGlyArgAlaVal---GlyAlaHisSerTrpValileasProAsnAspIle 809
DB 5224 GTAAACATCGGTATCCATCGCAACACCAATTTAAGTCCGCAAGACAT----- 5277
QY 810 AsnArgLeuValProIleGlyAlaValGlyGluLeuValileGlnSerProGlyLylAla 829
DB 5278 TTACAAACCAATCCCAATCGCGTAACCAAGAAATTAATATATGTGTGTGACGAGGTGCC 5337
QY 830 ArgAspTyrIleValProProProGluLylSerProPhePhe-----Thr 845

DB 5338 AAAAGATATGGCAACCTCCAGACTTAACAGAGAAAGATTTCATCAATCACTCAACA 5397
QY 846 AspIleProserTrpTyrProAlaAsnThrPheProAspGlyAlaLylLeuTyrArgThr 865
DB 5398 GTCAACAGTCACACAGTCAACAGTCACACAC-----TTATATTAACA 5439
QY 866 GlyAspLeuAlaArgTyrAlaSerAspGlySerIleValCylleuGlyArgIleAspSer 885
DB 5440 GCGCATGCGCTCGATATCTCCAGATGTAACTTAATAATCTGGTAGATTAGATTAT 5499
QY 886 GlnValLylSerArgGlyGlnArgValGluLeuGlyAlaIleGluThrHisLeuArgGln 905
DB 5500 CAAGTCAAAATTCGCGGTTTCCGATTGAATGGAATAATGAGAGATATTAGCAAA 5559
QY 906 GlnMetProAspAspLeuThrIleValGlnAlaThrLysAspSerGlnSerAlaAsn 925
DB 5560 CATCCCAAAATATCAACAGACAGTATGTA-----AGCGCAAGAAATGAACAGGA 5610
QY 926 SerThrSerleuilealaphleuileGlySerSerTyrPheGlyAsnArgProSerAsp 945
DB 5611 GAACAGCGTTATGTCCTTATCATGTC-----CCCAATTCT 5646
QY 946 AlaHisIleLeuAspHisAspAlaThrLylAlaAlaIleAsnIleLylLeuGlnValLeu 965
DB 5647 CAGGATGTGGGAAGCAATGATTTACAGCAATTCCTCCCAANA-----CTC 5694
QY 966 ProArgHisSerIleProSerPheTyrIleCysMetLeuGlnLeuProArgThrAlaThr 985
DB 5695 CCAAAATATATGATCTCTGGGGTGTGTGCATTAACAGCTTAACTCCCTCAACCTAAT 5754
QY 986 GlyLylSerAspArgArgLysArgIleMetGlyLylAspIleLeuAspLylGlnThr 1005
DB 5755 GGTAACTTGAACCTTAAGCTTATACC-----ACTCCCAATACC 5793
QY 1006 GlnGlyAlaIleValGlnGlnAlaProAlaProIleProValPheAlaAspThrAlaAla 1025
DB 5794 CAATCAACAGTAATGAACCCCTCGCACACA-----ACAGAGAA 5835
QY 1026 LylLeuHisSerIleTrpValGlnSerLeuGlyLylAspProAlaThrValAsnValGly 1045
DB 5836 GTTTTGGCGATTTTGGGAGTGGTGTGGTGCAG-----TCGGTGGTATGAG 5889
QY 1046 AlaThrPhePheGlnLeuGlyLylAsnSerIleThrAlaIleLylMetValAsnMetAla 1065
DB 5890 GATATTTCTTTGATTTTGGGGGACATCTCTGTCGCGACGCGGTATATTTCTCAAGTA 5949
QY 1066 ArgSerVal---GlyMetAspLeuLylSerAsnIleTyrGlnHisProThrLeuAla 1084
DB 5950 CCGGAGGTATTTGGTGTAGATTAACATAGTAATCTGTTGAAGTCCGAAATTTGCCG 6009
QY 1085 GlyLylSerAlaValLylLylAspProLeuSerTyrThrLeuIleProLylSerThr 1104
DB 6010 GATTTACCCAGAGTAATGAACAATAGTACACCAAGAAATTAACCAATTTAACCGATTGCT 6069
QY 1105 HisGlnLylProValGlnSerTyrSerGlnLylArgLeuTrpPheLeuAspGlnLeu 1124
DB 6070 CGCACTGTAACTTACTTATCTTTTGGCCAGACAGCTTTTGGATTATTAAGCCAGTTA 6129
QY 1125 AspValGlySerLeuTrpTyrLeuIleProTyrAlaValArgMetArgIlyProValAsn 1144
DB 6130 GAACCGGATAGCCCTTTTATATATCTTTGGCGGTGCAAAATCGGGGATATATCCAC 6189
QY 1145 ValAspAlaLeuArgArgAlaLeuAlaLylLeuGlnLylArgHisGluThrLeuArgThr 1164
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QY 1165 ThrPheGluAspGlnAspGlyValGlyValGlnIleValHisGluLylLeuSerGlnLyl 1184
DB 6250 CATTTCTTAATGTGATGAGACAGCTGTTTGAAGATGTGTGATTTGATGTCAAT 6309
QY 1185 MetLylValIleAspLeuCygllySerAspLeuAspProPheGlnValLeuAsnGlnGlu 1204

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Db      6310 ATACAGTGAATGATTATTCAGGGA-----TTACCGGAATTGAAACAAGCAGCAGCTG 6363
Qy      1205 Gln-----ThrThrProPheAnleuSerSerGluAlaGly--- 1216
Db      6364 CAGAGTGGCGGGAAGTCAAGCGCAGACAGCTTTGATTTG-----GCTGGTTTG 6414
Qy      1217 ---TTPArgAlaThrLeuLeuArgLeuGlyGluAspAspHisIleLeuThrIleValMet 1235
Db      6415 TTGTGGCGGCTGGCGGTGTAATAATTGGGGAGGGAATCAGGATTAATTGTTGACTTTG 6474
Qy      1236 HisHisIleIleSerAspGlyTyrSerIleAspValLeuArgAspLeuAsnGlnLeu 1255
Db      6475 CATCATATTAATGCTGATGCTGTGCTGTGGGTGTGTGTTGTTGGGAAATTTCTCGGCA 6534
Qy      1256 TySer-----AlaAlaLeuValAspSerIleAspProLeuSerAla 1269
Db      6535 TTGCGCGAGGCTCCCGAGGGAAGCCCAAGACGCAAGAGAGAGAG----- 6582
Qy      1270 LeuThrProLeuProIleGlnTyrSerAspPheAlaLeuTyrGlnIleAspGlnPheIle 1289
Db      6583 -----AGGATTCAAGTATGTGATTTGCTTTTGGCAGAGAGAGTGTGCGG 6630
Qy      1290 GluGln-----GluValGlnLeuAsnTyrTyrIleValGlnLeuValAspSerSerPro 1307
Db      6631 GGGAGGCTTTTAAAGGAACAATTGGAGTATTTGGCGGAGCAGTTG---GAGTCTGCGCG 6687
Qy      1308 Ala-----LysIleProThrAspPheAlaArgProAlaLeuLeuSerGlyAspAlaGly 1325
Db      6688 GTGATGTGTGAATTACCGCATGATTAACCCGCTCGGCTGACAGCTTTT--TCGGGGGGC 6746
Qy      1326 CysValHisValThrIleAspGly--GluLeuTyrGlnSerLeuArgAlaPheCysAsnGln 1345
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Qy      1345 ValSerThrThrSerPheValValLeuLeuAlaAlaPheArgAlaIleHisTyrArgLe 1365
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Qy      1365 ValThrAlaValAlaAspAlaValIleGlyThrProIleAlaAsnArgAsnArgProGluLe 1385
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Qy      1385 ValAspIleIleGlyCysPheValAsnThrGlnCysMetArgIleAsnIleAspHisIle 1405
Db      6927 GGAAGGCTTATGTTGTTGCTTACACCTGCTGCTTAAGTCTGATTTGAGTCTAA 6986
Qy      1405 SerThrPheGlyThrIleuIleAsnGlnValValIleThrThrAlaIlePheGluAs 1425
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Qy      1425 ValAspIleProPheGlnArgValValSerAlaLeuGlnProGlySerArgAspLeuSe 1445
Db      7047 TCAGATTTTACCTTTTGAACAATTGTAAGTGTCTCAACCA---GTGCGATGCTCAG 7103
Qy      1445 TyrThrProLeuAlaGlnLeuIlePheAlaValHisSer-----GlnIleVal 1461
Db      7104 TCATTCGCCCTCTTTTCAAGATGCTGCTGTCAAAATTTTACCTTTGCCAGAGTTGGA 7163
Qy      1461 PheGlnArgPhePheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1481
Db      7164 TATGGGGGAGATGAATGAGCAAGTAAATTAAGGCG-----GATAGTGTACAGC 7211
Qy      1481 ValGlnAspMetGlnPheHisLeuPheGlnGlnIleThrAspSerLeuValSerValAs 1501
Db      7212 AAAATTTGACTGACTGCTTGGTTCGAGCGAAACGCTCAAGCCTTAAGCTTAAGCTGA 7271
Qy      1501 nPheAlaAspGlnLeuPheLeuMetGlnThrValGluAsnValValArgValPhePheGln 1521
Db      7272 ATATATTAAGTATTAATTTCCAGCCACAATATTAAGCCTTAAGCTGAG--ACATTTAGAAA 7330
Qy      1521 ValLeuArgAsnGlnLeuGlnSerArgThrPro--ValSerIleLeuProLeuThr 1541
Db      7331 CATTAATTAACAGCATGATCTCAATCCGAAACGCAATATTAAGAAATTAACCTTA--- 7386

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Qy      1559 TyrProArgGlnSerSerLeuAlaAspValPheGlnThrGlnValSerAlaTyrProAspS 1579
Db      7442 ATCTTCAGCAG--TGTTTACATGATTAATTAAGCAAGGATGAGCAAAACCCGGAAA 7498
Qy      1579 LeuAlaValAlaAspSerSerCysArgLeuThrTyrThrGlnLeuAspArgGlnSerA 1599
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Qy      1619 LeuAlaProArgSerCysGlnThrIleValAlaPhePheGlnValLeuValAlaAsnLeuA 1639
Db      7619 GCGTTGACCTTCCCTAGATATGATTAATTCGGCTTAATGCTTACCAAGCTGACGCTG 7678
Qy      1639 ValThrLeuProLeuAspValArgSerProSerAlaArgValGlnAspIleLeuSerGlyL 1659
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Qy      1659 LeuSerGlyProThrIleValLeuIleGlyHisAsp-----ThrAlaProProAspIleG 1677
Db      7738 --TCCCAATGACAGTGTATCTACCCAGCAAAACAAATTAACCTCAAGCTCC 7795
Qy      1677 ValValThrAsnValGluPheValArgIleArgAspAlaLeuAsnAspSerAsnAlaAspG 1697
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Qy      1697 LysPheGluValIleGlnHisAspSerThrLysPro----- 1708
Db      7801 -----CCCATATTTCCCTAGACACCCCAATCCCAAGTCCCAATCCCAAGTCCCAAGTCC 7855
Qy      1709 -----SerAlaThrSerLeuAlaTyrValLeuTyrThrSerGlySerThrGlyArgProL 1727
Db      7856 CCAAGTCCCAACCAACCTAGCTCAATCATCATCACTCCGACACTACAGGCAATTCCTCA 7915
Qy      1727 ValGlyValMetIleGlnHisArg-----ValI 1736
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Db      7976 ACACAGACGAGATTAACAGGTGTTTACCTTC----- 8010
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Qy      1816 ValLeuArgValProArgArgLeuSerArgThrLeuMetPhePheLeuValValThrA 1836
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Qy      1836 spSerThrAla-----ProAspAlaLeuAspAlaGlnGlyLeuT 1849
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 QY 1904 lylleGlyValMetGlyGlnLeuValValThrgIAspGlyLeuAlaArgGlyTy 1922
 DB 8423 CCGTTGGCAATACCCGGGAAATTTACTCTCAGTGGCGGATGAGTTAGCAAGAGTTACTGGA 8482
 QY 1923 --SerAspIysAlaLeuAspGlyAsnArgPheValHisIleThrValAspGln---- 1940
 DB 8483 AGCGTCCAAATTTGACGAGAGAGGTTTAAACAGTCAACAGTCAACAGTCAACAGT 8542
 QY 1941 --ThrValIysAla--TyArgThrgIAspArgValArgTyArgIleGlyAspGly 1959
 DB 8543 CAACAGTCAACACTCTCTACAAAACAGCGATCGCGCTGTAT--CTTCCAGATGTGA 8599
 QY 1959 euIleGluPhePheGlyArgMetAspThrGlnPheIysIleArgGlyAsnArgIleGlu 1979
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 QY 2019 lSeRgluAsnAspIysGlyGln----- 2026
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 DB 8891 ACCGTTTGTCT-----TTACCAATACCTGATTTATCGCCAGTCACC----- 8931
 QY 2056 eAlaPheIysGlyTyTrpThSerMetTyAspGlySerGlnIleAspPheAspGluMet 2076
 DB 8932 -----ACCACAAACCGCACCCGACACCCATAGCAACAAATTAATTA 8974
 QY 2076 lEgIuTrp-----LeuGlyGluThrThrArgThrLeuHisAspAsnArgSerIeu 2093
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 QY 2093 lAsnValleuGlnIleGlyThrcIySerGlyMetIleuPheAsnLeuAspSerArg 2113
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 US-10-329-079-46
 ; Sequence 46, Application US/10329079
 ; Publication No. US20030198981A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FARMET, Chris
 ; APPLICANT: ZAZOPOULOS, Emmanuel
 ; APPLICANT: STAFRA, Alfredo
 ; TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
 ; FILE REFERENCE: 3002-1105
 ; CURRENT APPLICATION NUMBER: US/10/329, 079
 ; CURRENT FILING DATE: 2002-12-24
 ; NUMBER OF SEQ ID NOS: 66
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 46
 ; LENGTH: 15738
 ; TYPE: DNA
 ; ORGANISM: Streptomyces refuineus
 US-10-329-079-46
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 QY 49 lLeuAspProCysThrProPheGlnLeuAspMetIleAspCysAsnAlaLeuAspGln 68
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 5, 2004, 19:00:24 | Search time 464 Seconds
(without alignments)
4793.223 Million cell updates/sec

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US-09-482-788-2

Perfect score:

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Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched:

824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters:

1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blonsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MTN=0 -ALIGN=15
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5004.5	31.0	46899	1	US-08-471-119A-1
2	1715.5	10.6	7374	4	US-09-252-991A-9100
3	1641.5	10.2	6573	4	US-09-252-991A-9183
4	1618	10.0	10023	4	US-09-252-991A-6997
5	1517	9.4	11601	2	US-08-222-617A-3
6	1517	9.4	11601	2	US-08-222-617A-24
7	1506.5	8.9	7537	4	US-09-252-991A-71
8	1429	8.9	6968	4	US-09-710-279-759
9	1428	8.9	29555	4	US-08-956-171E-206
10	1428	8.9	29555	4	US-08-781-986A-206
11	1425.5	8.8	7215	3	US-09-134-001C-627
12	1383	8.6	1713	1	US-08-471-119A-4

13	1342.5	8.3	11444	2	US-08-222-617A-26	Sequence 26, Appl
14	1342.5	8.3	12364	2	US-08-222-617A-1	Sequence 1, Appl
15	1307.5	8.1	7911	4	US-09-252-991A-9182	Sequence 9182, Ap
16	1220	7.6	4403765	3	US-09-103-840A-2	Sequence 2, Appl
17	1220	7.6	4411529	3	US-09-103-840A-1	Sequence 1, Appl
18	1144.5	7.1	4411529	3	US-09-103-840A-1	Sequence 1, Appl
19	1143.5	7.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl
20	1141	7.1	3315	4	US-09-252-991A-8892	Sequence 8892, Ap
21	1129	7.0	77536	4	US-09-410-551B-1	Sequence 1, Appl
22	1129	7.0	77536	4	US-09-940-316B-1	Sequence 1, Appl
23	1128	7.0	4236	4	US-09-252-991A-7057	Sequence 7057, Ap
24	1061.5	6.6	6858	4	US-09-252-991A-1219	Sequence 1219, Ap
25	1014.5	6.3	4242	4	US-09-252-991A-7056	Sequence 7056, Ap
26	913	5.7	3602	4	US-09-710-279-3430	Sequence 3430, Ap
27	855	5.3	2219	3	US-08-510-646B-17	Sequence 17, Appl
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34	798.5	5.0	68750	3	US-09-568-472-1	Sequence 1, Appl
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38	755.5	4.7	3456	4	US-09-252-991A-7025	Sequence 7025, Ap
39	745	4.6	3981	4	US-09-328-352-760	Sequence 760, Appl
40	731	4.5	2022	4	US-09-252-991A-8890	Sequence 8890, Ap
41	716	4.4	4563	4	US-09-252-991A-4765	Sequence 4765, Ap
42	684.5	4.2	2301	4	US-09-710-279-419	Sequence 419, App
43	681	4.2	2823	4	US-09-252-991A-7100	Sequence 7100, Ap
44	631.5	3.9	2634	4	US-09-710-279-4189	Sequence 4189, Ap
45	629.5	3.9	6129	4	US-09-489-039A-6882	Sequence 6882, Ap

ALIGNMENTS

RESULT 1
US-08-471-119A-1
Sequence 1, Application US/08471119A
Patent No. 5827706
GENERAL INFORMATION:
APPLICANT: Leteuer, Ernst
APPLICANT: Schneider, Elisabeth
APPLICANT: Schoergerdoffer, Kurt
TITLE OF INVENTION: Cyclosporin Synthetase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 5827706art1s Corporation
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471, 119A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kasenooff, Melvyn
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8474
TELEFAX: 201 503 8807
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

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2665 AspAsnLeuVal-----GlnSerIleThrAsnGluIleValGly 2678
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2699 MetAlaSerGluIleAspProGlnLeuGluLeu-----GlnGluIleIleGlnAspIleTyr 2717
45273 ATCCAGCGCATGTTGATCTGACATGAGAACGCTGACAGCAACCCCTGACATGTAT 45332
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45447 AGCGCTGCGCGCTCTGTCGACACTTGGACATATTCGAACCGGTGCTGTCAAGA 45506
2778 SerGlyLeuLeuTyrGlnValAlaLeuSerCysLeuAspLeuProIleGlnValIleGlu 2797
45507 GCGGCGCGCTTCAACAGTGTCTTCTGTCATCTGATCTGATCTGCGAGTCACTGAG 45566
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45567 ACCGAGCAAGATGATGATGAGTGTCTCTCGCGCTGATGAACAGACAGCAGAGCCC 45626
2818 ValArgLeuGlyHisProLeuIleArgPheThrIleIleLeuGlnThr-----LysSerMet 2836
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2837 ArgValIleMetArgIleSerHisAlaLeuTyrAspGlyLeuSerLeuGlnHisValAla 2856
45687 CGACTTGTCTCCGAATGTCTCATCTCCCTTACGACGCGCTTGAGTCTTGAACATGTCTC 45746
2857 ArgLysLeuHisMetLeuTyrAsnGlyArgSerLeuLeuProHisGlnPheSerArg 2876
45747 AACGCTTACATGCTGTTGACAGTGAATGAACACTTTCGCAACACCAAGTTTGGTCTC 45806
2877 TyrMetGlnTyrThrAlaAspGlyArgGluSerGlyHisGlyPheThrPalaAspValIle 2896
45807 TACATGATCAACATGTGTACCGACGTGACAGAGGCTTACCAATTTTGGCGCATCTATTCTT 45866
2897 GlnAsnThrProMetThrIleLeuSerAspAspThr-----ValValAspGlyAsnAspAla 2915
45867 CAGGCTCTTCAATGATACCTCTGAAGCGCTCTGTGCGCGCCCTCGA--GGCCATGAGGCC 45925

QY 2916 chrVyslysalaleu-HisIleuSerIyVIlleValAsnIleProSerGlnValLeuAArgI 2995
 Db 45926 GTCTGCCGCTACAGGCAAGACGTCACAAATCCATCAGGATCCCTCTCGCGCACTCAAG-- 45983
 QY 2935 ySerSerAsnIleIleThrGlnAlaThrValPheAsnAlaIaIaCysAlaLeuValIeue 2995
 Db 45984 -----AAGCGCATTAACGAGGGGAGCCCTTTACACGCGCGCGCTCTCTCTTGGCTGC 46036
 QY 2955 rArgGluSerAspSerIyAspValValPheGlyArgGlleValSerGlyArgGlnGlyLe 2975
 Db 46037 CAACCAATACCAAGGTGCAGAGCGTCGTCCTTGCGCGCGCTCTTATCTGGACACAGAGATCT 46096
 QY 2975 uProValGluIyurGlnAspIleValIGlyProCysThrAsnAlaValProValArgAlaHi 2995
 Db 46097 CTCATTAACCTGCCAAGACATCGTGGACCTTGCATCAACAGAGGCTGTGGCCGTTTCG 46156
 QY 2995 sIle---GluSerSerAspTyraAsnGlnLeuLeuHisAspIleGlnAspGlnTyLeuLe 3014
 Db 46157 GATGACGAGGGCGCACACATAGGGGTGTCTCTCGCGCCATTCAAGACCACTACACCAG 46216
 QY 3014 uSerLeuProHisGluThrIleGlyPheSerAspLeuIyAsArgAnCyThrAspTrpPr 3034
 Db 46217 CAGCTTCGCGCACAGACCTTGGGCTTGCAGAAAGTGAAGGAAGTCAAGACTGACGACTGAC 46276
 QY 3034 oGluAlaIleThrAsnPheSerCyCysIleThrTyHisAsnPheGluTyHisProG1 3054
 Db 46277 TGAATGCACCAAGAGATTCAAGTTCGTGATTCGCTTCCAGAACTCAACCTGACCTCGA 46336
 QY 3054 uSerGlnPheGluGlnGlnArgValGluMet----- 3064
 Db 46337 GGCCGAGATTGAAGGCAAGCAGATTCGCTTGAGAGGTTTGCACGAAGATCAAGCAGC 46396
 QY 3064 ----- 3064
 Db 46397 CCAGGCAATGTCATGCCCCCAATGGCAGCAAGCAGCAAGATGCGACAGAA 46456
 QY 3064 ----- 3064
 Db 46457 TGGCGCAGACGGCAGATGGACGAATGGCAGCAATGTGTCCCATGCGAACCGATACAA 46516
 QY 3065 -----GlyValLeuThrIyPheValAsnIleGluMet-----AspG1 3077
 Db 46517 TGGTAGCAACGGGTCTCAATGAGCCCGCATAGCAAGCTGTTCACGCCGTGCGCATCAAGC 46576
 QY 3077 uProLeuTyraPheLeuAlaIleAgiIyGluValGluProAspAlaIaIaGlyLeuIySva 3097
 Db 46577 TCTGTTACAGATCTGGACATGTGGGATTCGCGAGCCGACCGCAGC---GTCAAGAT 46633
 QY 3097 lThrValIleAlaIyAsThrGlnLeuPheGlyArgIyArgValGluHisIleuLeuGluG1 3117
 Db 46634 TGGCATTTGTCGCGAGCGCGCATGCTTGGAGAGAAAGTCTGTGGCAGACGATCAATGA 46693
 QY 3117 uValSerIyThrPheGluGlyLeuAsn 3126
 Db 46694 ACTTGGAGACCATGCTCGCTTGGAGC 46721
 RESULT 2
 US-09-252-991A-9100
 : Sequence 9100 Application US/09252991A
 : Patent No. 6551795
 : GENERAL INFORMATION:
 : APPLICANT: Marc J. Rubenfield et al.
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 : FILE REFERENCE: 107196.136
 : CURRENT APPLICATION NUMBER: US/09/252, 991A
 : CURRENT FILING DATE: 1999-02-18
 : PRIOR APPLICATION NUMBER: US 60/074,788
 : PRIOR FILING DATE: 1998-02-18
 : PRIOR APPLICATION NUMBER: US 60/094,190
 : PRIOR FILING DATE: 1998-07-27
 : NUMBER OF SEQ ID NOS: 33142
 : SEQ ID NO 9100

```

; LENGTH: 7374
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9100

Alignment Scores:
Pred. No.: 6,02e-170 Length: 7374
Score: 1715.50 Matches: 586
Percent Similarity: 44.67% Conservative: 357
Best Local Similarity: 28.67% Mismatches: 754
Query Match: 10.64% Indels: 377
DB: 4 Gaps: 75

US-09-482-788-2 (1-3129) x US-09-252-991A-9100 (1-7374)
QY 430 TYRAERHIAENVAIIIEAPSERLEUQINHTHTHRYGLEULEQGLNINPHEGLNIVS 449
||| : : : : : ||| : : : : :
DQ 1348 TACGCCACCGAATCTGTGACGCCCTCCACCGCGAAGACGCTGGCGGCATTTGGCGCAAC 140
||| : : : : : ||| : : : : :
QY 450 LEUILLIYV--CYALEQGLNIFERPROLEUAEPLSEUSERMETCALAGLVALANLEU 468
||| : : : : : ||| : : : : :
DQ 1408 CTGTTGGCCGCGCATGTGCGCCAAACCA-----CGACAGCGCGCTGGCGCATTTGCCGCTG 146
||| : : : : : ||| : : : : :
QY 469 METHTNGIUTYARPAATGAGLU---ILEGISERTPAHSERGLINPROLEUGIV--- 486
||| : : : : : ||| : : : : :
DQ 1462 CTGATGCGCGCGGACGCGCGGACGACCTCTCCGATGGAACCCGGGCCAGCGCATGTC 152
||| : : : : : ||| : : : : :
QY 487 ---VALGNAERTHLEULIHIVHISGLUMELIULYVALAVALSERHISSEPROTHR 505
||| : : : : : ||| : : : : :
DQ 1522 GCGGCGACAGGACCTTG---CAGACGCGTTCCAGACGACGACGCGCGGACGCGCACAG 157
||| : : : : : ||| : : : : :
QY 506 LYETHRALIIEGLNALIETPAERGLYASPTTRHTYRSEGLIULYAEPAANVALSER 525
||| : : : : : ||| : : : : :
DQ 1579 GCGGTGTGCGGTATGCTCGACGACGACGAGTGAAGCTACGCGGACATGATGCGCGGCC 163
||| : : : : : ||| : : : : :
QY 526 SERATGLIENALAVAHISILEYSESERLEUGIYLEADAGLALGHLALALEIPEPO 545
||| : : : : : ||| : : : : :
DQ 1639 AATCGCTGGCGCATGCTGCTATGCGCGCGGTGGCGGTGGCGGAC-----GTGCGG 168
||| : : : : : ||| : : : : :
QY 546 VAL-----TYRPHIGLIYSESERIYSTRVALIIEALASERMETLEUALVALILEYUS 563
||| : : : : : ||| : : : : :
DQ 1630 GTCCGGCGCTGGCGCTGACGCTTCCGTGGACATGCTGCTGCGCTTCCGTGGCATCTCCAG 174
||| : : : : : ||| : : : : :
QY 564 SERGLIENALAPHERTHYLEUAEHPROBANAERPROFOALATGTHTALAGLVAL 583
||| : : : : : ||| : : : : :
DQ 1750 GCGCGCGCGCGCTACCTGCGCTTGGACCGCGCGCGCGGACGACGCGCTGCGCATATC 180
||| : : : : : ||| : : : : :
QY 584 VALTHRGINTHTAGLALATHYVALALALEUHTSERIYVLEHNIATGGLIUTHYVALGIN 603
||| : : : : : ||| : : : : :
DQ 1810 CTCGACGACAGTGGGAGTACGGCTTGTGTCGACCCGAGGCGCATCTGTCGACGACCTGCGG 186
||| : : : : : ||| : : : : :
QY 604 LYSLEUVALGIY---ARGCYVALIYVALIAPARPAIGLIULENGLINSERVALSERALA 622
||| : : : : : ||| : : : : :
DQ 1870 CGGACGCGCGGGGTGAGAGTGTGCGCATCGACGAGCATGCTGTGAGACGCTACGCGCGAG 192
||| : : : : : ||| : : : : :
QY 623 SERAPARPHESERISERILEUTHRYSESERGINAPLEUALATYRVALIIEPHERTHSER 642
||| : : : : : ||| : : : : :
DQ 1930 AGCATTCGCGCTCGGACGCTATCG---GGGACAACTGGCTACGTATCTATATCTGCG 198
||| : : : : : ||| : : : : :
QY 643 GLYSERTHTGILYARPROLYEGLIYLEMELIEGLIHNIV-----ARGALAPHE 658
||| : : : : : ||| : : : : :
DQ 1987 GGGCTGACCGGACAGCCGACAGGCGCATGTGTCACCCGACGACGCGCTGGCGCGCTGTC 204
||| : : : : : ||| : : : : :
QY 659 SERISERCYVALALEUPLYRPHGLYALASERLEUGIYILEANSERAPRHTHTAGLALAEU 678
||| : : : : : ||| : : : : :
DQ 2047 AGCGGACCGAGGCGCTGGTGGCTTGAC-----GACGGGACGCTGGGACATTTG 209
||| : : : : : ||| : : : : :
QY 679 GINPHEGLIUTHINIALAPHEGLYALACYULENGIULIEMETHRTHRYLEAEN 698
||| : : : : : ||| : : : : :
DQ 2098 ---TTCCATTCGCTGCGCTTGCATTTGCGGTGGGAATCTTGGCGCGCGTGGCTAT 215
||| : : : : : ||| : : : : :
QY 699 GILYGLIYCYVALIYVILE-----PROSERAPRPAARPAATG 710
||| : : : : : ||| : : : : :

```

Dh 2155 GCGGGGTCCTGATGTCGCGCAATGGGTGACCGCTTCGCGGAAGACTTACCGT 2214
Qy 711 MetAsnSerIleProSerPheIleAsnArgTyrAsnValAsnTrpMetMetAlaThrPro 730
Dh 2215 CTG-----CTGTGCGCGAAGCGGTGAACGGTCTCAACCAACGACCGG 2256
Qy 731 Ser-----TyrMetGlyThrPheSerProGluAspVal-----Pro 742
Dh 2257 TCGCGCTTCAAGCAACTGATGCGCGTGTCCCGCCGACATGGCGACGCAACGACCGG 2316
Qy 743 GlyLeuAlaThrLeuValLeuValGlyGluGlnMetSerSerSerValAsnAlaIleTrp 762
Dh 2317 GCGCTGCGCTACGATCTTCGTGTGTAGCGCTGTGATCTGCAGACCTTCGCGCGTGG 2376
Qy 763 AlaProIleu-----GlnLeuLeuAsnGlyTyrGlyGlnSerGluSer 777
Dh 2377 TTCACAGGCTTTGGCCGATTCGCCAGCCGCACTGTGAACATGTACGACATCAGCAAC 2436
Qy 778 SerSerIleCybPheAlaSerAsnMetSerThrGluPro----- 790
Dh 2437 ACG-----GTACACGTAACTACCGCTCGGTGAGCGAAGCGACCTGGAA 2481
Qy 791 -----AsnAsnMetGlyArgAlaValGlyAlaHisSerTrpValIleAspPro 806
Dh 2482 GGTGGCTGTGTCAGTCCGATGCGCGGAACTCCCGGACCTGTCTGTGATCATCTTGAC 2541
Qy 807 AsnAspIleAsnArgLeuValProIleGlyAlaValGlyLeuValIleGluSerPro 826
Dh 2542 CGTGACCTGAACCGG-----GTGCGCGCGCGCGCGGTGGCGAGCTGTACATCGTGGCGCC 2598
Qy 827 GlyTyrIleAlaArgAspTyrIleValProProProProGluIleValSerProPhePheThrAsp 846
Dh 2599 GGTCTGCGCGCGCTACTGAGCGCGCGCGGTGTGATGTCGACCGCTTC----- 2649
Qy 847 IleProSerTrpTyrProAlaAsnThrPheProAspGlyAla-----LysLeuTyrArg 864
Dh 2650 GTGCGG-----AACCCGTTCCCGCGCGGTGCGCGGACGCGCTTACCGT 2694
Qy 865 ThrGlyAsnProLeuAlaArgTyrAlaSerAspGlySerIleValCysLeuGlyArgIleAsp 884
Dh 2695 ACCGGCGACCTGGACGCGTTCGAGCGGATGCGCAATTCGAGTACATCGGCGGTATGAC 2754
Qy 885 SerGlnValIleValIleArgGlyGlnArgValGluLeuGlyAlaIleGluThrHisLeuArg 904
Dh 2755 CACGAGGTGAAGTTCGCGGTTCGATCGACATGCGGTGAGATCGAAGCGCGCTGCC 2814
Qy 905 GlnGlnMetProAspArgLeuThrIleValValGluAlaThrLysArgSer---GlnSer 923
Dh 2815 -----GGTCTGCGCGCGGTGACGCGATGCGGTGCTGGCGCCATGACGCG 2859
Qy 924 AlaAsnSerThrSerLeuIleAlaPheLeuIleGlySerSerTyrPheGlyAsnArgPro 943
Dh 2860 GTGCGCGCGACGCACTGTGTGCGGATACGTGTGCGGACCTG-----GCG 2904
Qy 944 SerAspAlaHisIleLeuAspHisAspAlaThrLysAlaIleAsnIleLysLeuGlnGln 963
Dh 2905 GAGGATCCGACGCTCTG-----CGGAGAGTCGCTCGCGGAGTCCCTGAAACGCG 2952
Qy 964 ValLeuProArgHisSerIleProSerPheTyrIleCysMetLeuGluLeuProArgThr 983
Dh 2953 CACCTGCGGAGCTACATGATGCGCGCATCTGATGCTGTGAGCGGATGCGCTGACG 3012
Qy 984 AlaThrGlyLysIleAspArgArgArgLeuArgIleMetGlyLysAspIleLeuAspLys 1003
Dh 3013 GTCAATGGCAAGCTGCAACCGGACGCGCTTG-----CCG 3045
Qy 1004 GlnThrGlnGlyAlaIleValGlnGlnAla---ProAlaProIleProValPheAlaAsp 1022
Dh 3046 CAACCGGATGCGAGCTGTGCGACAGCGCTATCGAGCGCC-----GTTAGCGAG 3096
Qy 1023 ThrAlaIleLysLeuHisSerIleTrpValGlnSerLeuGlyIleAspProAlaThrVal 1042
Dh 3097 CTGGAGCAGCGCATCGCATCTGGCGGAGATCTCTGGAGTGGAA-----CGGAGTT 3150

Qy 1043 AsnValGlyAlaThrPhePheGluLeuGlyGlyAsnSerIleThrAlaIleLysMetVal 1062
Dh 3151 GCGCTGACGACAACCTTCTTCAACTGGCGGCTGATCTGTGCTGCTACCCGCGTCAAT 3210
Qy 1063 AsnMetAlaArg---SerValGlyMetAspLeuLysValSerAsnIleTyrGlnHisPro 1081
Dh 3211 TCTCGGCTTCCAGAGCAGCAGCAGTGTGACGCAAGCTGTGAAGCGTGTTCAGCGCGCG 3270
Qy 1082 ThrLeuAlaGlyIleSerAlaValAlaValGlyAspProLeuSerTyrThrLeuIlePro 1101
Dh 3271 GTTCTGGAACGCTTCCCGCAGGATTTGGAACGACAGCGGATCGGCTGACAGATPACG 3330
Qy 1102 LysSerThrHisGluGlyProValGluGlnSerTyrSerGlnGlyArgLeuTrpPheLeu 1121
Dh 3331 CTTCGCGATCGGAGCAACGTTGGACCTGCTCTGCTGACAGAGCGTCACTGATTCCTC 3390
Qy 1122 AspGlnLeuAspValGlySerLeuTrpTyrLeuIleProTyrAlaValAlaArgMetArgGly 1141
Dh 3391 TGGCACTGAGCGCGGAACCGCGGCTTACATATTCGAGTCCGCTTGGCGCTACCGCGG 3450
Qy 1142 ProValAsnValAspAlaLeuArgArgAlaLeuAlaLeuGluGlnArgHisGluThr 1161
Dh 3451 CGGCTGACGTGATGCTTGTCAACGACGCTTGACAGCCTGTGCGCGGATGAAC 3510
Qy 1162 LeuArgThrThrPhe-----GluAspGlnAspGlyVal 1172
Dh 3511 TTGCGTACCGCTTCCGCTGAGAGGAGCGGTTCGTACACAGAGATGAACCTGCGGTT 3570
Qy 1173 GlyValGlnIleValHisGlyLysSerGlnGluMetLysValIleAspLeuCysGly 1192
Dh 3571 AGCGTTTCCATCAGACGCGGAACGTTCCGTGAAGAAAGCGCTGATC----- 3615
Qy 1193 SerAspLeuAspProPheGluValLeuAsnGlnGluGlnThrTrpProPheAsnLysSer 1212
Dh 3616 -----GAACGATPACAGGCCATGCTTGTGACGACCTTCACTGCACTGGA 3657
Qy 1213 SerGluAlaGlyTrpArgAlaThrLeuLeuArgLeuGlyGluAspAspHisIleLeuThr 1232
Dh 3658 CGGCGCGCGCTGCTGCGCGGTGAACCTGTTCACCTGCGCCGAACGACCATGTACTG 3717
Qy 1233 IleValMetHisIleIleSerAspGlyTrpSerIleAspValLeuAspArgAspLeu 1252
Dh 3718 CTGCTCAGACCAACATGCTGTCGAGGTGTGCTGATGAGGTGATGAGGAACCTG 3777
Qy 1253 AsnGlnLeuTyrSerAlaAlaLeuLysAspSerLysAspProLeuSerAlaLeuThrPro 1272
Dh 3778 GTCCAGCTCAT---GCCGCTTATAGCCAGGCTGACCTGCTG-----TTGCCAGCC 3828
Qy 1273 LeuProIleGlnTyrSerAspPheAlaLysTrpGlnLysAsp-----GlnPheIleGlu 1290
Dh 3829 CTGCGCATCCAGTACGCGGACTAGCGCTGTGACAGCGACGTGATGAGCGCGGGAA 3888
Qy 1291 GlnGluLysGlnLeuAsnTyrTrpLysLysGlnLeuLysAspSerSerProAla---Lys 1309
Dh 3889 AAGAGCGCAGATTGGGTGCTGACCGCTGTGCGCGGCGGACGCGCGTCTGGAG 3948
Qy 1310 IleProThrAspPheAlaArgProAlaLeuLeuSerGlyAspAlaGlyCysValHisVal 1329
Dh 3949 TTGCGCTGATGCGCGCGCTTCCGCGCGGACAGCATGTGTGCGCGGATGCGGTTTC 4008
Qy 1330 ThrIleAspGlyLeuLysTyrGlnSerLeuAspAlaPheCysAsnGluHisAsnThrThr 1349
Dh 4009 GAGCTACCAAGGAACCTGTCGAGGCGCTGAGAGCTTGTGCGCAGCTGAAGCGCCAGT 4068
Qy 1350 SerPheValValLeuLeuAlaIleAlaPheArgAlaAlaHisTyrArgLeuThrAlaValGlu 1369
Dh 4069 AGTTTCATGCTGTGCTGCGCTGCTGTCACAGCCCTGTTGATGCTTACACGCGGACGCG 4128
Qy 1370 AspAlaValIleGlyThrProIleAlaAsnArgAspArgProGluLeuGluAspIleIle 1389
Dh 4129 GATATCGGTCTCGGTGCGGATCGCATTCGCAACCGCGTGAAGACCGGCGGTGATC 4188

Db 6217 CAGCGCTGGCCGACCCGATGCGAGCTTTCGACAGAGCCGATACGCCGCCGAGTAC 6276
 QY 2057 AspPheIysGly-----TrrThrSerMetTyrAspGlySerGlnIleAsp 2071
 Db 6277 GACCTGAGAGAGCCGATCGACGACATGTGGCCGAGATCCCGGAGTGGAAACGGGTGGC 6336
 QY 2072 PheAspGluMetHisGluTrpLeuGlyGluThrThrArgThrLeuHisAspAsnArgSer 2091
 Db 6337 CTGACACGAC----- 6345
 QY 2092 LeuGlyAsnValLeuGluIleGlyThrGlySerGlyMetIleLeuPheAsnLeuAspSer 2111
 Db 6346 -----AATTCTTTCGAACTGGGC---GGTACTCATGTGTGCTGCTGATGCTTAAGAG 6396
 QY 2112 ArgLeuGluSerTyrValGlyLeuGluProSerArgSerAlaAlaPheValAsnIys 2131
 Db 6397 CGGATCGCGCAT----- 6417
 QY 2132 AlaThrGluSerIleProSerLeuAlaGlyValAlaIysValGlnValGlyThrAlaThr 2151
 Db 6418 GCTACGCTGACATCAGCCCACTGATGACCATGCCAGCTCGCGAACAAGCGCGCATGC 6477
 QY 2152 AspIleGlyGlnValAspAsnLeuHisProAspLeuValValLeuAsnSer----- 2168
 Db 6478 ATCGAGGGGAGCGCGCTGAG-----TCGTTGCTGTGGTCCGCTCAACGGTAGCGCGAA 6531
 QY 2169 -----ValIleGlnTyrPheProSerSerGlyTyrLeuAlaGlnIleAlaAspThr 2185
 Db 6532 GGTTCGCGCGCTTTCATGTCATCCAGT----- 6561
 QY 2186 LeuIleHisLeuProAsnValGlnArgIlePhePheGlyAspValArgSerGlnAlaThr 2205
 Db 6562 -----TTGCGCTCTGTGCACTGTTACAAAGACC 6588
 QY 2206 -----AsnGluHis-----PheLeuAlaAlaArgAlaIleHis 2216
 Db 6589 CTCGCCATGCGCGCTCGGAGCTGATCCGCTCAAGGGGTGTGTCTGCTCGGCTGCTGCTG 6648
 QY 2217 ThrLeuGlyIysAsnAlaThrIys---AspAspValArgGlnIysMetAlaGluLeuGlu 2235
 Db 6649 GCGGCTGTGTCGAGAGTCCGCGAGTGGACATGATGTTGCTGGCAATACGCCGAG----- 6702
 QY 2236 AspMetGluGluLeuLeuValGluProAlaPhePheThrSerLeuIysAspArgPhe 2255
 Db 6702 ----- 6702
 QY 2256 ProGlyLeuValGlnHisValGlnIleLeuProIysAsnMetGluAlaValAsnGluLeu 2275
 Db 6703 -----CAATTGCTGAGAGACACCCCGAAGGGGTTCACACTG 6741
 QY 2276 SerAlaTyrArgTyrAlaAlaValAlaHisValArgGlySerLeuGlyAspGluLeuVal 2295
 Db 6742 GCGGAGTGC-----TCGCTCGCGCGCAACTTCGGC 6771
 QY 2296 LeuProValGluIysAsp-----AspTrpIle 2304
 Db 6772 ATGAGATTCGCGCGCGCGCTGAGACAGCGTGGCGGAGGTGCTTTCGTCGCGCTGATC 6831
 QY 2305 AspPheGlnAla 2308
 Db 6832 GATGCGCGCGCA 6843

RESULT 3

US-09-252-991A-9183
 ; Sequence 9183, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252.991A
 ; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 9183
 ; LENGTH: 6573
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (5574)
 ; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
 US-09-252-991A-9183

Alignment Scores:

Pred. No.	Score:	Length:	Matches:
3	46e-162	6573	571
1641	50	571	317
Percent Similarity:	38.96%	Conservative:	758
Best Local Similarity:	25.05%	Mismatches:	633
Query Match:	10.18%	Indels:	59
DB:	4	Gaps:	59

US-09-482-788-2 (1-3129) x US-09-252-991A-9183 (1-6573)

QY 430 TyrAspHisAsnValIleAspSerLeuGlnThrThrArgLeuGlnIlePheGlyHis 449
 Db 1339 TATGCCAGGATGCTGTCGAGGCTCGACCGCTGACCGCTGCTGCTGCTGCTGCTGCTG 1398
 QY 450 LeuIleIysCysLeuGlnSerProLeuAspLeuSerMetAlaGluValAsnLeuMet 469
 Db 1399 CTCCTGCGCGCATGCTGCGCGCAACCGGCGC---CGGCGGTGCGCGGATGGCGCTGTG 1455
 QY 470 ThrGluTyrAspArg-----AlaGluIleGluSerTrpAsnSer 482
 Db 1456 CTGACGAGAGCGCATTCCTGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 1515
 QY 483 GlnProLeuGluValGlnAspThrLeuIleHisIleGluMetLeuIysValAlaSerHis 502
 Db 1516 TTGCGCGCGCTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTC 1563
 QY 503 SerProThrIysThrAlaIleGlnAlaTrpAspGlyAspTrpThrTyrSerGluLeuAsp 522
 Db 1564 ---CGCGAGCGCGAGGACTGCGCGTGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1620
 QY 523 AsnValSerSerArgLeuAlaValHisIleIysSerLeuGlyLeuArgAlaGlnAla 542
 Db 1621 GCCCGCGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1677
 QY 543 IleIleProValTyrPheGluIysSerIysTrpValIleAlaSerMetLeuAlaValLeu 562
 Db 1678 CTGATGGAGATTCGCGCGTGGAGCGCTGCGTGGATGATGATGATGATGATGATGATG 1737
 QY 563 LysSerGlyAsnAlaPheThrLeuIleAspProAsnAspProProAlaAlaGlnIleGln 582
 Db 1738 AAGCGCGTGTGCTATGTCGCGTGGACCGACCTATCCGAGAGACCGTTGGCTGAC 1797
 QY 583 ValValThrGlnThrArgAlaThrValAlaLeuThrSerIys----- 596
 Db 1798 ATGCTGAGAGACAGCGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1857
 QY 597 ---LeuHisArgGluThrValGlnIysLeuValGlyArgCysValAlaValAspAspGlu 615
 Db 1858 CTTTGCACGAA-----GGGCTGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1896
 QY 616 LeuLeuGlnSerValSerAlaSer---AspAspPheSerSerLeuThrIysSerGlnAsp 634
 Db 1897 CTGAAACGGAGCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1956
 QY 635 LeuAlaTyrValIlePheThrSerGlySerThrGlyAspProIysGlyIleMetIleGlu 654
 Db 1957 CTGACCTATGATCTACACTCGGCTCGACCGAAACCCAGGCGCGTGGCCATGAC 2016

Db 4024 CGCGTGAAGCGCTTGCCCAACGCGAGGTGCGAGTACCTTCATGTTCTGCGCGCTCG 4083
 QY 1358 PheArg11a1aHis1TyArgLeuThra1aValGluAspAlaVal1IleGlyThrPro1Ie 1377
 Db 4084 TTCAGCGCGCTGCTGATTCGCTACAGCGGTACAGCGGATATCCGTGCGCGTCCGCTC 4143
 QY 1378 AlaAsnArgAnhArgProGluLeuGluAsp1Ile1IleGlyCysPheValAsnThrGlnCys 1397
 Db 4144 GCCAATCGCAACCGGTCGAACCGAGCACTGATCGGGTTCCTGCTCAACACCCAGGTG 4203
 QY 1398 MetArg1IleAsn1IleAspHis1AspThrPheGlyThrLeu1IleAsnGlnValLeuAla 1417
 Db 4204 CTCAGGCGCCGATTCGATGGCAGATGGGTTCACCGCATTCCTGCGCACCGTTCGCGAG 4263
 QY 1418 ThrThrThrAla1aPheGluAsp1IleProPheGluArgVal1aSerAlaLeu 1437
 Db 4264 CGCTCGCTGAGAGCGAGCGGCGACACAGACTTCCGCTTCAGACAACTGGTGGAAAGCTTGG 4323
 QY 1438 GlnProGlySerArgAspLeuSerSerThrProLeuAlaGlnLeu1IlePheAlaValHis 1457
 Db 4324 CAACCG---GAGCGCATCTCAGCCAGACCGCGCTGTTCCAGGTGCTATTC-----AAC 4374
 QY 1458 SerGlnLysAspLeuGlyArgPheLysPheGlnGlyLeuGlnSerValProValProSer 1477
 Db 4375 TACACGCGGAGCGGCGGCGAGCACGCGTTCGCGAAGTTCGCGGAGCATGACATCGAAAG 4434
 QY 1478 LysAla1aTyR-----ThrArgPheAspMetGluPheHisLeuPheGlnGluThr 1493
 Db 4435 CAGCGCGTGGAAAGCCATACGGCGCAGTTCGCTGCTGCTGATACCTGTGAGTCCGAG 4494
 QY 1494 AspSerLeuLysGlySerValAsnPheAlaAspGluLeuPheLysMetGluThrValGlu 1513
 Db 4495 TCGGACATCTGGGCGCGCTGTGATGCGACGCGATCATCTGATGCTTCGACCGGAGAG 4554
 QY 1514 AsnValValArgValPhePheGln1IleLeuArgAsnGlnLeuGlnSerSerArgThrPro 1533
 Db 4555 CGCGTGTGATCGGCAATTGGCAGAACCTTCTGAT----- 4587
 QY 1534 ValSer1IleLeuProLeuThrAspGly1IleValThrLeuGlnLysAspValLeu--- 1552
 Db 4588 ---GCGATCTCTGGGATGCTCTGAC-----GCTGCGCTGGAGAGCTGGACATGCTCGAC 4638
 QY 1553 -----AsnValLysHisValAspTyProArg 1561
 Db 4639 CGCGAGAGCGCGAATCATCGGCGAGCTCTGAAACCGCAGCATTCGGGCTATCCGCA 4698
 QY 1562 GluSerSerLeuAlaAspValPheGlnThrGlnValSerAlaTyRProAspSerLeuAla 1581
 Db 4699 ACGCCGCTGTATCACCGAGAGTGGCGAGCGGCGGTATGGCGCGGATGCGGTGGCG 4758
 QY 1582 ValValAspSerSerCysArgLeuThrTyRThrGluLeuAspArgGlnSerAsp1IleLeu 1601
 Db 4759 GTGATCTTCAGACGAGGAAAACTACCTACCGCCAGCTGTGATGACCGGGCCAAACCGCTG 4818
 QY 1602 AlaGly1TriPheArgArgArgSerMetProAlaGluThrLeuValAlaValPheAlaPro 1621
 Db 4819 GCCCATCGTTGATCGCCGAGCGGTGCGGCCCGAAGTGGCGGTGGCGATGCGCATCGAG 4878
 QY 1622 ArgSerCysGluThr1IleValAlaPhePheGlyValLeuLysAlaAsnLeuAlaTyRLeu 1641
 Db 4879 CGGAGCGCGGAGATCATGTGGCTCTGCGGTGTGAAGCGCGCGCGCTTACGTG 4938
 QY 1642 ProLeuAspValArgSerProSerAlaArgValGlnAsp1IleLeuSerGlyLeuSerGly 1661
 Db 4939 CCCTGTGATATCGAATACCGCGCGAGCGCTGCTGATCATGATGCGAGACATCGCGCG 4998
 QY 1662 ProThr1IleValLeu1IleGlyHis1AspThrAlaProProAsp1IleGluValThrAsnVal 1681
 Db 4999 CACCTGCTGCTGACCCATAGCAC-----CTGCTG 5028
 QY 1682 GluPheValArg1IleArgAspAlaLeuAsnAspSerAsnAlaAsp----- 1696
 Db 5029 GAGCGTCTCGCATCCCGAGGGGTGTCTGCTGCTGCTGATCGCGAGAGAGTGG 5088

QY 1697 ---GlyPhe-----GluVal1IleGlnHisAspSerThrLysProSerAla 1710
 Db 5089 GCGCGCTTCCCGCTCATGATCAAGAGTGGCGCTGAC-----GGC 5130
 QY 1711 ThrSerLeuAlaTyRValLeuTyRThrSerGlySerThrGlyArgProLysGlyValMet 1730
 Db 5131 GACACCTGGCTCATGTGATGATCTACCTCCGCTCCACCGCGCATGCGCCAGAGGCGGTGGCG 5190
 QY 1731 IleGlnHis---ArgVal1IleLeuArgThrValThrSerGlyCys1IleProAsnTyRPro 1749
 Db 5191 GTGCTCCACGCTCCGTGATGCCCATATGCTGACCAACGCGCAGCGCTTCGAGATGACC 5250
 QY 1750 SerGlnThrArgMetAlaHisMetAlaThr1a1aPheAspGlyAlaSerTyRGlut1Ile 1769
 Db 5251 CGGAGAGCATCGAGCGTGCATTCATGCTGCTGCGCTTCGACGCTTCCACGAAAGCTGG 5310
 QY 1770 TyRSerAlaLeuLeuPheGlyArgThrLeuValCysValAspTyRmetThrThrLeuAsp 1789
 Db 5311 ATGCACCCGTTGATCAACGCGCGCGGTGCTGATCGCGACAGACAGCTGTGCTGCGCG 5370
 QY 1790 AlaArgAlaLeuLysAsp-----Val 1796
 Db 5371 GAACGAGCTTACGCGCGAGATCATTCGCGAGGCTTAAAGTGGGCTTCCCGCGCTG 5430
 QY 1797 PhePheArgGlnHisValAsnAla1aSerHisValThrSerSerGlnAspValPro 1816
 Db 5431 TACCTGACGAA-----CTGCGCAGCATGCGAGCGGACGCGCAATCCGCGCGCG 5481
 QY 1817 LeuArgValProArgArgLeuSerArgThrLeuMetPhePheLeuValValThrAsp 1836
 Db 5482 GTACGGGTG-----TATTGCTTCGCGCGCGGAC 5508
 QY 1837 SerThrAlaProAspAlaLeuAsp---AlaGlnGlyLeuTyRglnGlyValGlnCysTyR 1855
 Db 5509 GCGGTGCGGAGCGCACATGATGACTGCGCGCGCGCGCTGAAACCGAATGCTGCTTC 5568
 QY 1856 AsnGly1TyRglnProThrGluAsnGlyValMetSerThr1IleTyRPro1IleAspSerThr 1875
 Db 5569 AACGATACGCGCGCGACCGAGACGAGGTGTGACCGCGCTGTGTGAAACGCGCGCGCG 5628
 QY 1876 GluSerPhe---1IleAsnGlyValPro1IleGlyArgAlaLeuAsnAspSerGlyAlaTyR 1894
 Db 5629 GATGCTCGCGCGCGCATCATGCGCATGCTGTGCTGTGCGCAACCTTACCGCGCTAC 5688
 QY 1895 ValValAspProGlnGlnGlnLeuValGly1IleGlyValMetGlyGlnLeuValValThr 1914
 Db 5689 ATCTTCGACGCGGAGTTGAACCTGCTGCCGTGAGCGGTGGCGGCGAATGTTACTGGGC 5748
 QY 1915 GlyAspGlyLeuAlaArgGlyTyRSerAspLys---AlaLeuAspGluAsnArgPheVal 1933
 Db 5749 GGGGAAAGGCTGGCGCGCGCTACCTGAGACGTCGCGCGCTGACCGCGCAGCGTTTGGTG 5808
 QY 1934 His1IleThrValAsnAspGlnThrValLysAlaTyRArgThrGlyAspArgValArgTyR 1953
 Db 5809 CCGGACCCCTTGGCGCGCGCGCGAGCGGCTGTACCGCGCGCGCATCTGACCCGCTGGG 5868
 QY 1954 Arg1IleGlyAspGlyLeu1IleGluPhePheGlyArgMetAspThrGlnPheLys1IleArg 1973
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 Db 5926 GGTCTCGCATTCGAATCGGAGAGATGAGAGCGCGCTGGCGAGATATCCGGGGGTGGCG 5985
 QY 1994 AspAlaAlaValValLeuGlnGlnAsnGluAspGlnAlaProGlu1IleLeuGlyPheVal 2013
 Db 5986 GAGCGCGTGTGTGGCGCCAG----- 6006
 QY 2014 ValAlaAspHisAspHisSerGluAsnAspLysGlyGlnSerAlaAsnGlnValGlnGly 2033
 Db 6006 ----- 6006

QY 2034 TRGlnAspHisPheGluSerGlyMetYrSerAspIleGlyLulIleAspProSerThr 2053
 Db 6007 -----CGGGGTGGC 6015
 QY 2054 IleGlySerAspPheGlyTyrThrSerMetYrAspGlySerGlnIleAspPheAsp 2073
 Db 6016 GTGGGCGACAGTGTGGGCTTAC----- 6039
 QY 2074 GluMetHisGluTyrPheGlyGluThrThrArgThrIleuHisAspAsnArgSerLeuGly 2093
 Db 6039 ----- 6039
 QY 2094 AsnValIleGluIleGlyThrGlySerGlyMetIleuPheAsnLeuAspSerArgLeu 2113
 Db 6039 ----- 6039
 QY 2114 GluSerYrValGlyLeuGluProSerArgSerAlaAlaIlePheValAsnLysAlaThr 2133
 Db 6039 ----- 6039
 QY 2134 GluSerIleProSerLeuAlaGlyLysAlaLysValGlnValGlyThrAlaThrAspIle 2153
 Db 6039 ----- 6039
 QY 2154 GlyGlnValAspAspLeuHisProAspLeuValIleuAsnSerValIleGlnTyrPhe 2173
 Db 6040 -----GTGGTGGCGCCGCGC 6054
 QY 2174 ProSerSerGluTyrLeuAlaGluIleAlaAspThrIleuIleHisLeuProAsnValGln 2193
 Db 6055 CCGGCGC-----GTGGCGGATTCG-----CCGGAAGCGCAG 6084
 QY 2194 ArgIlePhePheGluAspValArgSerGlnAlaThrAsnGlnHisPheLeuAlaAlaArg 2213
 Db 6085 -----GCGGAGTCCGCGCGCAG----- 6102
 QY 2214 AlaIleIleThrLeuGlyLysAsnAlaThrLysAspAspValArgGlnLysMetAlaGlu 2233
 Db 6102 ----- 6102
 QY 2234 LeuGluAspMetGluGluLeuLeuValGluProAlaPhePheThrSerLeuLysAsp 2253
 Db 6102 ----- 6102
 QY 2254 ArgPheProGlyLeuValGluHisValGluIleLeuProLysAsnMetGluAlaValAsn 2273
 Db 6102 ----- 6102
 QY 2274 GluLeuSerAlaTyrArgTyrAlaAlaValAlaHisValArgGlySerLeuGlyAspGlu 2293
 Db 6102 ----- 6102
 QY 2294 LeuValIleuProValGluLysAspAspTyrIleAspPheGlnAlaAsnGlnLeuAsnGln 2313
 Db 6102 ----- 6102
 QY 2314 LysSerLeuGlyAspLeuLeuLysSerSerAspAlaAlaIleMetAlaValSerLysIle 2333
 Db 6102 ----- 6102
 QY 2334 ProPheGluIleThrAlaPheGluArgGlnValAlaLaserLeuAsnSerAsnIleAsp 2353
 Db 6102 ----- 6102
 QY 2354 GluTyrGlnLeuSerThrIleArgSerSerAlaGluGlyAspSerSerLeuSerValPro 2373
 Db 6102 ----- 6102
 QY 2374 AspIlePheArgIleAlaGlyGluAlaGlyPheArgValGluValSerSerAlaArgGln 2393
 Db 6102 ----- 6102
 QY 2394 TrpSerGlnAsnGlyAlaLeuAspAlaValPheHisHisCysCysSerGlnGlyArgThr 2413

Db 6102 ----- 6102
 QY 2414 LeuValAsnPheProThrAspHisHisLeuArgGlySerAspLeuLeuThrAsnArgPro 2433
 Db 6102 ----- 6102
 QY 2434 LeuGlnArgLeuGlnAsnArgIleAlaIleGluValArgGluArgLeuArgSerLeu 2453
 Db 6103 -----TTGAAGACGGCGCTGCCGACGCC 6126
 QY 2454 LeuProSerYrMetIleProSerAsnIleValIleuAspLysPheMetProLeuAsnAla 2473
 Db 6127 CTGCGGAAATACATGGGCGCATCGCATCTGTTCCTGGCGCGGATGCCGTCGACGCCG 6186
 QY 2474 AsnGlyLysValAspArgGlyGluLeuSerArgAlaAlaLysValAlaPolyGlnGln 2493
 Db 6187 AACGGCAAGCTGACCGCAAGGCGCTGCCCGCGGATCGAGCCCTGTTCAGCAGCTC 6246
 QY 2494 ThrAlaAlaProLeuProThrPheProIleSerGluValGluIleLeuGlyGluGlu 2513
 Db 6247 TACGTGGCGCGCGCA-----AGCGATCTGAGCAACAGCTCGCGGGATC 6291
 QY 2514 AlaThrGluValPheGlyMet---LysValAspIleThrAspHisPhePheAsnLeuGly 2532
 Db 6292 TGGCGGAGGTCTCGCAATTGCAACAGGTGGGTCTGACGACAACTTCGAGCTTGGC 6351
 QY 2533 GlyHisSerLeuLeuAlaThrLysLeuIleSerArgIleAspGlnArgLeuLysValArg 2552
 Db 6352 GGGCACTCGTGTGGCGACCCAGCTGATGGCGCTACGCAACAGCAGCTGAG 6411
 QY 2553 IleThrValLysAspValPheAspHisProValPheAlaAspLeuLaserValIleArg 2572
 Db 6412 GTCCCGATCAAGTCGATGTTACCCGCGAGACACTGGGTGAGTTCTGCCAGCGCTGAG 6471
 QY 2573 GlnGlyLeuGlyLeuGlnGlnProValSerAspGlyGlnGlyLysAspArgSerAlaHis 2592
 Db 6472 ACCCTCAAGCGCAGAGCGCGCGTGGAAGATGCCCTGCTAAATCCCTGAGGCGC--- 6528
 QY 2593 MetAlaProArgThrGluThrGluAlaIleLeuCysAspGluPheAlaLysValLeu 2611
 Db 6529 -----CTCAACAGCTATCTGCGGATCACTTGMAAACTGATT 6567

RESULT 4

US-09-252-991A-6997
 ; Sequence 6997, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 6997
 ; LENGTH: 10023
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-6997

Alignment Scores:

Pred. No.: 2,44e-159 Length: 10023
 Score: 1618.00 Matches: 778
 Percent Similarity: 39.10% Conservative: 454
 Best Local Similarity: 24.69% Mismatches: 1231
 Query Match: 10.03% Indels: 694
 DB: 4 Gaps: 118

US-09-482-788-2 (1-3129) x US-09-252-991A-6997 (1-10023)

65 LeuAspLeuSerIleSerAlaIleGlyHisValTyrAspValPro-----79
 1669 ATGATCCGACGAC-----GCCGCTCAACAATCCCGCGCGCTCGCGCTG 1716
 80 ---ThrAspIleAspIleSerArgPheAlaLeuAlaTryptylValIleAsnGlnThr 98
 1717 CGCGCGACGCTGCGACGAGCGCGCTCGCGCGACCTTCGACGCGCTGTGCAACGCGCAC 1776
 99 ProAlaLeuArgAlaPheAlaPheThrSerAspSerGlyLeuThrSerGlnValIleLeu 118
 1777 GAAGCGTGGCGACGCGCTTCTCGACGCGGACGCGCGCTTCGACGCGATGACGAG 1836
 119 LysAspSerPheValPheSerTrpMetCysTrp--SerSerSerSerProAspGluVal 138
 1837 CGGCGCGACGTTT-----GCCTGGACGTTTCTGACGCTCGCGCGCTG--GC 1880
 138 ValArgAspGlnAlaAlaAlaAla-----147
 1881 CGAGCAGCAGACGCGCGCGCTCGCGCGACGCGCGGACGCGGACGCGCGCTT 1940
 148 -----SerGlyProArgCysAsnArgPheValLeuLeuGlnAspMetGlnThr 164
 1941 CGACCTGAAAGAGGCGCGCTGCTGCGG-----GTACGCTGTGCGCTGACGACGA 1994
 164 LysCysGlnLeuValTryptPheSerHisValLeuValAspValThrPheGlnGlnArg 184
 1995 GAGACACACGCTGCGGTGACCTCGCATCAGATGTCGCGCATGTGTCGCTGAACCT 2054
 184 GValLeu-----SerArgValPheAla-----191
 2055 GGTGCTGACGAAATTCGTGCGGCTCTACGCGAAGCTGCGCGCGCGCGCGACCT 2114
 191 -----191
 2115 GCGCGCGCTGAACTGACACGCGAGCTGCTGCTGCGACGCGACGAGTGGCTGACGC 2174
 192 -----AlaTyrLysHisGlnLys-----AspThrHisArgPro 202
 2175 GGGCGAGGCGCGCGCGCACTGCGCTTCTGCGCGGAAACGCTGGCGCACAG-----GGCGC 2211
 202 OGlnThrProGlnSerSerArgAlaThrAspThrAspSerGlnSerValIle 222
 2232 GGTGCTGGAACCTGCGACCGCATCCGCGCGACGCGCGCGCGCGCTGCGCGCGCGC 2291
 222 rMetSerCysGlnAspAsnAlaValSerAlaThrHisPheTrpGlnThrHisLeuAsnArg 242
 2292 CTACAGCTGCGCGGTGACGAGCGCTGCGCGCGGTATCCGCGAGCGCGCGCTG--GA 2348
 242 PLeuAsnAlaSerValPheProHisLeu-----SerAspHisLeuMetValProAsnArg 260
 2349 CATGAGCGCAGTCTCTTCATGTCGCTGCGCGCGCTCCAGCGCTGCTGCATCCCA 2408
 260 otherThrAlaGlnHisArgIleThrPhePro--LeuSerGlnLysAlaLeuSerArg 279
 2409 CACGCGGACGAGGCGAGATCCGATCGCGCTGCGCGCGACGCGCGACGCGCTGAGAC 2468
 279 nSerAlaIleCysArgThrAlaLeuSerIleLeuLeuSerArgTyrThr-----295
 2469 CAGAGGCGTGGCTGCTTCTTCATCAACCTGTGCTGCGCGCGCGCGCGCGCG 2528
 296 -----HisSerArgGlnAlaLeuPheGlnAlaValThrGln 307
 2529 CAGCGCTTGGCGCATTGTCTGCGCGAGGCTCGCGAGGCGACCTCGCGCGCGCGCA 2588
 307 uGlnSerLeuProPheAspLysHisTyrLeuAlaAspGlyThr--TyrGlnThrValAla 326
 2589 CAGAGCCTGCGCTTTCACGACGAGTCTCGCGCGCTGCGCGCGCGCGCGCGCTTCCA 2648
 326 aProLeuArgValHisCysGlnSerAsnLeuArgAlaSerAspValMetAspAlaIle 346
 2649 GGTGCTGTTCACCAACGACGAGCGCGACCTG-----TCGCGGTTCGCG 2690

346 rSerTyrAspAspArgLeuGlyHisValLeuAlaProPheGlyLeuArgAspIleArgAsnThr 366
 2691 CGCGCTGCGCGCGCTGCTGCGCGACGAGCTGCGCTGCGACAGCGCGCA-----2739
 366 rGlyAspAsnGlySerAlaAlaCysAspPheGlnThrValLeuLeuValThrAspGly 386
 2740 -----GCCAAGTTCGACCTGCAA-----2757
 386 rHisValAsnAsnGlyIleAsnGlyPheLeuGlnGlnIleThrGlnSerSerHisPhe 406
 2757 -----2757
 406 tProCysAsnAsnArgAlaLeuLeuLeuHisCysGlnMetGlnSerSerGlyAlaLeu 426
 2758 -----TCGACAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2792
 426 uValAlaTyr--TyrAspHisAsnValIleAspSerLeuGlnThrThrArgLeuGln 445
 2793 CTGAAATTCGACTACGCGCGGACCTTTCGACGAGCGCGACGATCCGCGGTTTCGCGC 2852
 445 nGlnPheGlyHisLeuLeu-----LysCysLeuGlnSerPro 457
 2853 GCAATACCTGAGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTGCTT 2904
 457 oLeuAspLeuSerSerMetAlaGlnValAsnLeuMetThrGlyTyrAspArgAlaGln 477
 2905 -----GGCATATCGCGCTGTGTCGACGCGCGAGCGCGCGCGCGCGCGCT 2945
 477 eGlnSerTrpAsnSerGlnProLeuGlnValGlnAspThrLeuLeuHisHisGlnMetLe 497
 2946 CGCGGATGGGAGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGCTGCGA 3005
 497 uLysAlaValSerHisSerProThrLysThrAlaIleGlnAlaTyrAsp--GlyAspTr 516
 3006 GCGGCACTGTCGACGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 3062
 516 rPThrTyrSerGlnLeuAspAsnValSerSerArgLeuAlaValHisIleLysSerLeuGln 536
 3063 CGGCTACCGCGCACTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3122
 536 yLeuArgAlaGlnGlnAlaIleIleProValTyrPheGlnLysSerLysTrpValIleAl 556
 3123 CGTC--GGCGCGGACGCTGCGGTAGCGATCGCGCGCGCGCGCGCGCGCGCGCGCTGCT 3179
 556 aSerMetLeuAlaValLeuLysSerGlyAsnAlaPheThrLeuIleAspProAsnAspArg 576
 3180 CGGTCTGCTGCGCATGCTCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 3239
 576 oProAlaArgThrAlaGlnValAlaThrGlnThrArgAlaThrValAlaLeuThrSerLys 596
 3240 CAGGAAAGCGCTGCGCTCAATGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3299
 596 sLeuHisArgGlnThrValGlnLysValGlyArgCysValValValAspAspGlyLe 616
 3300 CATCTGTTGAGCGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 3359
 616 uLeuGlnSerValSerAlaSerAspAspPheSerSerLeuThrLysSerGlnAspLeuAl 636
 3360 CAAGCTGCAACATGCG 3419
 636 aTyrValIlePheThrSerSerGlySerThrGlyAspProLysGlyIleMetIleGlnHisArg 656
 3420 CTAGCTCATACACCTCGCGCTCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3479
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 3480 GGGCGCTGCGCGCGCGCTGCAATGATGACGAGCGACCATGACCGCTTCACGCGCGCGCGCT 3539
 676 gAlaLeuGlnPheGlyThrHisAlaPheGlyAlaCysValLeuLeuGlnIleMetThrThrLe 696
 3540 GGTGATCAGAGAGCGCGCGGTGAGCTTCGACGTCGTGCGGTGAGTGTTCGCGCGCT 3599

Qy	696	uIlleAnGlyGlyCy-----ValCyIlleProSerThAspAraSerAraMetAenSe	713
Db	3600	GGTACC---GGTTGGCGCGGTGCTTCCTGCGCGCCCGGACGAGACCGCATCCGCGCG	3656
Qy	713	rIlleProSerPheIleAsnArgTyraAnValAsnTriMetMetAlaThrProSerTyMe	733
Db	3657	CTGTGTGGAACTGGATGGCGGCAAGTTCCGGGGTATCAACAGCTGCATTCTGGCCGCTGCT	3716
Qy	733	tGlyThrPheSerProGluAraValProGlyLeuAlaThr-----Le	747
Db	3717	GCAACTGTTGATC-----GACGAACCGCGGTGCGCGCTGGCGGACAGCTGCAGCGCT	3770
Qy	747	vValleuValGlyGluGlnMetSerSerVal---AsnAlaIleTrp-----AlaPr	764
Db	3771	GTTCCTCGCGCGCGGACGCGCTTCGCGGAGACTCGCAACCGCATGTTTCAACCGCTGCC	3830
Qy	764	oLyLeuGlnLeuLeuAsnGlyTyrglyGlnSerGlyuserSer-----	779
Db	3831	GGCGGTGGCCCTGCATACCGGCTACGGGCGGACCGAAGCCGCATCAACGTCAACCCATTG	3890
Qy	780	-IleCyPheAlaSerAsnMetSerThrGluProAsnAsnMetGlyAraGAlaGlyAl	799
Db	3891	GCAATGCGCGCGGAGACGCGCGGACGCTTGGCGG-----ATGCGCGACGCGTGGGCA	3944
Qy	799	aHisSerTrpValIleAspProAsnAspIleAsnArgLeuValProIleGlyAlaValG	819
Db	3945	CGTGTCTGCGCGCGTGGAGCGCGGCGGCAAGTTGAC---CTGCTGGCGGCGCGGCTGCGCG	4001
Qy	819	yGlyLeuValIleGluSerProGlyIleAlaArgAspTrtLeValProProProProG	839
Db	4002	CGACTGTGCACTGGCGCGGCTGGGCTGGGCGCGGCGGCTACTGGGGCGCGCGCGCTGAC	4061
Qy	839	uLySerProPheThrPheThrAspIleProSerTrpTyraAlaAsnThrPheProAspG	859
Db	4062	CGCGGACGCGCTTCGCGCGCATCGGCTGCG-----GGCGTGG	4100
Qy	859	yAlaLyLeuTyraArgThrGlyAraPheLeuAlaArgTyraIleSerArgGlySerIleValCy	879
Db	4101	CGAAGCGCTGTACCGCACCGCGCGACCGCGCGGCTGGAAACCGCACGCGCTGTGGATATA	4160
Qy	879	sLeuGlyArgIleAspSerGlnValLyIleArgGlyGlnArgTyraGlyLeuGlyAlaI	899
Db	4161	CTCTGGCGCGCTGCACAGCAAGTGTACGTGCTGCTGCTGCGCATCGAGCGCGAGAAAT	4220
Qy	899	eGluThrIleuTyrglnGlnGln-----MetProAspAraPheThrIleValGAlaI	917
Db	4221	CCAGGCAACGCTGCTGCGCGACCGCGGGGTGCCCGCGCGGTATGCTGATGTCGCGAAG	4280
Qy	917	aThrLyArgSerGlnSerAlaAsnSerThrSerIleuIleAlaPheLeuIleGlySerSe	937
Db	4281	CGTGCGCGGACGCGAG-----TTGGTCGGG---TA	4307
Qy	937	rTyrrPheGlyAsnArgProSerAraPheIleIleuAsnIleAraIleAlaThrTyValaI	957
Db	4308	CTAATCTGGCGCTGTGCGCGCGGAGCGA-----GAAACCGACGAAACGAGCTGT	4358
Qy	957	eAsnIleLyLeuGlnGlnValIleProArgHiserIleProSerPheTyrrIleCyMe	977
Db	4359	GGCGCGCGCGCTTACAGCGCGGAATCTGCGGAATACATGATCTCCCGCGCATGTGATGCGCT	4418
Qy	977	tLeuGlyLeuProArgThrAlaThrGlyLyIleAspArgTyraGlyLeuArgIleMetG	997
Db	4419	GGCGGACATGCGCTCGGCGCGGAGCGCACTGGATGACGCGGCGGCTG-----	4467
Qy	997	yLyAspIleLeuAspLySerGlnThrGlnGlyAlaIleValGlnGlnAlaProAlaProI	1017
Db	4468	-----CCGGA	4472
Qy	1017	eProValPhe-----AlaAspThrAlaIleLyLeuH	1028
Db	4473	GCCGGTCTGGACGACGCGCGACAGCTGCAGCGCGGACGCGCATGCG	4532
Qy	1028	sSerIleTrpValGlnSerLeuGlyIleAspProAlaThrValAsnValGlyAlaThrPh	1048

Db	4533	CGTGAATCTGGAGCCGAAGTCTCGGCCTG-----CCGCGGGTCCGGCTTCGGCCGACGATTT	4586
Qy	1048	epheglnuleuylgylanserlierthralalelysevalasmetalaarg--Se	1067
Db	4587	CTTGAGCTGGCGGGGATTTCTCGTGGCCACCGCATCGTTCCGCCACCCCGCAGGC	4646
Qy	1067	rvalglymetaspleulysvalseasnilletyrglnhiiprothirleualaglyle--	1086
Db	4647	CTGGCAGCTCGAACCTGGCCGTGGCCGCGCTGTGGAGCCGACCACTGGAGGCTTCTG	4706
Qy	1087	-----serlialvallysglyaspproulensertyrthileuileiprolly	1102
Db	4707	CGAACAGSTCCGCGAGGCCAGCGCCGCGGACGTACCGACAGCCACGGCGGATTCGCCG	4766
Qy	1102	sserthrhisglnulprovalgluinsertyrseryserglnlyargleutrpheleus	1122
Db	4767	CATGACCGCGAGAGCGCGGTGGCGGTCTCTACTCTCGAGCAGGCGAMGTGTTCTCTG	4826
Qy	1122	pglnleuaspvalglyserleutrptryrleuileprotyralavalargmetarglypr	1142
Db	4827	GCAACTGGAGCCGAGCAGCCCGCGCTTCMAAGTCCGCGCCCTGGCAGCCCTCGACGGGCC	4886
Qy	1142	ovalasnyalaspalaleuargalalaleualaleuenglunarghlsigluthle	1162
Db	4887	GCTGACCTGGCGCGCTTCGAGCGCGCGCTACAGCCCTGTGTGACGCCACAGAACCT	4946
Qy	1162	uargthrthrphegluaspghlnaspglyvalglyvalglnilevalhinsglnlylseu	1182
Db	4947	GGCAGCACACGTTCCCGACGCTCGAGCGGTCCGCTACAGCGCGGTGACCGCGCATGCGG	5006
Qy	1182	rglnulmetlysvallleaspleucysglyseraspleuaspProheglu-----	1199
Db	5007	CCTGCACATGGACTGGCAGCAGCTTCTCCGCGCTCGACCGCAGCAGCCGCGCAGCAGCT	5066
Qy	1200	-----valleuamnglnluginthtrProphenleuenserSerlualaglytr	1217
Db	5067	GCAGACCTTCGCCGACAGCGAGCGCAGCCGGCTTCGACCTTAGAGCGGGCGGTGCT	5128
Qy	1217	pargalathrleuaurgleuaglygluaspasphisilleuuthrillevalmethisih	1237
Db	5127	GCGGTCGTCAGTGTGAAGATGCGCGAGCGGAGACACTGCTGTGTGACCTCGACCA	5166
Qy	1237	sileliseraspglytppserileaspvalleuarghraspheunanglnleutyse	1257
Db	5187	CATGCTCCACGAAGGCTGGCGATGGACATCTTCGCCCGAACCTGGCGCGCTCTACGA	5246
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RESULT 5
US-08-222-617A-3
Sequence 3, Application US/08222617A
Patent No. 5882879
GENERAL INFORMATION:
APPLICANT: Veenstra, Annemarie E.
APPLICANT: Martin, Juan P.
APPLICANT: Garcia, Bruno D.
APPLICANT: Gutierrez, Santiago
APPLICANT: Barredo, Jose L.
APPLICANT: Von Doehren, Hans
APPLICANT: Palisosa, Harriet
APPLICANT: Van Liemp, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois

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COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-Apr-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 11601 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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LOCATION: 388..11526
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FEATURE:
NAME/KEY: CDS
LOCATION: 8050..8052
OTHER INFORMATION:
OTHER INFORMATION: /note= "NNN=GCC, AGU, AGC, UCU, UCC, UCA, or UCG;"
OTHER INFORMATION: Xaa=Ala or Ser "
US-08-222-617A-3
Alignment Scores:
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Score: 1517.00 Matches: 730
Percent Similarity: 39.70% Conservative: 504
Best Local Similarity: 23.49% Mismatches: 1282
Query Match: 9.41% Indels: 593
DB: Gaps: 124
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 QY 1020 PheAlaAspThrAlaAlaLysLeuHisSerIleTrpValGlnSerLeuGlyIleAspPro 1039
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 QY 1060 LysMetAlaAsnMetAla-----ArgSerValGlyMetAspLeuLysValSerAsnIleTyr 1078
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 QY 1079 GlnHisProThrLeuAlaGlyIleSer-----1087
 Db 6208 AGCCATCGCATTCGAAGCTTGTCTCAGTGAATTCAGGGGTTGGAAGAGCTGACAG 6267
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 Db 6319 -----GCCAGGAAGAACTCATGTTCAATCAAGAGTTC 6351

QY 1125 -----AspValGlySerLeuTrpTyrLeuIleProTyrAlaValArgMet 1139
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 QY 1140 ArgGlyProValAsnValAspAlaLeuArgArgAlaLeuAlaLeuGluGlnArgHis 1159
 Db 6406 CACCATGATCTGTCTGATCTGATGAGAGAGCTTGGGAGATGCTGCTCGACACAC 6465
 QY 1160 GluThrLeuArgThr-----ThrPheGluAspGlnAspGlyValGlyAlaGln---Ile 1176
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 QY 1177 ValHisGlnLysLeuSerGluGluMetLysValIleAspLeu-----CysGlySerAsp 1194
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 Db 6766 TTGAGCGCTTCATGCTGATCGCTTACAGACACACAG-----GCTCCGCGCACTGGCCA 6819
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DB 7687 GGAAATCTCTCATGAGGCTCTTCGAGACATCGGCTGACCCCGGACCCCATCGCA 7746
QY 1582 ValValAspSerSerCysArgLeuThrTyrThrGluLeu---AspArgGlnSerAspIle 1600
DB 7747 ATTGCGTACGGGACCGAGAGCTCTCTGACTCCGAATCAAGACGGGCAAAACAGCTC 7806
QY 1601 LeuAlaGlyTyrLeuArgArgArgSerMetProAlaGluThrLeuValAlaValPheAla 1620
DB 7807 GTACATTTGATCATCTCTTCTGCGAGATTTGTAGCAGACGACGCAATCGCTTTCTTTG 7866
QY 1621 ProArgSerCysGluThrIleValAlaPhePheGlyValLeuLysValAlaLeuAlaTyr 1640
DB 7867 GACAAAGCATCATGATGTGATGCTCTCTGCGAGTTGGAAGCGCGGTGCCGATAT 7926
QY 1641 LeuProLeuAspValArgSerProSerAlaArgValGlnAspIleLeuSerGlyLeuSer 1660
DB 7927 GTGCCCTTGACCCGACATATCGTGGCAGAGACGAGCTCATCTTGAGAGAACTCAT 7986
QY 1661 GlyProThrIleValLeuIleGlyHisAspThrAlaProProAspIleGluValThrAsn 1680
DB 7987 GCCAGAGACCTCATCACTAGAAAGCAGCAGC---CCGAGGGGAGGAAACGTCGCAAT 8043
QY 1681 ValGluPheValArgIle-----ArgAspAlaLeuAsnAspSerAsnAlaAspGlyPhe 1698
DB 8044 GTTCANNNGTGGTCTTGACAGCCCGGAGACCTTAGCTGCTCAACGACGCTCAAG 8103
QY 1699 GluValIleGluHisAspSerThrLysProSerAlaThrSerLeuAlaTyrValLeuTyr 1718
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QY 1719 ThrSerGlySerThrGlyArgProLysGlyValMetIleGluHisArgValIleIleArg 1738
DB 8158 ACTCGGAGAACCAAGCAAGCAAGGAGGCTCTGGTGAGACCAAGACGATGATCCAG 8217
QY 1739 ThrValThrSerGlyCysIleProAsnTyrProSerGluThrArgMetAlaHis----- 1756
DB 8218 ---CTGCGCAATTCCTCATCGAGCGATATCTTCGCGAGACCAACGGGTCTCAAGCCGCTG 8274
QY 1757 ---MetAlaThrIleAlaPheAspGlyAlaSerTyrGluTyrIleTyrSerAlaLeuLeu 1774
DB 8275 CTCTTCTCTGCTCACTACGCTTCGACTTCTCTTGAACAGCTGTCTCTCAAGCTTTG 8334
QY 1775 PheGlyArgThrLeuValCysValAspTyrMetThrThrLeuAspAlaArgAlaLeuLys 1794
DB 8335 GGAGGAAACAAAGCTATC---ATTCCACCAAGAGAGGCTTCACGACGACGATTTCTAC 8391
QY 1795 AspValPhePheArgGluHisValAlaSerHisValThrSerSerSerGlnAsp 1814
DB 8392 GAATCGGGCGGAGAGAGATATCTTATCTCAGCGGACGCGCTCGGTGTCAGCAG 8451
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DB 9095 -----CGAGTATCCGTGACACCTGACCGCAACCTTCCCGCTAC 9135
QY 2060 YThrThrSerMetTyrAspLysGlnIleAspPheAsp---GluMetHisGluThrLeuG 2080
DB 9136 ATGTGCTCAAGTACAGATTCACCAAGTTGAGAGGATCTCTCCCGTGAACCGTATGGGAG 9195
QY 2080 LysGluThrThrArgThrLeuHisAspAsn-----ArgSerLeuGlyAsnVal 2096
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QY 2096 euGluIleGlyThrGlySerGlyMetIleLeuPheAsnLeuAspSerArgLeu---GluSer 2115
DB 9256 CGAAATTCACAGAGA-----AACCTTGCCAGCTTTGGGACATCT 9297
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DB 9298 CTCTTAGGCTCGACCATGCGGATTTGACGACGACTGTTCGCGAGCGGCGACAGC 9357
QY 2136 IleProSer-----LeuAlaGlyLysAlaLysValGlnValGlyThrAlaThrAspIle 2153
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Qy 2319 LeuLeuLysSerSerAlaAla-----Ala 2326
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RESULT 6
US-08-222-617A-24
/ Sequence 24, Application US/08222617A
/ Patent No. 5882879
/ GENERAL INFORMATION:
/ APPLICANT: Veenstra, Annemarie E.
/ APPLICANT: Martin, Juan F.
/ APPLICANT: Garcia, Bruno D.
/ APPLICANT: Gutierrez, Santiago
/ APPLICANT: Barredo, Jose L.
/ APPLICANT: Von Doehren, Hans
/ APPLICANT: Palissa, Harriet
/ APPLICANT: Van Liempt, Henk
/ APPLICANT: Montenegro, Eduardo P.
/ TITLE OF INVENTION: A Method for Influencing Beta-Lactam
/ TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
/ TITLE OF INVENTION: Quantities of ACV Synthetase
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
/ STREET: 300 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/222,617A
/ FILING DATE: 04-APR-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ REFERENCE/DOCKET NUMBER: 97,157
/ INFORMATION FOR SEQ ID NO: 24:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11601 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ ORIGINAL SOURCE:
/ ORGANISM: Acremonium chrysogenum
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 388..11526
/ OTHER INFORMATION: /function= "Enzyme"
/ OTHER INFORMATION: /product= "ACV Synthetase"
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 8050..8052
/ OTHER INFORMATION:
/ OTHER INFORMATION: /note= "NNN=AGU, AGC, UCU, UCC, UCA, or UCG"
/ US-08-222-617A-24

Alignment Scores:
Pred. No.: 1,71e+148 Length: 11601
Score: 1517.00 Matches: 730
Percent Similarity: 39.70% Conservative: 504

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Best Local Similarity:		23.49%	Mismatches:	1282
Query Match:		9.41%	Indels:	593
DB:	2	Gaps:	124	

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OY	22	SerHis-----GIYAsPserProLeuAsnSerTYRGluGlnLeu	35
DG	3043	GGCCACCGCAGCAAGCGGCCCATGTTCAGGACACAGCTAGTGCGCAGCAATTGGACAAAGGC	3102
OY	36	PheHisleuTYRGlyLeuAspSerSeraTYGLELuallelYSProCythrProPhe	55
DG	3103	TTTGTTCATTCATTCACCAAGAAGAACCTGCCAG-----	3138
OY	56	GlnleuAspMetIleasPCysAsnAlaleuAspArgInserAlalleGYHIsAlalVal	75
DG	3139	-----GCGTACCACTGACATTCATGATC---CAC-----	3165
OY	76	TyrAspValProThrAspIleAspDileSeraArgPheAlaleuAlatPLYSgluIleval	95
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OY	96	AsnGlnThrProAlaleuArgAlaPheAlaPheThrsSerAspSerGlyVsrThsSerGln	115
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DG	3337	GAGAAAGACGCTGCTGGCGCTGGACACAATCCAAGGAGACACTTGTGAAGTACCAT	3396
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OY	186	LeuSerArgValPheAlaAlaTyrlYsHis-----Glu	196
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DG	3571	CAGACCGTACTCTACCTACACTGCGCAGACGATPACTGACGACCAACAG-----	3618
OY	206	GlnSerSerAspAlaThrAspThrAspSerGlnSerValSerValSerMetSerCys	225
DG	3619	-----GACGACCAATCTGCACTTGTGGGCGCAGACAGATCGGACAGATCGAAGCGCTGC	3672
OY	226	GlnAspAsnAlaValSerAlaThrHisIvherTrpGlnThrHisleuAsnAspLeuAsnAla	245
DG	3673	GACATGAATGGCGTG-----CTGAATGAGCCAGCGCA	3705
OY	246	SerValPheProHisLeuSerAspHisleuMetValProAsnProThrThrAlaglu	265
DG	3706	TACAAGHGCCC---CTGGCGCGATATGACCAAGTC-----CCGACAGACAGGCGAG	3753
OY	266	HisArgIleThrPhePro-----LeuSer	273
DG	3754	CAGACCAATCACTGCGCCCTGGACAACCTCCATGACGCTGTGTGCGGAAAGAACTTCC	3813
OY	274	GlnLYsAlaIleuSerAsnSerAlalleCysArgThrAlaleuSerilleuLeuSerArg	293
DG	3814	AGTGTGCGATACCCCTTCATTCATTCATTCACAGACGCTGTGGACACTGTGTCTTCACACT	3873

QY 294 TyrThrHisSerAspGluAlaLeuPheGly---AlaValThrGluGlnSerLeuProPhe 312
 Db 3874 TATGAGAGGACACCCACAGCATCACCAGCATCTCCGGCCGTACCTGCCGTC 3933
 QY 313 AspLeuHisIleTyrLeuAlaAspGlyThrTyrGlnThrValAlaProLeu-----Arg 329
 Db 3934 CCGGGAATTAGCGCTGTGTCTCTCTTCTATCAACACACTCCCTATGATCTTGATCAC 3993
 QY 330 ValHisCysGlnSerAsnLeuArgAlaSerAspValMetAspAlaIleSerSerTyrAsp 349
 Db 3994 ACCGTCTGCCAGAT-----ATGACAGCGCTCGAGCGCATTTAGCATGTCCAA 4041
 QY 350 AspArgLeuGlnIleLeuAlaProPheGlyLeuArgAspIleArgAsnThrGlyAspAsn 369
 Db 4042 GGCACAGTCAACGCCATGAATCCCGGGGCAACGTGACGCTCGACCATAGCAAGAAC 4101
 QY 370 GlySerAlaAlaCysAspPheGlnThrValLeuLeuValThrAspGlySerHisValAsn 389
 Db 4102 GACCTCAAGCACGGGCTTTCGACACCTCTTCCTCGAGACTACCCAAACCTCGAC 4161
 QY 390 Asn-----GlyIleAsnGlyPheLeuGln 397
 Db 4162 ACCGAGACGGGGAGAAAGCAGAGAGAGCTCAAGTTCACATCAAGGGTGGCAGGAG 4221
 QY 398 GlnIleThrGluSerSerHisPheMetProCysAsnAsnArgAlaLeuLeuHisCys 417
 Db 4222 AAGCTCAGTTACCG-----CTGGCCGATGATGGCCCAAGAG 4257
 QY 418 GlnMetGluSerSerGlyAlaLeuLeuValAlaTyr-----TyrAspHis 432
 Db 4258 GACGGCCACAGCGGAGCTGTTTACGCTGTCTATCGGGCGAGCTTTCACAGGAGAG 4317
 QY 433 AsnValIleAspSerLeuGlnThrThrArgLeuLeuGlnIlePheGlyHisLeuIleLys 452
 Db 4318 TCCATTCAGGCGCTCTCGACACTGTCCGG-----GACACCTCGATGATATTCTCGGG 4371
 QY 453 CysLeuGlnSerProLeuAspLeuSerSerMetAlaGluValAsnLeuMetThrGluTyr 472
 Db 4372 AACATTCATGCCCTATC-----CGCAACATGAGTACCTCTCTCGAAC 4416
 QY 473 AspArgAlaGluIleGluSerTyrAsnSerGlnProLeuGluValGlnAspThrLeuIle 492
 Db 4417 CACAGCGCGAGCTCGCAAGTGAATGCCACCGCTTCGAGTACCCCAACACCACTAC 4476
 QY 493 HisIleGluMetLeuLysAlaValSerHisSerProThrLysThrAlaIleGlnAlaTyr 512
 Db 4477 CACGCCATGTCGATCCGAGCGCAGCGCAGCAAGCCGCAAGTGGCCGTGTAGAG 4536
 QY 513 AspGlyAspTyrThrTyrSerGluLeuAspAsnValSerSerArgLeuAlaValHisIle 532
 Db 4537 GATATCAGGCTGACCTACCGGAGCTCAACAGCCGTGCCAATGCGCTGTACTCTC 4596
 QY 533 LysSerLeuGlnLysLeuArgAlaGlnGlnAlaIleIleProValTyrPheGluLysSerLys 552
 Db 4597 CTCTCCAGCGCGCTATCCAAACGACAGCTGTGCGGTGATCATGACCAAGAGGAG 4656
 QY 553 TyrValIleLeuSerMetLeuAlaValLeuLysSerGlyAsnAlaPheThrLeuIleAsp 572
 Db 4657 CACATGATTCACGACATCTCTCGCGTCTGAAHAAACGGGTGAGCTTACGTCGATGAC 4716
 QY 573 ProAsnAspProProAlaIleArgThrAlaGlnValAlaThrGlnThrArgAlaThrValAla 592
 Db 4717 CCTGATACCTGACCAAGCATCCAGTATCTCGAGATACGGGGCTCTGCGAGTC 4776
 QY 593 LeuThrSerLysLeuHisArgGluThrValGlnLysLeuValGlyArg-----CysVal 610
 Db 4777 ATCAGCGACAGTCTCTATATGACCGGTGCGGAGCATCCCAACACCGCTTCTGTT 4836
 QY 611 ValValAspAspGluLeuLeuGlnSerValSerAlaSerAspAspPheSerSerLeuThr 630
 Db 4837 ATCCAGTCGACCTTGTGCTTCAACTCCCGCCAGCCAGTTCCTCCGCTCAAACTGC 4896

QY 631 LysSerGlnAspLeuAlaTyrValIlePheThrSerGlySerThrGlyAspProLysGly 650
 Db 4897 AACCCAGACCGCTCGCTCATCATCATGATACATACATCCGGCACCTCGCAACCCCAAGGCT 4956
 QY 651 IleMetIleGluHisArg-----AlaPheSerSerCysAlaLeuLysPhe 665
 Db 4957 GTCATGTGAGAGCACACCGGTGATGATCTGTGCGCTTCACTCTGCGGCTC---TTC 5013
 QY 666 GlyAlaSerLeuGlnIleAsnSerAspThrArgAlaLeuGlnPheGlyThrHisAlaPhe 685
 Db 5014 GGC-----CTTGAAACACAGATGACGAGTCACTCTCGTTCTCGAATCACTGCTTC 5067
 QY 686 GlyAlaCysLeuLeuGlnIleMetThrThrLeuIleAsnGlyLysValCysIlePro 705
 Db 5068 GACCACCTTGTCCAGAGATGACGATGCCCTTCTACACGCTGAGACTCTTGTGATCTC 5127
 QY 706 SerAspAspAspArg-----MetAsnSerIleProSerPheIleAsnArgTyrAsnVal 723
 Db 5128 AACGACAGATGCGTGGCCAGCAAGAGAGGCTTTCACATGATACAGACCAACCGGCTC 5187
 QY 724 AsnTyrMetMetAlaThrProSerTyrMetGlyThrPheSerProGluAspVal---Pro 742
 Db 5188 ACGTACCTCGGGGACACCTTCGTCATCTCATGATGACAGTTCCACCGCTCCGGAC 5247
 QY 743 GlyLeuAlaThrLeuValLeuValGlyGluGlnMetSerSerSerValAsnAlaIleTyr 762
 Db 5248 CACCTGGCGCGCGATGCTGCGGAGGCGCTTCAGCAAGCCGGTA----- 5295
 QY 763 AlaProLysLeuGln-----LeuLeuAsnGlyTyrGlyGlnSerGlu 776
 Db 5296 TTGCACAGATCCGCGAGACGTTCCGGGTCTATCATCAACGGTATGACCGGACTGAG 5355
 QY 777 SerSerSerIleCysPheAlaSerAsnMetSerThrGluProAsnAsnMetGlyArgAla 796
 Db 5356 GTGTCTATCATCACTCCCAAGCGGCTTACCGTCCGGAGCGCGCAGACAGAGAGC 5415
 QY 797 ValGlyAlaHis-----SerTyrValIleAspProAsnAspIleAsnArg 811
 Db 5416 ATCGGTGGCAGGTGACCAACACAGCAGCATGACTGCTCTC-----AACGTGACATGAG 5469
 QY 812 LeuValProIleGlyAlaValGlyGluLeuValIleGluSerProGlyIleAlaArgAsp 831
 Db 5470 CGGTGCCATTCGGGGCGTGGAGAGCTTACTGTGTGGCGCATGGCGCTCGCGCA 5529
 QY 832 TyrIleValProProProGluLysSerProPhePheThrAspIleProSerTyrTyr 851
 Db 5530 TAC-----CACACCGGCGAGCTGACG-----GCTGACCGGTTG 5565
 QY 852 ProAlaAsnThrPheProAsp-----GlyAlaLysLeuTyr 863
 Db 5566 CTGTGCCAACCCCTTCCAGACGAGCAGAGAGACTTGAAGGCGGAATGCGCGTGTAT 5625
 QY 864 ArgThrGlyAspLeuAlaArgTyrAla-----SerAspGlySerIleValCys 879
 Db 5626 AAGACTGTGACTTGTGCTGCTGATCCACATGCAACCGGCAATGTGATGATCGAGTAC 5685
 QY 880 LeuGlyArgIleAspSerGlnValLysIleArgGlyGlnArgValGluLeuGlyAlaIle 899
 Db 5686 CTGGCGCGCAAGCATTTCCAGGTCAGATTCGAGGCGCAAGATTCAGCGTGGAGAGATC 5745
 QY 900 GluThrHisLeuArgGlnGlnMetProAspAspLeuThrIleValValGluAlaThrLys 919
 Db 5746 GAGGCGGCTCT---TCATCTATCCGGGCGATCAACATCCGTCTCTCGGCGCAAGGAC 5802
 QY 920 ArgSerGlnSerValAsnSerThrSerLeuIleAlaPheLeuIleGlySerSerTyrPhe 939
 Db 5803 CGCAAGATGACGGGAGAAAG-----TACTCTGTGGC-----TACTTC 5841
 QY 940 GlyAsnArgProSerAspAlaHisIleLeuAspHisAspAlaThrLysValIleAsnIle 959
 Db 5842 -----CTCTCTTCAGCAGGCTCCCTG-----TCCGCCAGCGCATCCGCGCG 5883
 QY 960 LysLeuGlnGlnValLeuProArgHisSerIleProSerPheTyrIleCysMetLeuGlu 979

Db	5884	TTATGCTCAGACGACCTGGCCCGGATTAACAGTGGTCTCTGGCAGCTGGTGGCCATGCGCAAG	5943
Qy	980	LeuProArgThrAlaArgIleGlyLysIleAspArgArgIleArgIleMetGlyLysAsp	999
Db	5944	TTCCCGCGTACCGTAGAGGGGAGAGCTGATGCAAGGCGCTTGGCCGGTCCAGAGATACA	6003
Qy	1000	IleLeuAspLysGlnThrGlnGlyAlaIleValGlnGlnIleProAlaProIleProVal	1019
Db	6004	GTCACGAGATGAC-----ATTTGCCACCG	6027
Qy	1020	PheAlaAspThrAlaAlaLysLeuHisSerIleThrValGlnSerLeuGlyIleAspPro	1039
Db	6028	CGTACCGAGGTGAGCGGCATCTTACGCTGGATCTGGTGTGACCTGTTGGAGATCCGGTC	6087
Qy	1040	AlaThrValAsnValGlyAlaThrPhePheGluLeuGlyIleAsnSerIleThrAlaIle	1059
Db	6088	GACAGGATCAGCATCTACAGTACGACTCTTCAAGTGGCGGCGACAGTCTCAAGATGAC	6147
Qy	1060	LysMetValAsnMetAla--ArgSerValGlyMetAspLysLysValSerAsnIleTyr	1078
Db	6148	AAGCTGTCTTGTGGTCCACTCGGAGCTCTCGATGGCCGTCAAGTGTCCGACATTGTC	6207
Qy	1079	GlnHisProThrIleuAlaGlyIleSer-----	1087
Db	6208	AGCCATCCGATATCGAAGCCTTGTCTCAGTGATATCAGGGTTCGACGAGTCAAG	6267
Qy	1088	-----AlaValIleLysGlyAsp--ProLeuSerTyrThrLeuIleProLysSerThr	1104
Db	6268	GATGTGGCTGTGTGGAGAGGCGCGTCCAGTCTTATATCCCCCTTATCCCT-----	6318
Qy	1105	HisGlnGlyProValGlnGlnSerTyrSerGlnGlyArgLeuTyrPheLeuAspGlnLeu	1124
Db	6319	-----GCCAGAAAGACTCATGTTTCATCCAGACGATCC	6351
Qy	1125	-----AspValGlySerLeuTyrTyrLeuIleProTyrAlaValArgMet	1139
Db	6352	GGCCATAGCGCGAGATCTGGTCT-----TACATGTGCTTTGGACGTCCAGCTT	6405
Qy	1140	ArgGlyProValAsnValAspAlaLeuArgArgAlaLeuAlaIleGlnGlnArgHis	1159
Db	6406	CACCATGATGTCTGTCTGAGTCCGCTTGAGAAAGCTCTCGCGGATGTCTGTCCAGACAC	6455
Qy	1160	GluThrLeuArgThr-----ThrPheGluAspGlnAspGlyValGlyValGln--Ile	1176
Db	6466	GAGGCTCTCCGGACTTGATCACCAGGACCCAGAAAGTCTCCGTGACATGCCAGAAAGT	6525
Qy	1177	ValHisGluLysLeuSerGlnGlnMetLysValIleAspLeu-----CysGlySerAsp	1194
Db	6526	CTCAGCGCGGAGGAAGCGCAAAAGCTCTTCTGTGATGTCTTGGCGCTGACCTCGAG	6585
Qy	1195	LeuAspProPheGluValLeuAsnGlnGlnGlnThrThrProPheAsnLeuSerGln	1214
Db	6586	ACGGAAGATGACGGGCGAGATGCCGAGAGTACCGCCACGCGCTTCAAGCTGACGAGGAA	6645
Qy	1215	AlaGlyTyrPArgAlaThrIleLeuLeuArgLeuGlyLysAspHisIleLeu-----	1231
Db	6646	CTCCCGATTCATGACGCTCTTACAGGTTGTAGGTATGGCCGACGCTCAGCTTGGC	6705
Qy	1232	ThrIleValMetHisHisIleIleSerAspGlyTyrSerIleAspValLeuArgArgAsp	1251
Db	6706	AGCATGTGCTGCCACATCTGCGCTTGTACCGGTGATGAGTATGTTTCAAGAGGAC	6765
Qy	1252	LeuAsnGlnLeuTyrSerLeuAlaIleuLysAspSerLysAspProLeuSerAlaLeuThr	1271
Db	6766	TTGAGACGCTTCTATGCGCTTCCATACGACAGACAAAG-----GCTGCCGCAACTGCCA	6819
Qy	1272	ProLeuProIleGlnTyrSerAspPheAla--LysTyrGlnLysAspGlnPheIleGlu	1290
Db	6820	ACCGTCCGCGTCAATATTAAGAGATGTCGATAGACACGCGCGGCTCTCCGGCGTAG	6879
Qy	1291	GlnGlnLysGlnLeu--AsnTyrTyrLysGlnLeuLysAspSerSerProAlaLys	1309

Db	6880	CACAGACGGTGTCTCCGGGAACTACTGGCTGGCGAAGCTCAAGTGCATGAGACGGCTTAT	6939
Qy	1310	ILProThraPhePheAlaArgProAlaLeuSerGlyAspAlaGlyCysValHisVal	1329
Db	6940	CTGGTCCCGGATCCCGCTCCGACCGCGCGACGTTTACTATACCCGGAAAGATCTCCAGTTC	6999
Qy	1330	ThrIleArgGlyLeuTyrcInSerIleuArgAlaPheCysAsnGluHisThrThr	1349
Db	7000	TCAACTACTCCCGAGAACCAACCGCGAGTGAAGAGCTGGCCAAAGCGGACGGTTCAAGC	7059
Qy	1350	SerPheValValLeuLeuAlaAlaPheArgAlaAlaHisGlyArgLeuThrAlaValGlu	1369
Db	7060	CTCTACACCGGTGTGGGGCGGCGCTACTCTTGTCTCTACGCTGATACCAACAGACGG	7119
Qy	1370	AspAlaValIleGlyThrProIleAlaAsnArgAsnArgProGluLeuGluAspIleIle	1389
Db	7120	GATATCAACGATGGTATATCCCGTTGGCGACCGTATACCATCCGGAATTGATCCGGTTC	7179
Qy	1390	GlyCysPheValAsnThrGlnCysMetCArgIleAsnIleAspHisAspThrPheGly	1409
Db	7180	GCGTCTTTGGTCACTTGGCTCCCTCTGGGGGTCAACGCTGTCACTGGACATTCATGGA	7239
Qy	1410	ThrIleuIleAsnGlnValIleValIleThrThrThrAlaAlaPheGluAsnGluAspIlePro	1429
Db	7240	---CTTATCCAGGACAGTGCAGAAAGAGCTTCCGATCCGACATCCACAGACTTGGCA	7296
Qy	1430	PheGluArgValValSerAlaLeuGlnProGlySerArgAspLeuSerThrProIleu	1449
Db	7297	TTCCAGAGACATCCACCAAGCTTCTTCATGTG---CAGACAGATCCACGCGCCATCCCTT	7353
Qy	1450	AlaGlnLeuIlePhe-----AlaValHisSerGlnLysAspLeu	1462
Db	7354	CTCCAGGCGCGGTTCACACTGGGAAAAAGTACCCGCCCATGTCCAGAGACACACTGCTT	7413
Qy	1463	GlyArgPheIysPheGlnGlyLeuGlySerValProValProSerIlyAlaIleTyThrArg	1482
Db	7414	CAGAGATCAAG-----CCGCCCTCGCTCTGCTTGGCGGCC-----AAG	7455
Qy	1483	PheAspMetGluPheHisIleuPheGlnGluThrAspSerLeuLysGlySerValAsnPhe	1502
Db	7456	TTTGATCTCAACGTCACGCGTAAAGAGAGCGTCAATTCGCTCAACGTCATCACTCAT	7515
Qy	1503	AlaAspGluLeuPheIysMetGlnThyValGluAsnValValArgValPhePheGluIle	1522
Db	7516	CTTACCAAGCTCTTCGAGAGAGAACCGTTCAGGGGTCAAGAAACCTTCATCTCCTT	7575
Qy	1523	LeuArgAsn---GlyLeuGlnSerSerArgThrProValSerIleLeuProIleuThrAsp	1541
Db	7576	CTTGACACACTGGCCCAACACAGAGCTTACACAAAGCTCTCGAAGCTGTCCGTTGAAGAT	7635
Qy	1542	GlyIleValThrLeuGluLysLeuAspValLeuAsnValLysHisValAspTyrProArg	1561
Db	7636	GGAGGTGTGATCCAGAGCG-----ACTAATCTTCAGCCCTCAAGCGGGAGACGC	7686
Qy	1562	GluSerSerLeuAlaAspValPheGlnThrGlnValSerIleAlaTyProAspSerLeuAla	1581
Db	7687	GGAATTCACATCCATGGGCTCTTCGAGGACATCTGGCGCTCGAACCCCGACCGCATCCCA	7746
Qy	1582	ValValaAspSerSerCysArgLeuThrTyThrGlnLeu---AspArgGlnSerAspIle	1600
Db	7747	ATTGCTGACGGACACAGAGATCTCTCTGATCTCCAACTCAACGAGCGGGCAAAACAGCTTC	7806
Qy	1601	LeuAlaGlyTrpLeuArgArgArgSerMetProAlaGluThrLeuValAlaValPheAla	1620
Db	7807	GTACTATTGATCATCTCTTCTGCCACAGTATTGTACACAGACAGCCGATCGCTCTTTTG	7866
Qy	1621	ProArgSerCysGluThrIleValAlaAspPheGlyValLeuLysAlaAsnLeuAlaTy	1640
Db	7867	GACAAAGACATCGATATGATGATGATGCTCTCTGACAGATTTGGAAAGCGCGGCTCGCATAT	7926
Qy	1641	LeuProIleuAspValArgSerProSerAlaArgValGlnAspIleLeuSerGlyLeuSer	1660
Db	7927	GTCGCCCTTACCCGACATATCTCGTGGAGAGGACTGATCTATCTTTGGAGAAATCTAGT	7986

QY 1661 GlyProThriIleValIleuIleGlyHisAspThrAlaProAspIleGluValThrAsn 1660
Db 7987 GCCAGACGCTCATCACCACCTAGAAAGACACG---CCGAGGGAGGAAACGTCGCAAT 8043
QY 1681 ValGluPheValArgIle-----ArgAspAlaIleuHisSerAsnAlaSerGlyPhe 1698
Db 8044 GTTCCANNNTGGTCTTGACAGCCCGAGACCTTACCTGCTCCACACGACTCAAG 8103
QY 1699 GluValIleGluHisAspSerThrIleProSerAlaThrSerIleuAlaIleuValIleuThr 1718
Db 8104 GAAACCCGACCAACGTACAGCGAAGAACCTGCC-----GACCTCGCATATGATATCTTC 8157
QY 1719 ThrSerGlySerThrGlyArgProGlyGlyValMetIleGluHisArgValIleIleArg 1738
Db 8158 ACCTCGGAGACACACAGGCAAGCCCAAGGGGTTCTGTGAGACACAGAGGTAGTCAG 8217
QY 1739 ThrValThrSerGlyCysIleProAsnTyrProSerGluThrArgMetAlaHis----- 1756
Db 8218 ---CTGGCAATCCCTCATCGAGCGATCTTCGCGACAGACCAACGGGTTCTACGCGCTG 8274
QY 1757 ---MetAlaThrIleAlaPheAspGlyAlaSerTyrAlaSerTyrGluIleTyrSerAlaIleu 1774
Db 8275 CTCTCTCTGCTCACTACGCTCTTCACTCTCTTGAACAGCTCTGCTCTCTGCTCTG 8334
QY 1775 PheGlyArgThrIleuValCysValAspTyrMetThrThrIleuAspAlaArgAlaIleuLys 1794
Db 8335 GGTGGAACAAGCTCATC---ATTCACACAGAGAGGGGTCTCAGCAGCAGAGCATTCAC 8391
QY 1795 AspValPhePheArgGluHisValAsnAlaIleSerIleValIleThrSerSerGluAsp 1814
Db 8392 GACATCGCGCGAGGAGGAAAGCTATCTCATCTCAGCGGAGCCCTCGGTGTCGACAG 8451
QY 1815 ValProIleu---ArgValProArgArgIleuSerArgThrIleuMetPhePheIleuVal 1833
Db 8452 ATTGAGCTCTCCGCTCTGCGCGAT-----CTTCACATGTCACCGCTGCG 8496
QY 1834 ValThrAspSerThrAlaProAspAlaIleuAspAlaGluIleuTyrGluIleValGlu 1853
Db 8497 GCGAGAGAGTTCACGCTAGTCAGTTGAGAAAGATGCGCTCCGCGCGGCG---CAG 8553
QY 1854 CysTyrArgIleuTyrGlyProThrGluAsnGlyValMetSerThrIleTyrProIleAsp 1873
Db 8554 ATCAACAACCGCATATGATCATCTGAG---ACGACCGGTATCAACATCATC 8601
QY 1874 SerThrIleuSerPheIleAsnGlyValProIleGlyArgAlaIleu-----Asn 1889
Db 8602 ACCACG-----TTCAAGGCGATGCCCCCTTTACCAAGCACTCTGCCACGGATCCCC 8655
QY 1890 AsnSerGlyAlaTyrValValAspProGluGluIleuValGlyIleGlyValMetGly 1909
Db 8656 GGAAGTCACGTCATACGTCGTAACAGCACGACTCAGGTGTTCTTTCAACGCTGTTGGC 8715
QY 1910 GluIleuValValThrGlyAspGlyIleuAlaArgGlyIleu---SerAspIleAlaIleuAsp 1928
Db 8716 GACCTCTACTTGGCGGTGAGCTGCTGTGTCGCGGTATCCTCAACAGATGCCCTTACC 8775
QY 1929 GluAsnArgPheVal-----HisIleThrValAsnAspGluThr 1941
Db 8776 AAGGAGGATTTATCCCAACCTTTCTACGAGCCGAAACAGCAAGTACAGTCGCC 8835
QY 1942 ValIleuAlaTyrArgThrGlyAspArgValArgTyrArgIleGlyAspGlyIleuIleGlu 1961
Db 8836 CAGAGACTATCAAGACTGAGATCTGTGCTTCGCT---GGAACCCCAACATCTCGAG 8892
QY 1962 PhePheGlyArgMetAspThrGluPheGlyIleArgIleAsnArgIleGluSerAlaGlu 1981
Db 8893 TATCTCGCGCGCAAGACAGCAGGTCAACCTGAGGGGCTTCGCGCATCGAGCTCTCGAG 8952
QY 1982 IleGluAlaIleuIleuAspSerSerValArgAspAlaIleValIleuGluGln 2001
Db 8953 GTGCGGATGCGCTCTAGCATCTCTGCTTTAAGAGGCTGCGTCATCCCAAGTAT 9012

QY 2002 AsnGluAspGluAlaProGluIleIleuGlyPheValValAlaAsp-HisAspHisSerGly 2021
Db 9013 GACAGGATGCG-----TCCGATTCACAGAGGTGACG 9045
QY 2021 uAsnAspIleGlyGluSerAlaAsnGluValGluGlyTyrGluAlaAspHisPheGluSerGly 2041
Db 9046 GCCATGCTGTCTACTATCAGCTCAACGCGGAACTGTGTGCGAAGCAT----- 9094
QY 2041 yMetTyrSerAspIleGlyGluIleAspProSerThrIleGlySerAspPhe---LysGly 2060
Db 9095 -----CGAGTATCCGAGACACCTGACCGCAACCTTCCCCCGTAC 9135
QY 2060 TyrThrSerMetTyrAspGlySerGluIleAspPheAsp-GluMetHisGluTyrLeuG 2080
Db 9136 ATGTCTCCCAAGCATGATCCACCACTGGAGAGATCTCTCCCGTGAACCGTGAATGGAG 9195
QY 2080 LysGluThrThrArgThrIleuHisAspAsn-----ArgSerIleGlyAsnVal 2096
Db 9196 CTGACCTGAACAGGCTCTCAACATCAAGTCTCCGACGCCAGAGCTTACACCGCTCCA 9255
QY 2096 euGluIleGlyThrGlySerGlyMetIleuPheAsnIleuAspSerArgIleu-GluSer 2115
Db 9256 CGAAATTCACAGAGG-----AACCTTGCCAGCTTGGGATCT 9297
QY 2116 TyrValGlyLeuGluProSerArgSerAlaAlaPheValAsnIleuValThrGluSer 2135
Db 9298 CTCTAGCGCTGCACCACTGCGGCAATTGACAGACGCTGTTTCCGCGGCGGAGACG 9357
QY 2136 IleProSer-----IleuAlaGlyLysAlaIleValGluIleValThrAlaThrAspIle 2153
Db 9358 ATCTCTCTCTCCGATTAAGGTGATCATTCACGCGCTTGAAGCGCAAGTACCGCTC 9417
QY 2154 GlyGluValAspAspIleuHisProAspIleuValIleuAsnSerValIleGluTyrPhe 2173
Db 9418 AAGGACATC---TACCTCCACCGCAGGCTCGAGCCCTA----- 9453
QY 2174 ProSerSerGluTyrIleuAlaGluIleAlaAsp-----ThrIleuIleHisLeuProAsn 2191
Db 9454 ---AGCGAAATGTCTGACCGACCAAGAGATAGAGGTACTCTGCCAGCGTCTCTCC 9510
QY 2192 ValGluArgIlePhePheGlyAspValArgSerGluAla-----ThrAsnGlu 2207
Db 9511 CTCGAGGAGCGAGACGAGGCGCAGGTGAGGCGAGCGACCGCTTCTCCCATTCAGGAC 9570
QY 2208 HisPheIleuAla----- 2211
Db 9571 TGGTCTCTTCAAGCCCTGATTAACCCGCTTACTGAAACCATGCTTACCATTCGA 9630
QY 2211 ----- 2211
Db 9631 ACCGCGGCACTTCGTCGAAGGGCTCCGGGTGCTCTGAAAGTCTGACAGAGCGCCAC 9690
QY 2212 -----AlaArgAlaIleHisThrLeuGly 2219
Db 9691 GACGTGCTGCTGACACTGCAACCGCGGAGCAAGATGCGCATGTTCTAGACCTTTGGC 9750
QY 2220 LysAsnAlaThrLys-----Asp 2225
Db 9751 CGTGACTGCGCGCAACTGCTGACTGCTGACCGACGAAAGCTTCAGAGACGAGAG 9810
QY 2226 AspValArgGluIleuMetAlaGluIleuGlu-----AspMetGluGluIleuLeu 2242
Db 9811 GATGTCCAGAGGCTCTGCGAGATCCATTCATTTCACTTCGAGATGAGACCCCTC 9870
QY 2243 ValGluProAlaPhePheThrSerLeuLysAsp-----ArgPheProGlyLeuVal 2259
Db 9871 TACACAGTGGCTATCATCCAGGTACAGAGAGGCTCCGCCGAGTGTGCTTGGCTGC 9930
QY 2260 GluHisValGluIleuProLysAsnMetGluAlaVal---AsnGluLeuSerAlaTyr 2278
Db 9931 CATCAGGTATGATGCACTGTGAGCTGGAACATTAATCTGCAAGACCTCGAGGCTCTC 9990
QY 2279 ArgTyrAlaIleValIleHisValArgGlySerLeuGlyAspGluLeuValIleuProVal 2298

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Db      9991 TATCATGAGACAGCCTTGTCCTCCAGAGCAGCGTGCAGAGTGTGCTAGCTGTC
Qy      2299 GtluYAspAspThrTrpIleAspPheGlnAlaAsnGlnLeuAsnGlnYsSerLeuGlyAsp
Db      10051 AGC-----GACTACAAATG---CCACTGTGAGAGGGCGCATTTGGAT
Qy      2319 LeuLeuYsSerSerAspAla-----
Db      10093 GTCTCTAGAGAAAGACAGTCCGCGGAGCTTGAGACCTGCTATCTGCATGGCGCGCTG
Qy      2327 IleMetAlaValSerIleProPheGlu---IleThrAlaPheGluArgIleVal
Db      10153 CTCACAGTGCAGAGAAAGTCTCGAGGGAACAGCAACAGCTGCTCTCCAGAGCCTGCG
Qy      2346 AlaSerLeuAsnSerAsnIleAspGluTrpGlnLeuSerThrIleAspSerSer-----
Db      10213 CTCGCTTGACTCCGGTATGATGATCTCTCATGGCCGCGGCTGCGCTGCG
Qy      2364 ---AlaGluGlyAspSerSerLeuSerValProAspIlePheArgIleAlaGlyAla
Db      10273 AAGCGCGCAGGGGAT-----GTCCCTCAGCTGCTCAGATGAGGCTCAGCGG
Qy      2383 GlyPheArgValGlu-ValSerSerAlaArgIleTrpSerGlnAsnGlyAlaLeuAspAl
Db      10321 CGC-----GAGATACTATCGACGCAACTGTGACGCTGACGCGGA-----CAGTC
Qy      2402 aValPheHisHisCysCysSerGlnGlyArgThrLeuValAsnProThrAspHis
Db      10366 GCGTGGTTCAGACAGTGTACCTTCGAGATCC---CCAAAGTGAACGCGCCG---
Qy      2422 sLeuArgGlySerAspLeuThrAsnArgProLeuGlnArgLeuGlnAsnArgAl
Db      10418 -CTCAGAGGCTGCTCG---ATGTCAGAGAGCG-ATGCGTGGGTCGCGAATAGGGTGT
Qy      2442 eAlaIleGluValArgGluArgLeuArgSerLeuProSerTyrMetIleProSerAs
Db      10473 CGGTACGGT-----CCAGCTCAGGATACGCGCGATC
Qy      2462 nIleValIleLeuAspLysMetProLeuAsnAlaAsnGlyValValAspArgLysGlu--
Db      10506 G-----TGCTGCGCCGCGCTGAGCTTCACTACCTTGCTGCGCTGACAGGCTTCTC
Qy      2482 ---LeuSerArgArgAlaLysValValProLysGlnGlnThrAlaAlaProLeuProth
Db      10560 GGGGGCTCAAGGGACTGACGCGTGCATGATGAA-----
Qy      2500 rPheProIleSerGluValGluValIleLeuCysGluGluAlaThrGluValPheGlyMe
Db      10597 -----GAGCAGATATCCGGTCCGACTGTCACACAGCGCT---GAGCAGTCCGGACG
Qy      2520 cLysValAspIleThrAspHisPhePheAsnLeuGlyGlyHisSerLeuLeuAlaThrLy
Db      10644 AAGCTCTCATGTGGATTTCACTTCTATCTGCGGCGCAGCTTGTG-----
Qy      2540 sLeuIleSerArgIleAspGlnArgLeuLysValArgIleThrValLysAspValPheAs
Db      10696 -----ATGATATGATGATGACAGCTGCGG
Qy      2560 pHisProValPheAlaAspLeuAlaSerValIleArgGlnGlyLeuGlnGlnInPr
Db      10719 CCACGGCGCAGAAATGAAATTCGTGCGACAGTTCGTAAC-----ACACTAATGATCTT
Qy      2580 oValSerAspGlyGlnGlyLysArgSerAlaHisMetAlaProArgThrGluThrG1
Db      10773 GATCAAAACACACAGACGAGGATTCACGCGACCTCTCCCTCGGATCGAGATC
Qy      2600 uAlaIleLeuCysAspGluPheAlaLysValLeuGlyPheGlnValGlyIleThrAspAs
Db      10833 CAGC-----TTACCCCTTATTTTGTCTTGAGAGGGCGACGACACGCG
Qy      2620 n-----PhePheAspLeu-----GlyGlyHisSerLeuMetAlaThrIlyLe
2624 n-----PhePheAspLeu-----GlyGlyHisSerLeuMetAlaThrIlyLe

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Db      10878 CGCTCCGCTTCTCTGCTCCACCTGCGAGGCGGAGCGGAGACTTACTTCCAAACAT
Qy      2634 uAlaValArgIleGlyHisAspLeuAspThrThrValSerValLysAspValPheAspHis
Db      10938 TGTCAAGGCTCTCCGAACTCG-----
Qy      2654 sProValLeuPheGlnLeuAlaIleAlaLeuAspAsnLeuValGlnSerLysThrAsnG1
Db      10960 -----AATCTGTGCTGTTCACAACTATTCACCGGAGAGAAAGACGCTCGG
Qy      2674 uIleValGlyLysArgGluMetAlaGluTyr-----SerProPheGlnLeuLeuPheTh
Db      11007 GACCATC-----GAGCGCTGCGCGAGTACTCTCTCCACATCCATCCATCCAGCC
Qy      2692 rGluAspProGluGluPheMetAlaSerGluIleLysProGlnLeuGlnGluGlnG1
Db      11061 GAGAGGGCCATACACATCTCTGCGCTGAGATTTGAGAGGATCTGCTGCTGAGCGGC
Qy      2712 eIleGlnAspIleTyrProSerThrGlnMetGlnLysAlaPheLeuPheAspHisThrTh
Db      11121 AAGCATTTACTGCGGAGGCTCACAAGATTCGACGCTGCGACTTATGATCG-----
Qy      2732 rAlaArgProArgProPheValProPheTyrIleAspPheProSerThrSer-----
Db      11176 -----TACTTGAATCCGCTCCGCTCAGGCGCAT
Qy      2750 ---GluProAspAlaAlaGlyLeuIle-----
Db      11208 CGGCCAATCGACGATGCTGCGCTTGGACCCCATATACACGCTTACCAACCGCTGCC
Qy      2758 ---LysAlaCysGlnSerLeuValAsnHisLysLeuAspIlePheArgThrValPh
Db      11268 GAGAGCTTACAGACGCGTGCATCTCTCACTAATACATGACCGCTGTTCAGAGCTAAC--
Qy      2774 eAlaGluAlaSerGlyGluLeuTyrGlnValValLeuSerCysLeuAspLeuProIleG1
Db      11325 -----
Qy      2794 nValIleGluThrGluAspAsnIleAsnThrAlaThrAsnGluPheLeuAspGlu---Ph
Db      11326 -----GAGACGAAATGACCGACGATGCGCAATGCGACGACAGCGCTGTATGATGCTT
Qy      2813 eAlaLysGluProVal
Db      11379 TGCCAGTGCCTTTTG

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RESULT 7
 US-09-252-991A-71
 ; Sequence 71, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 71
 ; LENGTH: 7527
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-71

Alignment Scores:
 Pred. No.: 9,66e-148 Length: 7527
 Score: 1506.50 Matches: 552
 Percent Similarity: 44.41% Conservative: 338
 Best Local Similarity: 27.54% Mismatches: 859

Query Match: 9.34% Index: 258
DB: 4 Gaps: 66
US-09-482-788-2 (1-3129) x US-09-252-991A-71 (1-7527)

QY 16 ThrProAlaSerPheCysSerHisGlyAspSerProLeu---AsnSerSerTyrGluGln 34
DB 1933 ACCCGCGGACTTC-----CCGCTGGCCGGGCTTTCCAGACGACG 1974
QY 35 LeuPheHisLeuTyrGlyLeuAspSerSerArgIleGluAlaIleLeuProCysTyrPro 54
DB 1975 CTGGATGAATTC---TCCTTGATTCCTGATTCGTCGGGACATCTATCCGTTGTCGCC 2031
QY 55 PheGlnLeuAspMetIleAspCysAsnAlaLeuAspIlySerGlnSerAlaIleGlyHisAla 74
DB 2032 ATGCAG-----CAGGCGCATCTGTTTCACAGT 2058
QY 75 ValTyrAspValProThrAsp-----IleAsp 83
DB 2059 CTTCATGGAACGGAAGCGACTATGTCACCACTGGCATGTATCGCGCATGGAC 2118
QY 84 IleSerArgPheAlaLeuAlaTyrIlyGluIleValaGlnInThrProAlaLeuArgAla 103
DB 2119 CCGGATCGCTTCGCGGACGCTGGCAGGCGCACCTCGATGCCATCGATCTGCGC--- 2175
QY 104 PheAlaPheThrSerAspSerGlyIlyThrSerGlnValIleLeuIlyAspSerPhe--- 122
DB 2176 -----AGCGATTCCTCTGGAAGACGCGTGCCT 2205
QY 123 -----ValPhe-SerTyrMetCysTyrPheSerSerSerSerProAspG1 137
DB 2206 CAGCGCTTGCAGGTGATTCGACGACGACGCGTGAAGCGCTGGCGCTGCCCGCCAGGC 2265
QY 137 uValIValArgAsp-----GluAlaAlaAlaIleAspGlyIyr 150
DB 2266 AGTGATCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 2325
QY 150 oArgCysAsnArgPheValLeuLeuGluAspMetGlnThrIlyLeuIlyCysGlnLeuValTr 170
DB 2326 CCGTGGACAGC---TTGGTGTGGTG---CCGCTGGCAATGGCGGATGACCTCATCTA 2381
QY 170 pThrPheSerHisAlaLeuValAspValThrPheGlnGlnArgValIleLeuSerArgValPh 190
DB 2382 TACCTATCACCACTCTGATGATGCTGAGACGACGACGACGACGACGACGACGACG 2441
QY 190 eAlaAlaTyrLeuHisGluIlyAspThrHisIlyArgProGluThrProGluSerSerAspAl 210
DB 2442 GCAGCGCTATGCG----- 2454
QY 210 aThrAspThrAspSerGlnSerValIleSerMetSerCysGluAsp----- 227
DB 2455 -----GGCAGAGAGGTAGCCGCTCCGCTGGGCGTTACGCGACCTATCGG 2501
QY 228 -----AsnAlaValSerAlaThrHisPheThrGlnInThrHisLeuAsnAs 242
DB 2502 TTGGTTGCAGAGCGCGCATGTGATGCGACGACGACGACGACGACGACGACGACG 2561
QY 242 pLeuAsn-----AlaSerValPheProHisLeuSerAs 253
DB 2562 CTTGGAAATGCCACAGCGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 2621
QY 253 pHisLeuMetValProAsnProThrThrThrAlaGlnHisArgIleThrPheProLeuSe 273
DB 2622 GCATCTCGCGGACGTGATCGGACGACGACGACGACGACGACGACGACGACGACG 2678
QY 273 rGlnIlyValLeuSerSerSerAlaIleCysArgThrAlaLeuSerIleLeuLeuSerArg 293
DB 2679 TCAGAACTCAAGCTCAACCTTGTG---CAGCGCGCTGGCGCTGCTGCTGCGACGG 2735
QY 293 gTyrThrHisSerArgGluAlaLeuPheGlyAlaValThr-----GluGlnSerIle 310
DB 2736 GCATCGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 2795

QY 310 uProPheAspIlyHisIleTyrLeuAlaAspGlyThrTyrGlnInThrValAlaProLeuArgVa 330
DB 2796 GCCAGCATGACGCGCAGATC-----GGTCTGTATTCATACACCTCGCGGTATCGC 2849
QY 330 HisCysGlnSerAsnLeuArgAlaSerAspValMetAspAlaIleSerSerTyrAspAs 350
DB 2850 CCGCGCGACCCACAGACAGCGCTCCGGAAATCTCGACAGGATGACGCGCTCAACT 2909
QY 350 pArgGluIlyHisLeuAlaProPheGlyLeuArgAspIle---ArgAsnThrGlyAspAs 369
DB 2910 GCGCTCGCGGACACAGACATAGCTCTGTACATCATCAGACGCTGGCGCGCGCATGC 2969
QY 369 nGlySerAlaAlaCysAspPheGlnInThrValLeuLeuValThrAspGlySerHisValAs 389
DB 2970 CCGCGAGGCTCTGTGAT-----AGCATCTGTGTGTTCAGAACTTCCCGCTGCG 3020
QY 389 nAsnGlyIleAsn-----GlyPheLeuGlnGlnIleThrGluSerSerHisPheMe 406
DB 3021 CAGAGCTTGCAGAGCTCCCGCATCTGAGATTCCTCCAGCCAAAGCACACAGCA 3080
QY 406 tProCysAsnAsnArgAlaLeuLeuLeuHisCysGlnMetGluSerSerGlyAlaLeuLe 426
DB 3081 G-----ACCACTACCCCTGACGCTGGGTACCCCTGGTAGAGCGCTGAGCTGCA 3134
QY 426 uValAlaTyr-----TyrAspHisAsnValIleAspSerLeuGlnInThrTyrGluLeu 444
DB 3135 GTACGCTTATGCGCGCGCATTTGACGACGACGACATCGCAGCATCGACGCTGACGCT 3189
QY 444 uGlnGlnPheGlyHisIleuLeuIlyCysGluGlnSerProLeuAspLeu-----SerSe 462
DB 3190 -----CATCTGTCATCTGCTGACAGCGAGATGCGGACACCCCGACGACG 3236
QY 462 rMetAlaGluValAsnLeuMetThrGluTyrAspArgAlaGln---IleGluSerTyrAs 481
DB 3237 GCTGGGAGAGCTGACCTGCTGACGCGCGGAGAACCCAGAGAGCGCTGCGGATGGCA 3296
QY 481 nSerGlnProLeuGluValGlnAspThrLeuIleHisGlnMetLeuValAlaIse 501
DB 3297 GCGA---CCGCTGAG---GCGCTGCGCGCGCGCGCGCGCGCGCGCTTTCGC 3344
QY 501 rHis-----SerProThrIlyThrAlaIleGlnAlaTyrAspGlyAspThrTh 517
DB 3345 GCATCAGGACGCTGCGCTGAGCGCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3404
QY 517 rTyrSerGluLeuAspAsnValIleSerArgLeuAlaValHisIleIlySerLeuGlyLe 537
DB 3405 CTATGCGCACTGATATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3464
QY 537 uArgAlaGlnGlnAlaIleIleProValTyrPheGluIlySerIlyThrValIleAlaSe 557
DB 3465 G---GCCGCGAAGCGCTGTGCGCATCGCTGCGCGCGCTCTTGCACCTGTGCTCGG 3521
QY 557 rMetLeuAlaValLeuIlySerGlyAsnAlaPheThrLeuIleAspProAsnAspProP 577
DB 3522 CTTGCTGGCATCTCAAGGTGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3581
QY 577 oAlaArgThrAlaGlnValAlaThrGlnInThrArgAlaThrValAlaLeuThrSerIlyLe 597
DB 3582 GAGCGCTGGCGTACATGTGGCGACGCGCGCGCGCGCGCGCTGCTGCTGCTGCTG 3633
QY 597 uHisArgGluThrValGlnIlyLeuValGlyArgCysValValValAspArgIleLeuLe 617
DB 3634 -----CAGAAACCTGCGCGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3689
QY 617 uGlnSerValSer-----AlaSerAspAspPheSerSerLeuThrIlyS---SerG1 633
DB 3690 GAAACCGCGCGCTGCGCGCGAGTGCATACGCGCGCGCTGCGCGAGTACCTGCGCA 3749
QY 633 nAspLeuAlaTyrValIlePheThrSerGlySerThrGlyAspProIlyAspIlyMetI1 653
DB 3750 GAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3809
QY 653 eGluHisArgAlaPheSerSerCysValAlaLeuIlyAspGlyAlaSerLeuGlyIleAsnSe 673


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Db      3810 CAGCCAGGCGGCGCTCGTCGCGCACTGCCAGCGGCGAGCGACGACCTACCGCGCGGCGCC 3869
Qy      673 rAspThrAlaAlaLeuGlnPheGlyThrHisAlaPheGlyAlaCysLeuLeuGluIle 693
Db      3870 GGGGAGCTGCGCACTTCAGTTCCCTCGATCGATTCGATGCGCTGCCAGAACACTT 3929
Qy      693 cThrThrLeuIleAsnGlyGlyCysValCysIleProSerAspAspArgMetAsn 713
Db      3930 CGTACCCTCTGCTGCGAGACCCGGGTCTGCTC--GGCGAGCGCGGACAGTGGAGCGC 3986
Qy      713 r-----IleProSerPheIleAsnArgTyraAsnValAsnTrpMetMetAlaThrPro 721
Db      3987 GCACACATCTGCGCGATGATGAGCGGCGACGCGGTGATATCTCATCTACCGCGCGC 4046
Qy      731 rTyMetGlyThrPheSerProGlu-----AspValProGlyLeuAlaThr 746
Db      4047 TTATCTTCAGCAACAGCGCGAGAGTTGCCACGCGCGCGCGGATCCGATACCGCGC 4106
Qy      746 rLeuValLeuValGlyGlnIleMetSerSerValAsnAlaIleTrpAlaProGlySle 766
Db      4107 CTGTATCTCTGCGCGGAGACCTGGGACGCCACTCTCTACCCAGAGCGCGTGCAGCC 4166
Qy      766 uGlnLeu--LeuAsnGlyTyGlyGlnSerGlySerSerIleCysPheAlaSerAs 785
Db      4167 TGAAGCTGGTTCACGCGCTACCGCTCCACCGAGCGGTGATCATCTCGGTGCGTGGCA 4226
Qy      785 mMetSerThrGluProAsnAsn-----MetGlyArgAlaValGlyAlaHisSerTr 802
Db      4227 CTGTGCGGCGAGAGGCGCGCTCCCGCTATCGCGCGCGCTCGTCCGCGCGCGCGC 4286
Qy      802 pValIleAspProAsnAspIleAsnArgLeuValProIleGlyAlaValGlyGlnLeuVa 822
Db      4287 CTCCTACTCTGAGCGGACCGCTCGACGCAATGTGCGCC--GGATGATCGCGAGCTGTA 4343
Qy      822 IileGlySerProGlyIleAlaArgAspTyriIleValProProProGluLysSerPr 842
Db      4344 CATCGGCGGCGCACTGCTGCTGCTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGC 4403
Qy      842 oPhePheThrAspIleProSerTrpTyriProAlaAsnThrPheProAspGlyAlaLys 862
Db      4404 TTTCGTGCGCGGATCCGTTCTCA-----GTTTCGCGCGCGCGCGCT 4442
Qy      862 uTyTrpArgThrGlyAspLeuAlaArgTyriAlaSerAspGlySerIleValCysLeuGlyAr 882
Db      4443 GATTCGACCGGGGACCTGGCGGCTTATCGCGTGCAGCGTCAAGTCAATATCTCGCGCG 4502
Qy      882 gIleAspSerGlnValLysIleArgGlyGlnArgValGluLeuGlyAlaIleGluThrH 902
Db      4503 GCGCGATCAGCAGATCAAGATCCGTGTTCCGATCGAGATCGCGCAATTCAGAGCCA 4562
Qy      902 sLeuArgGlnIleMetProAspAspLeuThrIleValGluAlaThrLysArgSerG 922
Db      4563 ACTGCTTGCACAC-----CCGATGTGCGCGGACAGCGGTGCTGCGCGCA 4607
Qy      922 n-----SerAlaAsnSerThrSerLeuIleAlaPheLeuIleGlySerSerTyriPheGlyAs 941
Db      4608 GGATGCGCGTGGTGGTCCGCTGCTGCGCGGCTTACCTGTGAGG----- 4650
Qy      941 nArgProSerAspAlaHisIleLeuAspHisAspAlaThrLysAlaIleAsnIleLys 961
Db      4651 -----CGTGAAGCT--ATGCGGGGTGAGAGACCTTCGCGGAGTGTGCGCACCTGGCT 4700
Qy      961 uGlnGlnValLeuProArgHisSerIleProSerPheTyriIleCysMetLeuGluLeuPr 981
Db      4701 GCGCGGAGCGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4760
Qy      981 oArgThrAlaThrGlyLysIleAspArgArgArgLysGluIleMetGlyLysAspIleLe 1001
Db      4761 GCTGAACGCGACGCGCAAGCTGATCGCAAGCGCTG----- 4797
Qy      1001 uAspLysGlnThrGlnGlyAlaIleValGlnGlnAlaProAlaProIleProValPheAl 1021

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Db      4798 -----CGAAGTGAAGCGGCTGCCCGCACAGCGCGGAGAGCTTCGCGGAGGGCT 4853
Qy      1021 aAspThrAlaAlaLysLeuHisSerIleTrpValGlnSerLeuGlyIleAspProAlaThr 1041
Db      4854 CGAACGTTCC-----GTCCAGCGATCTGGAGCGCGCTCTGAGTTCAG-----GG 4901
Qy      1041 rValAsnValGlyAlaThrPhePheGluLeuGlyGlyAsnSerIleThrAlaIleLys 1061
Db      4902 CATCGCGCGGAGAGAGACTTCTTCGAACCTCGCGGTCACTCCCTCAGCGCCACCGGGGT 4961
Qy      1061 tValAsnMetAlaArg--SerValGlyMetAspLeuLysValSerAsnIleTyriGlnH 1080
Db      4962 GGTCTGCGCGCTGCGCGAGATCTGGAGCTGAGCTGAGCTTCCTGCGATCTGTCGAGCG 5021
Qy      1080 sProThrLeuAlaGlyIleSerAlaValValLysGlyAspProLysSerTyriThr----- 1098
Db      5022 GCGGTCTCTGCAACTTCGCGCGCTTCCTGAGATCCAGCGGCGAGCGCTTGGCCCTGT 5081
Qy      1099 -----LeuIleProLysSerThrHisGlyGlyProValGlnGlnSerTyriSerGln 1116
Db      5082 GCTGCAAGTATTCGCGGA-----GTCCGCGAGCTGCTTTC-----TCGATGCTCAGCA 5132
Qy      1116 yArgLeuTrpPheLeuAspGlnLeuAspValGlySerLeuTrpTyriLeuIleProTyriAl 1136
Db      5133 ACCCATGTGGTCTCTGGAACCTGGAAGCTGGAAGCGCGCTATCATCTCCACCGCT 5192
Qy      1136 aValArgMetArgGlyProValAsnValAspAlaLeuArgArgAlaLeuAlaIleGlu 1156
Db      5193 ACTGCACGTGCGGCGTCTTGCACAGCGCGGCTTGCACAGCGCTTCGATTCGCTGTGT 5252
Qy      1156 uGlnArgHisGlyThrLeuArgThrThrPheGluAspGlnAspGlyValGlyValGln 1176
Db      5253 GCTCGCGCAGAGACCTTGGCGCACCCGCTTCAGAGAGTGAAGCGTGAAGCGCGCGCAGAC 5312
Qy      1176 eValHisGlyLysLeuSerGlnGluMetLysValIleAspLeuCysGly--SerAsp 1195
Db      5313 GATCTGCGCAACATGCGGTTCGCGCATTCCTGAGAGATTCGCGCGCGCGCGAGCAAGC 5372
Qy      1195 uAspProPheGlnValLeuAsnGlnGlnGlnThrThrProPheAsnLeuSerSerGluAl 1215
Db      5373 AACGTGCGGACAGCGGTGCGCGAGAAATCCCGCACCTTGCACCTGCTGCTGCGCGC 5432
Qy      1215 aGlyTrpArgAlaThrLeuLeuArgLeuGlyGlyAspAspHisIleLeuThrIleVal 1235
Db      5433 GCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5492
Qy      1235 tHisIleIleIleSerAspGlyTyriSerIleAspValLeuArgArgLeuAsnGln 1255
Db      5493 GCACATATCGTGTCCGACGCTTGTGTGATGATGATGATGATGATGATGATGATGATGAT 5552
Qy      1255 uTyriSerAlaAlaLeuLysAspSerLysAspProLysSerAlaLeuThrProLeuPro 1275
Db      5553 CTATGCGCGCGCGCGCGCGCGCAACA-----CCGACGCTGCGCGCATTCGACGCT 5603
Qy      1275 eGlnTyriSerAspPheAlaLysTrpGlnLysAspGlnPheIleGluGlnGlu-----Lys 1293
Db      5604 GCAGTACCGCGCATATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5663
Qy      1293 sGlnLeuAsnTyriTrpLysGlnLeuLysLysAspSerSerProAla--LysIleProTh 1312
Db      5664 GCAGCTGATTAATCTGAGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5723
Qy      1312 rAspPheAlaArgProAlaLeuLeuSerGlyLysAspAlaGlyCysValHisValThrIleAs 1332
Db      5724 CGACCGGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5783
Qy      1332 pGlyLysLeuTyriGlnSerLeuArgAlaPheCysAsnGlnHisAsnThrThrSerPheVa 1352
Db      5784 GGTGCGATTATTCGAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5843
Qy      1352 lValLeuLeuAlaAlaPheArgAlaAlaHisTyriArgLeuThrAlaValGluAspAlaVa 1372
Db      5844 GCTTCTGTTGGCTGCTTCCAGGTGCTTGAAGCGCTATAGCGGCGAGTCCGATATTCG 5903

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QY 1372 111eglyThrProileAlaAsnArgAsnArgProgluLeuGluAspIleileglyCysph 1392
DB 5904 CGTCGGGGTACTATGCGCAACCGCAACCGCGGAGGTGAGCGCTGATCGGCTTCTT 5963
QY 1392 eValaerThrGlnCysMetArgIleAsnIleAspHisAspThrPheGlyThrLeu1 1412
DB 5964 CGTCAATACCCAGGTGCTGGCTGGCCAGGTGATGCTGGCTGGCTGGCTGGCTGGCT 6023
QY 1412 eaenGlnValAlaThrThrThrThrAlaIlePheGluAsnGluAspIleProPheGlu1 1432
DB 6024 GGGCCCGGTCGAGAGCGCGCGCTGGCGCGCGAGCGCGCGAGATGCTGGCTGGCGCA 6083
QY 1432 gValValSerAlaLeuGlnProGlySerArgAspLeuSerSerThrProLeuAlaGln1 1452
DB 6084 ATGGTCGATGCTGCTGGAGCC---GAACGCAATCTGACGCAACGCCGTTGTTCCAGGT 6140
QY 1452 uIlePheAlaValHisSerGlnValAspLeuGlyArgPheLeuPheGlnGlyLeu1 1472
DB 6141 GATGTATTAACACCCAGAGC---GGCGAGCGCGAGAGATCCCAAGTCGATGG 6188
QY 1472 rValProValProSerIleValAlaTyr-----ThrArgPheAspMetGluPheH1 1488
DB 6189 TTGGACATGAGAGTGTGGCTGGAGCGGTGCTGGCGCAAGTTCGACCTTGGCTTGA 6248
QY 1488 sleuPheGlnGluThrAspSerLeuGlySerValAsnPheAlaAspGluLeuPhe1 1508
DB 6249 TACTGGGAAACCCCGAGCGCTGGGGGGCGCGCTGACCTGACGACGACGCTTTCGA 6308
QY 1508 sMetGluThrValGluAsnValAlaArgValPhePheGluIleLeuArgAsnGlyLeu1 1528
DB 6309 GGGCGGAGCGTCGAGCGCATGGCGCGCATTTGGCAGAACCTGCTGGCGCATGCGGA 6368
QY 1528 nSerSerArgThrProValSerIleLeuProLeuThrAspGlyIleValThrLeuGlu1 1548
DB 6369 GAACCGCGAGCGAGCGCTGACCTGCTGGCGATGCTGATGCGGAGAGCGGTGCGGATT 6428
QY 1548 sleuAspValAlaLeuAsnValHisValAspTyrProArgGlnSerSerLeuAlaAsp1 1568
DB 6429 GCTGGAAGCGTGAACCGCACTGCTGGCGAGTACCGCTGCAACGCGCGTGCACCGGTT 6488
QY 1568 lPheGlnThrGlnValSerAlaTyrProAspSerLeuAlaValAlaAspSerSerCys1 1588
DB 6489 GTTCGAGGACAGGTGACGCGCAACCGCGCGCGCTGGCTGGCGCGAGAGCG 6548
QY 1588 gIleuThrTyrThrGluLeuAspArgGlnSerAspIleLeuAlaGlyTrpLeuArgAs1 1608
DB 6549 CTTGACTACCGCGAGCTGAACCGCGCGCGAGCGCGCTGGCGATGCTGATCGAGCG 6608
QY 1608 gSerMetProAlaGluThrLeuValAlaValPheAlaProArgSerCysGluThrIle1 1628
DB 6609 CGGGGTCGTCGCGAGCGCGCTGGTGGCGTGGCGATGAGCGCTTCATCGAGATGCT 6668
QY 1628 lAlaPhePheGlyValLeuValAlaAsnLeuAlaTyrLeuProLeuAspValArgSer1 1648
DB 6669 GGGCGCTGATGCGCATCTCTCAAGCGCGCGCTGATGCTGATGCTGATGCTGATGCT 6728
QY 1648 oSerAlaArgValAlaAspIleLeuSerGlyLeuSerGlyProThrIleValLeu1 1668
DB 6729 CGAGAGCGCGAGCGCTGACATGCTGAGAGACAGCGGTGCTGCTGCTGACCGCGTC 6788
QY 1668 yHisAspThrAlaProProAspIleGluValThrAsnValGluPheValArgIleArg1 1688
DB 6789 GCACCTGAAGCTGCGTGGCGCGAGGTGTCAGCGATGACCTG----- 6834
QY 1688 pAlaLeuAsnAspSerAsnAlaAspGlyPheGluValIleGluHisAspSerThrLys1 1708
DB 6835 -----GATCGCGGTGCGCTGCTGAG-----GATTAACGTGAGCGCAACCC 6878
QY 1708 o-----SerIleThrSerLeuAlaTyrValLeuThrThrSerGlySerThrG1 1724
DB 6879 GATATTATCTCGATGCGAGCACTGCTATGATTAACACTCGGTTCCACCG 6938

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QY 1724 yArgProLysGlyValMetIleGluHisArgValIleIleAlaGlyThrValThrSerGly1 1744
DB 6939 CAAGCCCAAGGGCGCGCGCAACCGCATTCGCGCTGA---GCAACCGCTTGTCTGATG 6996
QY 1744 gIle-----ProAsnTyrProSerGluThrArgMetAlaHisMetAlaThrIleAla1 1762
DB 6997 CACAGCGCTATGAGCTGGCGGTGCGGTGACACGCTGTTGCGAAG---ACCCGTTCACTT 7055
QY 1762 eaerGlyAlaSerTyrGluIleTyrSerAlaLeuLeuPheGlyArgThrLeuValCys1 1782
DB 7056 GCACGTGTCGTGTGGAGATGTTCTTGCGCGCTGATGAGCGGGGCAAGTGTGTCGTC 7115
QY 1782 lAspTyrMetThrThrLeuAspAlaArgAlaLeuValAspValPhePheArgGluHis1 1802
DB 7116 CGCGCGCGCGACCATGCGATCGCGCGAAGCTGTGTGAGCTGATGATGATGATGATG 7175
QY 1802 lAsnAlaAlaSerHisValThrSer-----SerGluAspValProLeu1 1818
DB 7176 GCACAGCTGACATTCGTGCGCTGATGCTGAGCGGTGCTGAGAGCAAGACGTCGC 7235
QY 1818 gValProArgArgLeuSerArgThrLeuMetPhePhePheValValThrAspSer1 1838
DB 7236 CTCTGACACAGCTGAACGC-----ATGTTTGCAGCGCGAGCG 7277
QY 1838 rAlaProAspAlaLeuAspAlaGln-----GlyLe 1848
DB 7278 GCTGCCG-----GCGGACCGCGCAGACAGATGTTTGCACACCTGCGCGCGCGCT 7331
QY 1848 uTyrGlnGlyValGlnCysThrAsnGlyTyrGlyProThrGluAsnGlyValMetSer1 1868
DB 7332 C-----TATAACCTTTATGCGCGACGAGCGCGCGCATTAACGTCAC 7373
QY 1868 rIleTyrProIleAspSerThrGluSerPheIleAsnGlyValProIleGlyArgAla1 1888
DB 7374 CACTCG-----ACCTGCAATGAGAGAGGCAAGACGCGTCCGATGCGCGCGCGAT 7427
QY 1888 waenAsnSerGlyAlaTyrValAlaValProGluGlnGlnLeuValGlyIleGlyVal1 1908
DB 7428 CGCCCAACTGCGCTGACATCTTGTGCGCAACTGCAACCTGACCGGTACCGGTGCGCT 7487
QY 1908 tGlyGluLeu 1911
DB 7488 CGCGAGATG 7497

RESULT 8
US-09-710-279-759
; Sequence 759, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 759
; LENGTH: 6968
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-759

Alignment Scores:
Pred. No.: 1,41e-139 Length: 6968
Score: 1429.00 Matches: 576
Percent Similarity: 41.62% Conservative: 462
Best Local Similarity: 23.10% Mismatches: 1030
Query Match: 8.86% Indels: 426

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[illegible]

Dd		865	---CATATTGAAAAA-----	:::: :::		:: ::	906
Oy		406	MetProCysAsnAsnArgAlaLeuIleuLeuHisCysGlnMetGluSerSerGlyAlaLeu				425
Dd		907	-----TCTCATCATATACATCGTTATTAACAAT-----	GAAGCATCATCATTCGGG	951		
Oy		426	LeuValAlaTyrTyrAspHis-----	AsnVal	434		
Dd		952	GATTATAGAGTTTATTCCTCATGTGCAGGGTGTTTGATAGTTATTAATGACAAAGTT	101			
Oy		435	IleAspSerLeuGlnThrThrArgIleuLeuGlnGlnPhe---	GlyHisIleuLeuLeuCys	453		
Dd		1012	TATGTATGAATTAACTGTAAATACGTTAGTCAAAATTAATGAGATTTATATGCAAAATT	107			
Oy		454	LeuGlnSerProLeuAspLeuSerSerMetAlaGluValAsnIleMetThrGluTyrAsp	473			
Dd		1072	ACACAAAATTCATCATCTTATTA-----ATTAAAGATATAAAACTGACGATCGTCAGAT	1122			
Oy		474	ArgAlaGluIleGluSerTyrAsnSerGlnProLeuGluValGlnAspThrLeuIleHis	493			
Dd		1126	TTAGCTTAATATTAATGACATCATCTTCACAAAACANVAGCATTAATTAATGAGAGCTACT	118			
Oy		494	HisGluMetLeu-----LysAlaValSerHisSerProThrIyrThrAla	508			
Dd		1186	TATATAAACCGGTGTGAAAGATTCCAAAGCTCAAGGCCAACATCCCAGATGATTTGGG	124			
Oy		509	IleGlnAlaTyrAspGlyAspTyrThrTyrSerGluLeuAspAsnValSerSerArgLeu	528			
Dd		1246	TTGCATATAGAACAACAGATCCAGTGCATATCATCTTAATTAATCAATGTCGCAATCTTTA	130			
Oy		529	AlaValHisIleLeuSerLeuGlyLeuArgAlaGlnGlnAlaIleIleProValTyrPhe	548			
Dd		1306	GCATATAGATTGCGTTTAATCATCAGATTCAGAACCTAATGATATGATGTGGCATTTATAGCA	136			
Oy		549	GluIyrSerLysTyrPvalIleAlaSerMetLeuAlaValLeuLysSerGlyAsnAlaPhe	568			
Dd		1366	GAACCCAGCTTAGAATATTAATGGAATGTTAAGGATCTTGAAAGCTGGTCCAGCGTAC	142			
Oy		569	ThrIleuIleAspProAsnAspProProAlaArgThrAlaGlnValIleValThrGlnThrArg	588			
Dd		1426	ATACCATTTGATCCGATTAATCTCTAAGAAACAATGAATTAATTAATGAGACGCCAAA	148			
Oy		589	AlaThrValAlaLeuThrSerLysLeuHisArgGlnThrValGlnLysLeuValGlyArg	608			
Dd		1486	CCTAAAGCGGTGTACAC-----TATCGTACATCATTCANTCAGGTTTACTCTCA	153			
Oy		609	CysValValValAspAspGluLeuLeuGlnSerValSerAlaSerAspPheSerSer	628			
Dd		1537	-----ATCGATATAGAAATTGATGATTCGAT--TCAGAGAACATGATTTGATAC	158			
Oy		629	-----LeuThrLysSerGlnAspLeuAlaTyrValIlePheThrSerLysSerThr	645			
Dd		1585	CCGAGAGCGCATTAATGTTTCAGAAAGATATCGTTATGTCATCTATATACACAGAAACGACT	164			
Oy		646	GlyAspProLysGlyIleMetCileGluHisArgAlaPheSerSerCysAlaLeuLysPhe	665			
Dd		1645	GGTAAACCTTAAGGACACCTGCTGCCATATGAGGAATTCGATCGC---TTAATACCAAT	170			
Oy		666	GlyAlaSerLeuGlyIleAsnSerAspThrArgAlaLeuGlnPheGlyThrHisAlaPhe	685			
Dd		1702	CCAATATATGTCGAAATTGACGAACAAATCAACCCGCTTATTAATCAGAAACAGTACGCTTT	176			
Oy		686	GlyAlaCysLeuLeuGlnIleMetThrTrileuIleAsnGlyGlyCysValCysIlePro	705			
Dd		1762	GATGAGCAACCTTTGAATATATATGCTCCATATTAATGAGGACGGTACTCATTTACA	182			
Oy		706	SerAspAspAspArgMetAsnSer-----IleProSerPheIleAsnArgTyrAsnVal	723			
Dd		1822	TCTTAAGATAGCTTCTTAATCTCTCAATTCGTTAGATCAAGCATTAATCAGAAATAAAGTC	188			
Oy		724	AsnTyrMetMetAlaThrProSerTyrMetGlyThrPheSerProGluAspValProGly	743			

Db 1882 AACACGATGGTTACGATCTTTATTTAAATCAAAATTCGTACGACGATTCGACGCA 1941
 Qy 744 LeuAlaThrLeu-----ValLeuValGlyGluGlnMetSerSerSerValAsnAlaIle 761
 Db 1942 CTGAATCTTTACTTATTTACTTATTTGTCGGGAAGTG-----TTAAATGCTTAA 1992
 Qy 762 TyrAlaProLySerLeu-----GlnLeuLeuAsnGlyTyrGlyGln 774
 Db 1993 TGGGTTCACTTAAATTCGCGTACGATTCATCAAAATTAATCAATGTTATGACCG 2052
 Qy 775 SerGlnSerSerSerIleCyPheAlaSerAsnMetSerThrGluProAsnAsnMetGly 794
 Db 2053 ACAGAGATACCAACA-----TTTACTACAACTTTTCGAGT---CCACAAGAGATCCCT 2103
 Qy 795 ArgAlaVal-----GlyAlaHisSerTyrValIleAspProAsn 807
 Db 2104 TCACGATACCTATTTGGTTTACCTATTTAGTGAACGACGTTTATGTCATCGCAAGT--- 2160
 Qy 808 AspIleAsnArgLeuValProIleGlyAlaValGlyGluLeuValIleGlnSerProGly 827
 Db 2161 -----AATCGTATTTGTCGGCGTAGTGTTCCAGGTGAATTTGTCATTTGGTGCAGGT 2214
 Qy 828 IleAlaArgAspTyrIleValProProProProGlu-----LysSerPro 842
 Db 2215 TTAGCAAAAGTTATTTAAATCAACGTAACCTTACCTGACGCTTTTATTCAGTCACT 2274
 Qy 843 PhePheThrAspIleProSerTyrProAlaAsnThrPheProAspGlyAlaLyLeu 862
 Db 2275 TTTTACAAATGAATG-----CTT 2292
 Qy 863 TyrArgThrGlyAspLeuAlaArgTyrAlaSerAspGlySerIleValCysLeuGlyArg 882
 Db 2293 TATCGAAGCGGTGATTTAGTTCGCTTCAGAGAGATGCTATATGATTTATATAGTCGT 2352
 Qy 883 IleAspSerGlnValIleArgGlyAlaArgValGluLeuGlyAlaIleGluThrHis 902
 Db 2353 ATCGATACGACAGTAAATACGCGGTTTAAATAGAAATATATGCAAAATTTGAAAAACA 2412
 Qy 903 LeuArgGlnIleMetProAspAspLeuThrIleValAlaGluAlaThrLysArgSerGln 922
 Db 2413 TTA---GAAGCTATACGTATATTAATTAAGCTTACTATCGTTCGACAGCAAGACCA 2469
 Qy 923 SerIleAsnSerThrSerLeuIleAlaPheLeuIleGlySerSerTyrPheGlyAsnArg 942
 Db 2470 -----GATAAACAATAGTGCATATTATGACATCGCAATTA----- 2508
 Qy 943 ProSerAspAlaHisIleLeuAspHisAspAlaThrIleAlaIleAsnIleLysLeuGlu 962
 Db 2509 -----AAATCAACAGCTCAATTAAAGATATTTAAGT 2541
 Qy 963 GlnValLeuProArgHisSerIleProSerPheTyrIleCysMetLeuGluLeuProArg 982
 Db 2542 GAAACATTTACTGAAATATATGATATCTGTGCATTTTATGAAGTGCATCGATATCTATC 2601
 Qy 983 ThrAlaThrGlyLysIleAspArgArgArgLeuArgIleMetGlyLysAspIleLeuAsp 1002
 Db 2602 ACCATGAAATGGGAAATTAAGATGTGTCGTCATTA-----CCTGAAATTAATCTA 2649
 Qy 1003 LysGlnThrGlnGlyAlaIleValGlnGlnAlaProAlaProIleProValPheAlaAsp 1022
 Db 2650 AAGAAATATAGAAATTAATTAAGCAACGT-----AACGAT 2685
 Qy 1023 ThrAlaIleLysLeuHisSerIleTyrPheValGlnSerLeuGlyIleAspProAlaThrVal 1042
 Db 2686 ATTGAAACGACACAGTTTCCGATTTTTCGAAAGAGATTTTACATGTTGAT-----CAGTA 2739
 Qy 1043 AsnValGlyAlaThrPhePheGluLeuGlyGlyAsnSerIleThrAlaIleLysMetVal 1062
 Db 2740 GGTGTTTAAAGATATATTTCTTTGAACTAGTGACACCTCTTGAAGCAACATTGTTGTA 2799
 Qy 1063 Asn---MetIleAsnSerValGlyMetAspLeuLysValSerAsnIleTyrGlnHisPro 1081
 Db 2800 AACCGTATTGAAGAAAGGTTAAAAACGTTTAAAGGTGATTTAAAGAAATGCGCT 2859

Qy 1082 ThrLeuAlaGlyIleSerAlaVal-----LysGlyAspProLeuSerTyrThr 1098
 Db 2860 ACTGTAGACGACCTTGACACAAATTAAGAACTGCAAAATGAT-----GCTATGAA 2913
 Qy 1099 LeuIleProLySerThrHisGluGlyProValGluGlnSerTyrSerGlnGlyArgLeu 1118
 Db 2914 GTGATTCCTCCAAACCAATGAATGATGATCAATATGATTTAAGTCGCTCAAAAGATAG 2973
 Qy 1119 TyrPheLeuAspGlnLeuAspValGlySerLeuTyrTyrLeuIleProTyrAlaValArg 1138
 Db 2974 TATCTTTTAGAAGGCAATCTTAAAGACAGCTGTATACATTCATCTTATGAGCA 3033
 Qy 1139 MetArgGlyProValAsnValAspAlaLeuArgArgAlaLeuAlaLeuGlnArg 1158
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 Db 3094 CATGAATATATTACGACACAAATATGTAATTGATGACAAATGAACGTATTCGCG 3153
 Qy 1179 GlnLysLeuSerGlnGluMetLysValIleAspLeuCysGlySerAspLeuAspProPhe 1198
 Db 3154 ACACATGTTTCGCTGATTTTGAAGGTACG-----ACATCTTAGCAAGACG 3204
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 Db 3205 CAAGATATTATTCATCATCATTTATGAAACGTTGATTTAGAACCAACAGTACAGATGCGA 3264
 Qy 1219 AlaThrLeuLeuArgLeuGlyGluAspAspHisIleLeuThrIleValMetHisIle 1238
 Db 3265 GTTAATATATATATGACGACCAACAAGATTA---TTATTTAGTACTCACTCAATAGT 3321
 Qy 1239 IleSerAspGlyTyrPheSerIleAspValIleuArgArgAspLeuAsnGlnLeuTyrSerAla 1258
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 Qy 1259 AlaLeuLysAspSerLysAspProLeuSerAlaLeuThrProLeuProIleGlnTyrSer 1278
 Db 3382 -----AAATCACTTACCTGAACCTTAAAGCTTCAGTATMAA 3414
 Qy 1279 AspPheAlaLysTyrGlnLysAspGlnPheIleGluGlnLysGlnLeuAsnTyrTyr 1298
 Db 3415 GATTTATGATGAGTGGATGGTGCACAGA-----GACTATCTTAAACCAACGCTTTTGG 3468
 Qy 1299 LysLeuGlnLeuLysAspSerSerPro---AlaLysIleProThrAspPheAlaArgPro 1317
 Db 3469 TTACAGCAATTTGAATATCAGTTCCAAATTTAAATAGCTTACGATTTTCTAGACCA 3528
 Qy 1318 AlaLeuLeuSerGlyAspAlaGlyCysValHisValThrIleAspGlyLysLeuTyrGln 1337
 Db 3529 AGTATTTAAACCAACCAACGCTATATATGTTGACGTTTCATTAACAATGCTCAACCAACG 3588
 Qy 1338 SerLeuArgAlaPheCysAsnGlnHisAsnThrThrSerPheValValLeuLeuAlaIle 1357
 Db 3589 CAATTAATCTTATATGAAACCAATCAAGTACACAGATTTTATGTTCTTTGCTAGGCA 3648
 Qy 1358 PheArgAlaAlaHisTyrArgLeuThrAlaValGluAspAlaValIleGlyThrProIle 1377
 Db 3649 ATCATGATATTATTCGACAAATATACACGTCAGACAGATATCCGTATGTAAGTATC 3708
 Qy 1378 AlaAsnArgAsnArgProGluLeuGluAspIleIleGlyCysAspPheValAsnThrGlnCys 1397
 Db 3709 AGTGGCGGTCTCATGCGCATCTGAAATAATATGTTAGGTGTTGCTTAATACACTTGTA 3768
 Qy 1398 MetArgIleAsnIleAspHisIleAspThrPheGlyThrLeuIleAsnGlnValValAla 1417
 Db 3769 TATCGTGTGACACACATGATCAAAAGACATGAGATCAATATGATGCTGAGGAAAGAG 3828
 Qy 1418 ThrThrAlaIlePheGluAsnGluAspIleProPheGluTyrValValSerAlaLeu 1437
 Db 3829 ATGTGCTAGGGGCAATATGAAATCATCAAGATATCTTTTGAAGCTTATGCAATGATCTT 3888

QY 1438 GlnProGlySerArgAspLeuSerSerThrProLeuAlaGlnLeuIlePheAlaVal--- 1456
 DB 3889 ----GTGATGAAAGAGATGCTTCAACATCCGTTATTGATGATGATGCTCGACTTCAA 3945
 QY 1457 HisSerGlnIleuAspLeuGlyArgPheLeuPheGlnGlyLeuGlnSerValProValPro 1476
 DB 3946 AATAATGAAACAATCATCGCAATTTTGGACATAGTCATGACATATTTCCA---CCT 4002
 QY 1477 SerValAlaIleThrArgPheAspMetGlnPheHisIleuPheGlnGlnIleuThrAspSerLeu 1496
 DB 4003 CAGTCACAAACAGCTAAATTTGATTTGTCTATTATTGAAAGAAAGCAAGATGACTAT 4062
 QY 1497 LysGlySerValAsnPheAlaAspGlnLeuPheLysMetGlnThrValGluAsnValVal 1516
 DB 4063 GTGCGTCAATTTGAATATATACAGATTATATTAACAAGACCATTCACTCATTTGCT 4122
 QY 1517 ArgValPhePheGlnIleuLeuArgAsnGlyLeuGlnSerSerArgThrProValSerIle 1536
 DB 4123 GAACAACCTTCAATGATTTATTAACATGTAATCTCCGAAACCTAAAAATTCAGAT 4182
 QY 1537 LeuProLeuThrArgPheGlyIleValThrLeuGlnIleuLeuAspValIleuAsnValHis 1556
 DB 4183 ATTAGTGAATAATGATGACTTA---TTAATTGTGTGAC-----AACCAT 4224
 QY 1557 Val-----AspTyrProArgGluSerSerLeuAlaAspValPheGlnThr 1571
 DB 4225 GTCAATGATTTGTTCTTAACTTCCCAAAATTAAGCATATACAGCACTTTTACATGAT 4284
 QY 1572 GlnValSerAlaTyrProAspSerLeuAlaValValAspSerCysValLeuThrTyr 1591
 DB 4285 GTCATATAAGCGAAGACAGATGATGTGACACTTAAATGATGATGACAAATGATGACGTAT 4344
 QY 1592 ThrGlnLeuAspArgGlnSerAspIleLeuAlaGlyTyrIleuArgAlaGlySerMetPro 1611
 DB 4345 CAAAGACTGATGATATTATTGTAATAGTATGCTCAACATTTGATGATCAAAATGGCATCAA 4404
 QY 1612 AlaGlnThrLeuValAlaValPheAlaProArgSerCysGlnThrIleAlaPhePhe 1631
 DB 4405 AAGGGGAACGTGATGCCCTTTTAACAGCAAGATTTGAAATGGTTCGTAATGAT 4464
 QY 1632 GlyValIleuValAsnLeuAlaTyrLeuProLeuAspValArgSerProSerAlaArg 1651
 DB 4465 GGTGATATTAAGAGTGGAGTCTTATGTACCTATGACGTACCTATCCCGATTAACGC 4524
 QY 1652 ValGlnAspIleLeuSerGlyLeuSerGlyProThrIleValIleuIleGlnHisAspThr 1671
 DB 4525 ATTGAAATTTATTTTGAAGAAGCTGAGTGCAGACAGCTGCTCATATGGAAGAAAGCAATA 4584
 QY 1672 AlaProProAspIleGluValThrAsnValGluPheValArgIleArgAspAlaLeuAsn 1691
 DB 4585 TCC-----TCACATATACCAAGTAAATTAAATTTGAAAGATATTGATATAC 4626
 QY 1692 AspSerAsnAlaAspGlyPheGluVal-----IleGlnHisAspSerThr 1706
 DB 4627 ACTGAAATATTAAGTTAAATATATGATATGACAGAGAAATTTGGAAGATGAT----- 4680
 QY 1707 LysProSerAlaThrSerLeuAlaTyrValLeuTyrThrSerGlySerThrGlyAspPro 1726
 DB 4681 -----ATGTATCATATTTATTCATCTGCAACACAGGAAGAACCT 4719
 QY 1727 LysGlyValMetIleGlnHisArgValIleIleArgThrValThrSerGlyCysIle--- 1745
 DB 4720 AAGGACGATACAGTAAACAAGTAAATATATTAATTAATTAAGTA-----TGTGCTGG 4770
 QY 1746 -----ProAsnTyrProSerGlnThrArgMetAlaHisMetAlaThrIleAlaPhe 1762
 DB 4771 ACAAAGACATCAATTTATCCGATGATGAGTATGATGCAAGTAACTTAATGTTGCTTC 4830
 QY 1763 ArgGlyAlaSerTyrGlnIleTyrSerAlaLeuLeuPheGlyArgThrLeuValCysVal 1782
 DB 4831 GATGCTTCGGCAACTGATTTCTACTGTAGTTTATTAATGATATCCGCTGTGCATTGCA 4890
 QY 1783 AspTyrMetThrThrLeuAspAlaArgAlaLeuLysAspValPhePheArgGlnHisVal 1802

DB 4891 ACATCACTTGAGCGGACCAATACAGATTTTATGAAAAGTTAATTTCCAAAGAAAATATC 4950
 QY 1803 AsnAlaAlaSerHisValThrSerSerSerGlnAspValProLeuArgValProValArg 1822
 DB 4951 ACCATGCACT-----ATTCACATTAAC 4974
 QY 1823 LeuSerArgThrLeuMetPhePheLeu-----ValValThrAspSerThrAlaPro 1840
 DB 4975 GTATATATGTGATGATCATCTTTCTATATCTTAAGTAACTGATACAGAGGTGGCCCAAGT 5034
 QY 1841 AspAlaLeuAspAlaGlnGlyLeuTyrGlnGlyValGlnCysTyr---AsnGlyTyrGly 1859
 DB 5035 ACTCCAGCATTTGTGCAACATTTTCAACATTTGATGATGATGATGATGATGATGATGATG 5094
 QY 1860 ProThrGlnAsnGlyValMetSerThrIleTyrProIleAspSerThrGlnSerPheIle 1879
 DB 5095 CCTTGTGAAAATACAGTTATACATCTTTGTGATATACAAAAGGTGACGCCATACCA 5154
 QY 1880 AsnGlyValProIleGlyArgAlaLeuAsnAspSerGlyAlaTyrValValAspProGlu 1899
 DB 5155 TCGACTATTTCCGATGGGAAACCGTTAGCTAAATGTTGATTTTATATATGTC---GGC 5211
 QY 1900 GlnGlnLeuValGlyIleGlyValMetGlyGluLeuValValThrGlyAspGlyLeuAla 1919
 DB 5212 GGTAACTATGTCGCGGTGATTTCCAGGTGAATTAATGATGATGATGATGATGATGATGAT 5271
 QY 1920 ArgGlyTyrSerAspLys---AlaLeuAspGlnAsnArgPheValHisIleThrValAsn 1938
 DB 5272 TCAGGATATTTAAACAGACCCGAACCTTTCGTGAATAATTTAATTAATTCCTTTGGG 5331
 QY 1939 AspGlnThrValLysAlaTyrArgThrGlyAspArgValArgTyrArgIleGlyAspGly 1958
 DB 5332 CCAAGA-----CACTTTATCCAAAGGTGATTTAGCAGATTTG---ATGCCAGATGGG 5382
 QY 1959 LeuIleGlnPhePheGlyArgMetAspThrGlnPheLysIleArgGlyAsnArgIleGly 1978
 DB 5383 CAATTAATTTCTTGTTAATATAGACAAAGCAAGTTAACTATGATGATGATGATGATGATG 5442
 QY 1979 SerAlaGlnIleGluAlaAlaLeuLeuArgAspSerSerValArgAspAlaAlaValVal 1998
 DB 5443 CTAGGTGAATTAAGAAATATCATTAATTCAGTATGATCTGTTACAGATACCGTTGTAAT 5502
 QY 1999 LeuGlnGlnAsnGlnLeuSerGlnAlaProGlnIleLeuGlyPheValValAlaAspHisAsp 2018
 DB 5503 TTAGCTTAACAGGATGAGCT-----GAAGTGTGATGCTTATGATGTTGGAAGTCAA 5556
 QY 2019 HisSerGlnAsnAspLysGlyGlnSerAlaAsnGlnValGlnGlyTyrGlnAspHisPhe 2038
 DB 5557 GAAGATGAAGTCAATATTTCAACAACATTTAAATCAATAT-----TTGCCTAATATACAG 5610
 QY 2039 GluSerGlyMetTyrSerAspIleGlyGlnIleAspProSerThrIleGlySerAspPhe 2058
 DB 5611 ATTCTTAAGACATTAACAGCTATTAAGCAAAAT---CAATTAACA---GGAAATGAT--- 5661
 QY 2059 LysGlyTyrThrSerMetTyrAspGlySerGlnIleAspPheSerGlnMetHisLeuIleTyr 2078
 DB 5662 -----AAGTGATGAGTCAAGATTAACCTGTACCTTAATGATGACCAAAAT 5706
 QY 2079 LeuGlyGlnThrThrArgThrLeuHisAspAsnArgSerLeuGlnLeuValIle 2098
 DB 5707 AAATTTGTCACACACATAT---AATATGAAACGAAATATACACAAATCGTT----- 5757
 QY 2099 GlyThrGlySerGlyMetIle-----LeuPheAsnLeuAspSerArgLeuGlnSer 2115
 DB 5758 -----AGCGAGAGTGTGACGATCGCTATGATGATGATGATGATGATGATGATG 5796
 QY 2116 TyrValGlyLeuLeuProSerArgSerAlaAlaPheValAsnLysAlaThrGlnSer 2135
 DB 5797 -----GACTCTTTGAATAGGCTGATCA 5823
 QY 2136 IleProSerLeuAlaGlyLysAlaLysValGlnValGlyThrAlaThrAspIleGlyGln 2155

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Db      5824 CTAGATGCTATGCTGATGATCAAACTA-----AAA 5856
Qy      2156 ValAspAspLeuHisProAspLeuValLeuAsnSerValIleGlnTyrPheProSer 2175
Db      5857 TCAAATGGCATAC-----ATTACAAATGCAAGATGATATCA---TTTAAACT 5904
Qy      2176 SerGlnTyrLeuAlaGlu-----IleAlaAspThrLeuIle--- 2187
Db      5905 GTTCGTTATATACCTATACACAGAAAAAGCCAAACACTACACAGAGATATTACCA 5964
Qy      2188 ---HisLeuProAsnValGlnArgIlePhePheGlyAspValArgSerGlnAlaThrAsn 2206
Db      5965 GATCATCTACCAATTAATCAATCTTGGTT-----GAAAGACGATACCACTAAATAATCA 6018
Qy      2207 GlnHisPheLeuAlaAlaArgAlaIleHisThrLeuGlyLeuAsnAlaThr----- 2223
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Qy      2223 ----- 2223
Db      6079 GCGCATATTAAATGATGAATGCAAGATGATGCTGATCAATTAATCATGATTGTCAGA 6138
Qy      2224 LysAspAspValArgGlnLysMetAlaGluLeuGlnAspMetGluGluLeuLeuVal 2243
Db      6139 GGTCAATGATTCATCAATCAAGCTAAACTAACTGGAATAATAT-----TTA 6183
Qy      2244 GluProAlaPhePheThrSerLeuLysAspArgPheProGlyLeuValGlnHisValGlu 2263
Db      6184 AATTGTTATTTGATACGCTCATGTCATGATTA-----TTAATGAAAGCATTTGAT 6234
Qy      2264 IleLeuProLysAsnMetGlnAlaValAsnGluLeu-----SerAlaTyrArgTyr 2280
Db      6235 ATTATTTTACCGATTTATCAGAACTGACCATCTTATTATTCATTCAGCC-----ATT 6288
Qy      2281 AlaAlaValAlaHisValArgGlySerLeuGlyAspGluLeuValLeuProValGluLys 2300
Db      6289 GATACATATTTTCATGCT--GGAGCTCGTACACATACCTT-----GGC 6330
Qy      2301 AspAspTrpIleAspPheGlnAlaAsnGlnLeuAsnGlnLysSerLeuGlyAspLeuLeu 2320
Db      6331 GATGATCAAAACATTTTCGATGTCATAGTAAAGTACACAGATTAATGATTTAGCT 6390
Qy      2321 LysSerSerAspAlaAlaIleMetAlaValSerLysIleProPheGlnIleThrAlaPhe 2340
Db      6391 AAGCATTAATAAGCAATTAATCTATATATCAACGATA----- 6429
Qy      2341 GluArgGlnValValAlaSerLeuAsnSerAsnIleAspGluTyrGlnLeuSerThrIle 2360
Db      6430 -----AGTGGGCTACCGTA 6444
Qy      2361 ArgSerSerAlaGluGlyAspSerSerLeuSerValProAspIlePheArgIleAlaGly 2380
Db      6445 TTGGAATACATCAACAGCATATTACATTTTCGAAAAAAGTTATATATAA---GGC 6498
Qy      2381 GluAlaGlyPheArgValGlnValSerSerAlaArgIleTyrSerGlnAsnGlyAlaLeu 2400
Db      6499 CAGGTTA---TTTACATCACCATACACTAAAGTAAAGTTAATAGCGAGATTAAGGTGTA 6555
Qy      2401 AspAlaValPheHisHisCysCysSerGlnGlyArgThrLeuValAsnPro-----Pro 2418
Db      6556 GAAGCGGTTATGAAGTTTACGCTCAAGCTCAATTAAGATTAAAGAAATCTGCAAGAGTCT 6615
Qy      2419 ThrAspHisHisLeuArgGlySerAspLeuLeuThrAsnArg 2432
Db      6616 TCTACTGACCATTAATAATGAAAAATTTTAAACAATTAATGCT 6657

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RESULT 9
US-08-956-171E-206/c
; Sequence 206, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi

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/ Patrick S. Dillon
/ Craig A. Rosen
/ Steven C. Barash
/ Michael R. Fannon
/ TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
/ NUMBER OF SEQUENCES: 5256
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Human Genome Sciences, Inc.
/ STREET: 9410 Key West Avenue
/ CITY: Rockville
/ STATE: Maryland
/ COUNTRY: USA
/ ZIP: 20850
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 Inch, 1.4Mb storage
/ COMPUTER: HP Vectra 486/33
/ OPERATING SYSTEM: MSDOS version 6.2
/ SOFTWARE: ASCII Text
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/956,171E
/ FILING DATE: 20-Oct-1997
/ CLASSIFICATION: <Unknown>
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 60/009,861
/ FILING DATE: January 5, 1996
/ APPLICATION NUMBER: 08/781,986
/ FILING DATE: January 3, 1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mark J. Hyman
/ REGISTRATION NUMBER: 46,789
/ REFERENCE/DOCKET NUMBER: PB248P1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (240) 314-1224
/ TELEFAX: (301) 309-8439
/ INFORMATION FOR SEQ ID NO: 206:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 29555 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-08-956-171E-206

Alignment Scores:
Pred. No.: 2,9e-138 Length: 29555
Score: 1428.00 Matches: 646
Percent Similarity: 39.61% Conservative: 458
Best Local Similarity: 23.18% Mismatches: 1028
Query Match: 8.85% Indels: 657
DB: Gaps: 109

US-09-482-788-2 (1-3129) x US-08-956-171E-206 (1-29555)
Qy      194 LysHisGluLysAspThrHisArgProGluThrProGluSerSerAspAlaThrAspThr 213
Db      27274 AACCATCCATTAAACAAAGCTTTATATCAACGATATTGATGATGATGACATCAATA 27215
Qy      214 AspSerGlnSerValSerValSerMetSerCysGluAspAsnAlaValSerAlaThr 233
Db      27214 GATATGGCATCGTTGGCT--GTTAGTGTATATTAGCTATATCAATTAATGATCAACAA 27158
Qy      234 His-----PheTyrGlnThrHisLeu---AsnAspLeuAsnAlaSer 246
Db      27157 CATGATGTCATTAGGTATACATGATGATCACTACATTACCAATGATTTACACGGAAT 27098
Qy      247 ValPheProHisLeuSerAspHisLeuMetValProAsnProThrThrAlaGluHis 266
Db      27097 ATTTGGCCG-----TTTACGTTTAAATGATGTCGCAAAATATGTCGCAATTACAGTCCG 27053
Qy      267 ArgIleThrPheProLeuSerGlnLysAlaLeuSerAsnSerAlaIleCysArgThrAla 286
Db      27052 CGTTTTCACACAGATTTTATTAATGATGTCGCAAAATATGTCGCAATTACAGTCCG 26993

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QY 287 LeuSer11euleuSerArgTyrThrHisSerAspGluAlaLeuPheGluAlaValThr 306
 DB 26992 AGCTTCGCTT-----TCACTAGACGCTATTTT----- 26963
 QY 307 GluGlnSerLeuProPheAspLysHisTyrLeuAlaAspGlyThrTyrGlnThrValAla 326
 DB 26963 ----- 26963
 QY 327 ProLeuAlaGValHisCysGlnSerAsnLeuAlaGAla-----SerAspValMetAspAla 344
 DB 26962 -----CATTTGTTATCATCATATGATGCTGTGTTGTAATGATGTTATTTGAGGAT 26915
 QY 345 L1eSerSerTyrAspAspArgLeuGlyHisLeuAlaProPhe----- 358
 DB 26914 GTACATCAATATAGATATGATGACATACATCTTTAGCCGATATGAAATTTTCCACATCA 26855
 QY 359 ---GlyLeuArgAsp11eArgAsnThrGlyAspAsnGlySerAlaAlaCysAspPheGln 377
 DB 26854 CACGGGCTTCAAAATTTATATATAC-----AGTCACAGCATATGATTTGCTC 26810
 QY 378 ThrValLeuLeuValThrAspGlySerHisValAsnAsnGlyLeuAsnGlyPheLeuGln 397
 DB 26809 TCATATGACAGCGCTGAGTGAC-----TTAGTTCGAAATATTTATTTTG 26768
 QY 398 Gln11eThrGlySerSerHisAspMetProCysAsnAsnArgAlaLeuLeuLeuHisCys 417
 DB 26767 CAAATTAAGTCAAAATAATGCA-----AATTAACGA----- 26738
 QY 418 GlnMetCysSerGlyAlaLeuLeuValAlaTyrTyrAspHisAsnVal11eAspSer 437
 DB 26738 ----- 26738
 QY 438 LeuGlnThrThrArgLeuLeuGlnGlnPheGlyHisLeuLeuLeuCysLeuGlnSerPro 457
 DB 26738 ----- 26738
 QY 458 LeuAspLeuSerSerMetAlaGluValAsnLeuMetThrGlyTyrAspArgAlaGlu11e 477
 DB 26737 -----ACAAGTCAAGTCACTTAATTTGATGACAGACGCTGATATTCATTTAT 26687
 QY 478 GluSerTyrAspSerGlnProLeuGlyValGlnAsp-----ThrLeu11e 492
 DB 26686 GACGATATCATTTAGTTGCTGAGATGATGATGATGCGCAACAGTTGTTACCTTATTT 26627
 QY 493 HisHisGluMetLeuLysAlaValSerHisSerProThrTyrThrAla11eGlnAlaTyr 512
 DB 26626 GAGCAACA-----GTTGAAGCAACGCCGAATCATGTCGCTGCGCA-----TTT 26582
 QY 513 AspGlyAspTyr---ThrTyrSerGlyLeuAspAsnValSerSerArgLeuAlaValHis 531
 DB 26581 GACGGAGTGTTTTAACTATCAACATTTAAATGACACGCCGGAATGATTTAGCACACCGT 26522
 QY 532 11eLysSerLeuGlyLeuArgAlaGlnGlnAla11eLeuPro-----Val 546
 DB 26521 -----TTGAGAAACCAAGTATGCTGTTGACCTAATGATCGTGCCTGTC 26477
 QY 547 TyrPheGlyLysSerLysTyrVal11eAlaSerMetLeuAlaValLeuLysSerGlyAsn 566
 DB 26476 ATAGCTGAAATAAGTTGATGAGATGATTAATGACGATGATGCTGTGTTGAAGCTGTGGG 26417
 QY 567 AlaPheThrLeuLeuAspProAsnAspProProAlaArgThrAlaGlnVal11eThrGln 586
 DB 26416 GCTTAGTGCCAAATGATCCGAATCATCAAGTGATGTCAGAGATTCATTTTAAAGAT 26357
 QY 587 ThrArgAlaThrValAlaLeuThr---SerLysLeuHisArgGlyThrValGlnLysLeuVal 606
 DB 26356 GTAAAGCGCTAAAGTTGTAATACGATACCAAGCTTTATATGAAATGTTAAACAAATAAT 26297
 QY 606 1-----GlyArgCysValValValAspAspGluLeu 617
 DB 26296 AATCACATGATTTGTAATAGATAGCGTGGAAAAATTTGATATATC----- 26251
 QY 617 uGlnSerValSerAlaSerAspPheSerSerLeuThrLysSerGlnAspLeuAlaTyr 637

DB 26250 -----TTTCTAATGTAAACAGCTTA---GAAGATCATGCTTA 26217
 QY 637 Val11ePheThrSerGlySerThrGlyAspProLysGly11eMet11eGlnHisArgAl 657
 DB 26216 TGTATTTTAAACGCTGGGCAACCTGTGTAACCTTAAGGACACTAATTCGACCGAGG 26157
 QY 657 aPheSerSerCysAlaLeuLysPheGlyAlaSerLeuGly11eAsnSerAspThrArgAl 677
 DB 26156 TATTTGCTGCTGCTGCATCA-----AATCATTTATGACATTTAAATGAAGACGACGAT 26100
 QY 677 AleuGlnPheGlyThrHisAlaPheGlyAlaCysLeuLeuGly11eMetThrThrLeu11 697
 DB 26099 TTGTTATGACGAATCATAGCTTTTGATGCTGCAACATTTGAATATATGTCGATGCT 26040
 QY 697 eAsnGlyGlyCysValCys11eProSerAspAspArgMetAsn-----Ser11eP 715
 DB 26039 CAATGGTGGAACCTGATTTGCTTAAAAAAGAACATTTAATTCATTAACGCGTGA 25980
 QY 715 oSerPhe11eAsnArgTyrAsnValAsnTyrMetMetAlaThrProSerTyrMetGlyTh 735
 DB 25979 ACAATTAATCAATGAATGACGCTTAACTATGCTGTTAACCTCTCATATTATTAATCA 25920
 QY 735 rPheSerProGlyAspValProGlyLeuAlaThrLeu-----ValLeuValGlyGlu1 753
 DB 25919 GATTGCTAGTGAACGAATGAGATTTGTAACGCTTAAGATATTATTTATTTGCTGAGA 25860
 QY 753 mMetSerSerValAsnAla11eThrAlaProLysLeu----- 766
 DB 25859 AGTA-----TTGAAATCTAAGTGGGTGATTTGCTTAAATCAAAACCGAACATCC 25809
 QY 767 -GlnLeuLeuAsnGlyTyrGlyLysSerGlySerSer11eCysPheAlaSerAsn 786
 DB 25808 TCAAATTAATTAATGATTAAGTATGACCAACTGAATAACCTTTTCAACAGACGATTAAT 25749
 QY 786 tSerThrGlu---ProAsnAsn-----MetGlyArgAlaVal---GlyAlaHisSerTyr 802
 DB 25748 ACTAACAAGTTCCAATGATGATTCCTATTCGTTAAACGATTCGCGTTCATGTTTA 25689
 QY 802 pVal11eAspProAsnAsp11eAsnArgLeuValPro11eGlyAlaValGlyGluLeuVal 822
 DB 25688 TATCATGCAAGGC-----GAGCGTCGCTGCGGTGATTCCTGGAATAATATG 25638
 QY 822 11eGlySerProGly11eAlaArgAspTyr11eAlaProProProProGlyLysSerPro 842
 DB 25637 TACAAGTGCCTTGGGTAGCTGACGCTATTTAAATCAACCGAATGACACAGATTA 25578
 QY 842 oPhePheThrAsp11eProSerTyrTyrProAlaAsnThrPheProAspGlyAlaLysLe 862
 DB 25577 ATTTATCAAAAGAT-----TCAAATATA-----AATCAGCTGAT 25545
 QY 862 uTyrArgThrGlyAspLeuAlaArgTyrAlaSerAspGlySer11eValCysLeuGlyArg 882
 DB 25544 GTATTAAGAGTGTGATATCGTTGTTGTTACCCGATGCGCAACATGATTAATTAATTCG 25485
 QY 882 g11eAspSerGlnValLys11eArgGlyGlnArgValGluLeuGlyAla11eGlnThrHis 902
 DB 25484 AAAGCAACAACAGTTAAGATTTGAGAGGTTTACGATTAAGTTTTCAGAGTTAG----- 25430
 QY 902 sLeuArgGlnGlnMetProAspAspLeuThr11eValAlaGluAlaThrLysArgSerG 922
 DB 25429 -----CATGCGTCAAGGATATACA 25410
 QY 922 nSerAlaAsnSerThrSerLeu11eAla-----PheLeu11eG 935
 DB 25409 AGCTAATTAATAAGCAAGTTGTATTGTTCAAAATCATGATCAAGATCAGATATTCGTT-- 25352
 QY 935 ySerSerTyrPheGlyAsnArgProSerAspAlaHis11eLeuAspHisAspAlaThrLys 955
 DB 25351 -----GCTTATTA-----GAAGCATGCATCACTTATCACTAATATAAGATTA 25308
 QY 955 sAla11eAsn11eLysLeuGlnGlnValLeuProArgHisSer11eProSerPheTyr11 975

Db	25307	ATCA-----	-CAATTAGSTAGACCTTAACGGAGTACATGATACAGTTAA	TTTCA	25257
Qy	975	ECyMeLeuGIuLeuProArgThrAlaThrGIuYvLIeAspArgArgLeuArgI			995
Db	25256	GCAATATTGACGAATTCCTTACTTAATTAATGGGAATTTGATTAAGCAATTCGCTAT			25197
Qy	995	eMeCjYUvAspRIleLeuAspYvSGINthrGInGlyAlaIleValGInGlnAlaProI			1015
Db	25196	CATG-----GACATATGTCAT-----			ACCGATTC 25173
Qy	1015	APrOILeProValIhPheAlaAspThrAlaAlaYvLeuHiseRIleTrpValGInSerLe			1035
Db	25172	CTATGTGACACCGAGTACAGTACATCCGAACCTTGCTATGCCAAATTTTTCGAGATTTT			25113
Qy	1035	uGIYIleAspProAlaThrValAsnValGIyAlaThrPhePheGInLeuGIyYvAsnSe			1055
Db	25112	ACATGTGAT-----CAAGTAGGTATTCATGATTAATTTCTTGATTAATGATGGCCATTC			25059
Qy	1055	RIleThrAlaIleYvMeCValAsn--MeCAlaYvSerValGIyMeCAspLeuYvA			1074
Db	25058	ATTAAAGCAACCTTAATGGTGAATCCGATAGAGCCATCTACACGGAAACGATTCACAT			24999
Qy	1074	ISerAsnIleTrpGInIhSProThrLeuAlaGIyIleSer---AlaValIleGIyAs			1093
Db	24998	TGTGTGATTTATTAACAAGCCATGTATTTGAACATGCAACAGCAATTCGTAAGTTCA			24939
Qy	1093	pProLeuSerTYrThrLeuIleProYvSerThrHISGInGlyProValGIuGInSerTY			1113
Db	24938	AGAACAAACATATGATAGATTCACGAACCTATATGTTAAAGATGATTAATGTGTAGCTC			24879
Qy	1113	rSerGInGIyArgLeuTrpPheLeuAspGInLeuAspValGIySerLeuTrpTYrLeuI			1133
Db	24878	TGCACAAAGCGTATGATTTATTTATGTGAATCAACACATTAAGATACGGTGTATACGT			24819
Qy	1133	eProTYrAlaValArgMeCArgIyProValAsnValAspAlaLeuArgAlaLeuAl			1153
Db	24818	ACCTTTTATTAGCGCGGTATCATACAACTTAATGTACCTCAATTCGCACACACAGTGA			24759
Qy	1153	aAlaLeuGInGInArgHISGInThrLeuArgTYrThrPhe-----GluAspGlnAs			1170
Db	24758	GCGTTTGTATACGGGACACTGATTTACGAACCAATATATGTGTGATGATGATAG--			24701
Qy	1170	pGIYValGIyValGInIleValHISGInYvLeuSerGIuGInMeCLeYvAlIleAspLe			1190
Db	24700	-----GTTCCACAAACGATATTGTGGCAGATGGTCAGTT-----			24668
Qy	1190	uCYvGIySerAspLeuAspProPheGIuValLeuAspGInGInGInThr-----			1206
Db	24667	-----GACTTTGAAGATTTAACCCGATTTTACCGATGAACACAGA			24627
Qy	1207	-----ThrProPheAsnLeuSerSerGIuAlaGIYTrpArgAlaTh			1220
Db	24626	AATCATGCCCAATTGTGACACTTTTAAATTGGAAGAACCAAGTCAAATTAAGAGTGAG			24567
Qy	1220	rLeuLeuArgLeuGIyGInLeuAspHISIleLeuThrIleValMeCHisIleIleSe			1240
Db	24566	ATTACATTAGAGTCCCTTACATGCATAC--CTCTTATATGATACCAATCATATCATTA			24510
Qy	1240	rAspGIYTrpSerIleAspValLeuAspArgAspLeuAspGInLeuTYrSerAlaIle			1260
Db	24509	TGACGGTATGTAGTATATACATTAATGATGATCTTAAACGACTTATATCAACATTAAT			24450
Qy	1260	uLYAspSerLYAspProLeuSerAlaLeuThrProLeuProIleGIYTYrSerAspH			1280
Db	24449	A-----TTGTTAACCACTTAATTTGCATATTAAGACTA			24417
Qy	1280	eAlaLYeTrpGInLYAspGInPheIleGIuGInGlyuYvGInLeuAsnTYrTrpLYeLY			1300
Db	24416	TATGAGAGTGATGTGCGCATCGTATATGACGAACAAATATAGCAA-----TATGTGTTATC			24363
Qy	1300	SGInLeuLYAspSerSerPro--AlaLYSIIeProThrAspPheAlaArgProAlaIe			1319
Db	24362	TCAATTCAAAATGATAGTACTTATTTAAAGCTTATACCAACGATCTTATATGACCAAAAT			24303

QY	1319	uLeuSeRgLYaRPaLaGlycYsValInIhValThrIleAaRdGlyLeuTyRGlInSeR	1339
DB	24302	TAAGAAGCAAAATGGAGCAATGATGTCATTTACAAAGAAATCAACAATATGACAGCTACT	24243
QY	1339	uAGxAlaPhSeCyAaInGlnIhIaAaThrThRSeRPhaValIaLeuAlaAlaPhaR	1359
DB	24242	TCAAAGATATGTAAGAAAGCATCAAAATTCATGTTTATGTTCTTTATGAGTGTGCAT	24189
QY	1359	gAlaAlaNIhTYaRgLeuThRaLaValGIaAaRaLaValIleGlyThRProIleAlaA	1379
DB	24182	GACSTGTGTAAAGTAAGATATGCTCGAAAGATGATGTTGTTCGCGTAAGTGAATGATGTC	24123
QY	1379	naRxAaNaAaRgProGlyLeuGlyAaRleIleGlyCySPhaValAaThRGIInCySeAaR	1399
DB	24122	GCGATATGCAATAAGGACGAGCAAAATGCTAGGACATGTTGCTAAATACCTGTGATATAG	24065
QY	1399	gIleAaNIleAaRNIhIaAaThRPhaGlyThRleuIleAaInValIyAlaThRTh	1419
DB	24062	AGGGCAACCGATACCTGATTAATATGTGACACAGTTTTCAAAGAGTTAAAGGAATATAG	24003
QY	1419	rThRaAlaRPhaGlyAaInGlyAaRleIleProPhaGlyAaRValIaSeRaIleuGlnR	1439
DB	24002	TTTGGAGCGATACGAGATCAAAATACCCATTCGATGATTTTAAGTAAGACTTATGATCA	23943
QY	1439	oGlySeRaRgAaRleuSeRSeThRrProLeuAlaGlnleuIlePhaAlaValIhIaSeRGI	1459
DB	23942	A---TCAATGATGTCCTCACGGAATCATATTATGATGTCATGTTAGTACTCAAAACAA	23886
QY	1459	nLyA-----AaRleuGlyAaRgPhaIyRPhaGlyLeuGlyAaRleuGlyAaRleuA	1475
DB	23885	TGAAGCAAGATCATGCTCATTTTGGGCAATGATTAATTAACACATTCAA-----	23837
QY	1475	lProSeRaLyAlaTyThRrAaRgPhaAaRmeTGIuPhaNIleuPhaGlyThRzAaRSe	1495
DB	23836	-CCCAATTCAGTACGCGGCAAAATTTGATTTATCTTTCATCATTTGAAGAAAGTGCATGA	23778
QY	1495	rLeuLyAGlySeRaValAaRPhaAlaAaRgIleuAaRPhaIyAaRmeTGIuThValGIuAaR	1515
DB	23777	CTAATACATCAATATTCAGATATTAATCCGATTTATATCTCAGAAACAGTTGCTACAT	23718
QY	1515	IValAaRValAaRPhaGlyIleuAaRgAaInGlyLeuGlnSeRSeRaThRProVaISe	1535
DB	23717	GGGTATCAATATGATG---ATTATGATTTATTTATTTTGAACATCAAGATCACTTAA	23661
QY	1535	rIleuAaRProLeuThRzAaRgLyIleValThRleuGlyAaRleuAaRPhaValIeAaR	1554
DB	23660	AATTTGATGATATCCAAACGGC-----ACGAGAAATCTTAAATTTGGGTCAATACGA	23607
QY	1555	-----LyaNIhValaAaRPyThRProAaRgIuSeRSeRaValAaRPhaGlnTh	1571
DB	23606	TGTTAAAGATCGAATGCTTAATGTCCGGGAAATTAATCATATCAATAGTACTTAAATGA	23547
QY	1571	rGlnIValSeRaIaTyRProAaRSeRaValaValIaAaRSeRSeCyAaRgLeuThTy	1591
DB	23546	AGTTGTCTCACAGCAAGATTAATCATGTGGCTAGTCATCAAGAAATTTGACATGACGTA	23487
QY	1591	rThRGIuAaRPaRgIInSeRaRleIleuAlaGlyThRleuAaRgATgATgSeRmeCP	1611
DB	23486	TGAAGCAATTCGCAACATATGTGATGCGACATGCTCTCTCAATAGCTGTGG	23427
QY	1611	oAlaGlyThRleuValaAlaAaRPhaAlaProAaRgSeCySglnThIleValAlaAaRPha	1631
DB	23426	CAATGTCMAACGGGTGCTTGTTCACAGACGTAAGTTTGAATGATTTGGCGCATGTT	23367
QY	1631	eGlyValIyAlaNIhAaRleuAlaTyRleuAaRProLeuAaRPaRgSeRProSeRaIaR	1651
DB	23366	GCGACAGATTAAAGTATGTCATCTTAATATACCTATGCAATATGATTTCCGAATTAACG	23307
QY	1651	gValGIaAaRPIleuSeRgLyLeuSeRgLyProThrIleValIleuIleGly-----H	1669
DB	23306	ACAAGGTGCAATTTTGGAGAGTCTAAAGTAAGTACGACATGCTTAAGGGCTGAAT	23247


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Db 21389 TGCAGGTAAATATATGTCTCTACGATTAAGTGTGGAACTTATTGATATAGACACAGA 21330
QY 2334 -----Prophag 2336
Db 21329 AGATGTGACATTTTCASAGCGGATGTCTATTAAGGGCACTACTACATACCATATAC 21270
QY 2336 uilethralphe-----gluarglnvalvalaleuSerleuamSerleuamleap-- 2353
Db 21269 ACCGAGCAAAATTTATAGTAAATTAAGATTAAGAACTGTAAATATGCTTATGATGCG 21210
QY 2354 -----glutprglnleuSerth 2359
Db 21209 TCGGATTTGACGTGTCTGTAATTTGACGAATCCTTACAAATGGAAGATGGCTATGAGAAA 21150
QY 2359 rileargSerSerleuagluylapSerSerleuSerleuValproaphlephargileal 2379
Db 21149 TATTAAGACATACCGCT-----TTTTCATGTGATATGATGATTTGTTACAA----- 21104
QY 2379 aglygluaglylpheargvalgluvalSerSerleuarglnltpSerlenglyal 2399
Db 21104 ----- 21104
QY 2399 aleuapralvalphehihiScyScySerenglnlyArgThrleuvalampheroth 2419
Db 21103 -CTGATTTGTATC-----GGGGTTAGCATGGCTGAATGCTGT 21066
QY 2419 rARPHiHiLeuAarglySerAerleuThrAen-ArgProLeuGlnAargleuGlna 2439
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QY 2439 smAarglilealilegluvalAarglyleuAargSerleuProSerTyweti 2459
Db 21006 CACCACAAATCATTTTACCATGTG-----CTATCAGCT----- 20975
QY 2459 leProSeranillevalleuamsplysmetProleuamAalaAarglyls--Vala 2478
Db 20974 -----AATAAAMGCCGGGAAATCTTTGTGAATGCCGTTA 20938
QY 2478 spAarglyleuSerAarglaleuvalProlysglnlthralaIaprol 2498
Db 20937 AGGGCAAA----- 20930
QY 2498 eudProthRheProIleSerGluvalgluvalileuCysegluvalaThrGluvalP 2518
Db 20929 -----GAATTTGAACCTGTCAGCATGATCTTTAATGAAATTT 20890
QY 2518 heglwelyValaPleleThrAphleAenleuGlylHISerleuA 2538
Db 20889 TACAGAAACAA-----GACATGTACGAACGATTTGATTAAGTGTGACC 20842
QY 2538 lathrlyleuileSerAarglleAerGlnAargleuValAarglleThr----- 2554
Db 20841 GTGAAACAACAATGACATGATGATGATCAACATTTAATAAATATGATACATCA 20782
QY 2555 -----Vallysa 2557
Db 20781 GTGAAAAATGGCCAAACGATTAACATAATGGCTGTATCTATGGGCAAAATATATCAAAA 20722
QY 2557 spvalPheaphleProvalPhealaleuSerleuileSerleuilelearglnlyleuclyl 2577
Db 20721 CAATATTCAATTAAGTAAGTGAAGAACTTATGACAGATTTGTTATGATCAATTCACAGATA 20662
QY 2577 euglnlInprovalSerAerGlyglnlyGlnAerAerSerleuAhiMetAlaproargt 2597
Db 20661 ACTTGAAGAAATGATTAAGAAATTAATACCAAACTCGTTGCTATATAAAAAACGGGCTA 20602
QY 2597 hrgluthrgluvalileuCyseAerGluPhealaleuValleuGly-----Pheg 2614
Db 20601 CAGTCAACTATAGATACATCAATCAATTAACATCAAGATGGAGATATTTTATGTC 20542
QY 2614 lvalaglylilethraAerAenPhe----- 2621
Db 20541 AATATGAATTCACATGACACAGCTTTATTTACCATGAATGACATTAATCATCTTTCGC 20482

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QY 2622 -----PheAerleuGlylHISerleuMetAlathrlyleuAalaAargl 2638
Db 20481 CACGAGTAAAGCAGATATATGTTCAACACAAATCGTATGGACAGCCCATCTATGAGCT 20422
QY 2638 leglylHISerleuAerPthThrValSerVallyAerPhealPheaphleProvalLeuP 2658
Db 20421 TATCATTAATGATTAATCTTATATGCTGTGTGTGAT-----AAGAACAGTT----- 20372
QY 2658 hegluvalaleuAerAenleuValGlnSer----- 2670
Db 20371 -----GGTATGTATATGAAAGATATACAGAGTTAGCTGCGGTAGCTTGTGA 20320
QY 2671 -----lysthrAenGluilelelGlnAer--lletyrProserThrglnMetGln--L 2724
Db 20319 CGTGTCTCTACAAACGAA-----GCACATCAAAATATGATTTAATGATTTT 20269
QY 2688 lInleuAerPheThr-----GluAerProglucluhemetalAerGluilelePProG 2706
Db 20268 ATCAAAATATGACACAAAGAAAGTTTACAAATGATGTGTAAGTTTATATCAAG 20209
QY 2706 lInleuGluLeuGlnGluilelelGlnAer--lletyrProserThrglnMetGln--L 2724
Db 20208 GATTGACATTTATGATATGACACAAATCAGCTTTTATCATATCAGTGAAGTGAAGTTCA 20149
QY 2724 ysaIapheleuPheAer 2729
Db 20148 AACAAATTTATTTTGAT 20132

RESULT 10
US-08-781-986A-206/c
; Sequence 206, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29555 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-781-986A-206

Alignment Scores: 2.9e-138 Length: 29555
Pred. No.:

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Dh 25637 TACAGTGGCTTTGGCTTACGAGCTTATTAAATCAGCAGATTTGACAGCATAA 25578
Qy 842 ophethrAspIleProserTrpIyProAlaasnThrPheProaspGlyAlaIysle 862
Db 25577 ATTTATCAAAAGAT-----TCAAAATATA-----AATCAGCTGAT 25545
Qy 862 uTyArgThrGlyAspLeuAlaArgTyAlaIAserAspGlySerIleValCySleuGlyAr 882
Db 25544 GTATTAGAGTGGTATCGCTTCTTGTTCACCGAGTGGCAACAATTAATTATATTCG 25485
Qy 882 gIleAspSerGlyValIysIleArgGlyValIAsnValGluLeuGlyAlaIleGluThrRh 902
Db 25484 AAAGCAAAACAAGTTAAGATTGAGGGTTTGGAGTTGAGTTGACAGAGTGAG----- 25430
Qy 902 sleuArgGlnGlnImerProAspAspLeuThrIleValIaGluAlaThrIysArgSerG 922
Db 25429 -----CATGCGCTCGAGCTATATCA 25410
Qy 922 nSerAlaAsnSerThrSerIleuIleAla-----PheIleuIleG 935
Db 25409 AGGTATTAAATMAAGCAGTTGTTATTTCAAAATCATGATCATGATATCGTT-- 25352
Qy 935 ySerSerThrPheGlyAsnArgProSerAspAlaHisIleLeuAspHisAspAlaThrI 955
Db 25351 -----GCTTATTAT-----GAAGCAGTCAATCATTCATCATTAATAAGATTAA 25308
Qy 955 sAlaIleAsnIleLeuLeuGlnGlnValIleuProArgHisSerIleProserPheTyri 975
Db 25307 ATCA-----CAATTAGGTATGACCTTACCGAGTACATGATACAGATTATTTTCA 25257
Qy 975 eCySmetLeuGlnLeuProArgThrAlaThrGlyIleAspArgArgArgIleuArgI 995
Db 25256 GCATTATTGACCAAAATTCCTATTACTATTAAATGGGAAATTAAGTAAGAAGCATTTGCC 25197
Qy 995 eMetGlyLeuAspIleLeuAspIlyGlnThrGlnGlyAlaIleValGlnGlnIleProAl 1015
Db 25196 CATG-----GACTATGTCGAT-----ACCGATGC 25173
Qy 1015 aProIleProValPheAlaAspThrAlaAlaIleLeuHisSerIleTrpValGlnSerIe 1035
Db 25172 CTATGTAGCAACCGAGTACAGTACCGAAACCTTGCTATGCCAAATTTTGGAGATATTTT 25113
Qy 1035 uGlyIleAspProAlaThrValAsnValGlyAlaThrPhePheGlnLeuGlyIysIle 1055
Db 25112 ACATGTGCAAT-----CAAGTAGCTATTCTGATTAATTTCTTGAATTAGCTGCCATTC 25059
Qy 1055 rIleThrAlaIleLeuMetValAsn---MetAlaArgSerValGlyMetAspLeuIysVa 1074
Db 25058 ATTAAAGCAACGTTAGTGGTGAATCGGATAGAGGCATCTACTGGGAAACGATTACAAAT 24999
Qy 1074 lSerAsnIleTyrglnIAspProThrLeuAlaGlyIleSer---AlaValIalIysGlyAs 1093
Db 24998 TGGTGATTATTTCAAAAGCAACTGATTTGAATTCAGCAACAGCGATTGGTATGCTCA 24939
Qy 1093 pProLeuSerTyThrIleuIleProIySerThrHisGlnGlyProValGlnGlnSerTy 1113
Db 24938 AGAACAACAACTAGAGTGAATTCAGAAACTATAGTTAAAGATGATTATGTCTGACCTC 24879
Qy 1113 rSerGlnGlyArgIleuThrPheLeuAspGlnLeuAspValGlySerIleuTrpTyrlleuI 1133
Db 24878 TGCAACAAAGCGATGATTTATTATGGAATTCAAACATTAAGATACCGGTATTAACGT 24819
Qy 1133 eProTyAlaValAlaArgMetArgGlyProValAsnValAspAlaLeuArgAlaLeuAl 1153
Db 24818 ACCTTTATTATGGCGTTATCATCAGAACTTAATGTAAGTCAATTTGGAGCAAGAGTGA 24759
Qy 1153 aAlaLeuGlnGlnArgHisGluThrIleuArgThrPhe-----GluAspGlnAs 1170
Db 24758 GCGTTTGATAGCGGACATGATGATTTTACGAACAATATTTGTTAGTATGATGAG-- 24701
Qy 1170 pGlyValGlyValGlnIleValHisGluIyLeuSerGlnGlnMetIyValIleAspIle 1190
Db 24700 -----GTTGCAACAACGATTGTGGCAGATGTGCAGTT----- 24668

Qy 1190 uCyGlySerAspLeuAspProPheGlnValIleuAsnGlnGlnThr----- 1206
Db 24667 -----GACTTGAAGAAGTTAACACCGCATTTTACGATGAAACAAG 24627
Qy 1207 -----ThrProPheAsnLeuSerSerGlnAlaGlyTyrrArgAlaTh 1220
Db 24626 AATCATCGCGCAATTTGTAGCACCTTTTAAATTTGAAAAACCAAGTCMAATTTGAGTGA 24567
Qy 1220 rLeuLeuArgLeuGlyGluAspAspHisIleLeuThrIleValIleMetHisIleIleSe 1240
Db 24566 ATACATTAGAAAGTCCCTTACATGCATAC---CTCTTATATGATACCGCATATTCATTTAA 24510
Qy 1240 rAspGlyTyrrSerIleAspValIleuArgArgAspLeuAsnGlnLeuTyrrSerAlaIle 1260
Db 24509 TCACGGTATGAGTAATATCAATTAATGAATGATCTTAAACGCACTTATATCAACATAAAT 24450
Qy 1260 uTyAspSerIyAspProLeuSerAlaLeuThrProLeuProIleGlnTyrrSerAspH 1280
Db 24449 A-----TTGTTACCACTTAAATTCMAATTAATAAGACTA 24417
Qy 1280 eAlaTyrrPglIlyAspGlnPheIleGlnGlnIlyGlnLeuAsnTyrrTyrrIyIy 1300
Db 24416 TAGTGAAGTATGCCATCGCATGATATGACGAACATAGACA-----TATTGTTATTC 24363
Qy 1300 sGlnLeuIyAspSerSerPro---AlaIyIleProThrAspPheAlaArgProAlaIe 1319
Db 24362 TCATTCAAAAGATGAAGTACTATTTTAACTTACCGACAGACTATGTTAGACCAATAT 24303
Qy 1319 uLeuSerGlyAspAlaGlyCyValHisValThrIleAspGlyGluLeuTyrrGlnSerIe 1339
Db 24302 TAAACGCAAAATGAGCAATGATATGTCATTACAAATGAATCAAAATGAGACGCTACT 24243
Qy 1339 uArgAlaPheCyAsnGlnHisAsnThrThrSerPheValIleuLeuAlaIleAspHear 1359
Db 24242 TCAAAAGTATGTAAGAAAGCATCAAAATCTGATTTTATGCTTATATGAGTGGTGCAT 24183
Qy 1359 gAlaAlaHisTyrrArgLeuThrAlaValGluAspAlaValIleGlyThrProIleAlaAs 1379
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Qy 1379 nArgAsnArgProGluLeuGlnAspIleIleGlyCySppheValAsnThrGlnCyMetAr 1399
Db 24122 GCGTATGCAATMAAGCAGCGAGGAATGCTAGGCACTTTGCTAAATCGTTGATATAG 24063
Qy 1399 gIleAsnIleAspHisIleAspThrPheGlyThrIleuIleAsnGlnValIyAlaThrTh 1419
Db 24062 AGGCAACCGTCACTGATTAATGTGCACACAGTTTATACAGAGCTTAAGGAATGAG 24003
Qy 1419 rThrAlaAlaPheGlnAsnGluAspIleProPheGlnAspValIleSerAlaLeuGlnPr 1439
Db 24002 TTTGAGAGCTACGACATCATGAMAATACCATTCGATGTTAGTAATGACTTAGATCA 23943
Qy 1439 oGlySerArgAspLeuSerSerThrProLeuAlaGlnLeuIlePheAlaValHisSerG 1459
Db 23942 A---TCAATGATGCGCTCAGCAATCCATTTATGATGATTTGATGATCAAAACAA 23886
Qy 1459 nTyS-----AspLeuGlyArgPheIyPheGlnGlyLeuGlnSerValIProVa 1475
Db 23885 TGAACGAATCATGCTCATTTTGGCATAGTAATTAACACACATTCAA----- 23837
Qy 1475 lProSerIyAlaTyrrThrArgPheAspMetGluPheHisIleuPheGlnGlnIuThrAspS 1495
Db 23836 -CCCAATCAGTACGCGCAAAATTTGATTTATCTTTCATCATCATGAAGAAGATGCGCATGA 23778
Qy 1495 rLeuIyGlySerValAsnPheAlaAspGluLeuPheIyPheMetGlnIuThrValGluAsnVa 1515
Db 23777 CTATACATCAATATGAGATATATACCGATTTATATCACTAGAAACAGTTGCTGAT 23718
Qy 1515 lValArgValPhePheGlnIleuLeuArgAsnGlyLeuGlnSerSerArgThrProValSe 1535
Db 23717 GGGTAAATCAATGATATG---ATTATGATGATTTATTTTGAAGCATCAAGATACACTACA 23661

QY	1535	rTlLeuPrLeuThrsApLylLeValThrLeuGluYLeuAspValLeuAsnVal---	1554
Db	23660	AAATTGTGATATCAACAACGCGC-----ACGAGAGAACTTTAAATTTGGCTCAATACGCA	23607
QY	1555	-----LYsHlValAspTYrProAGGluSerSerLeuAlAspValPheGlnH	1571
Db	23606	TGTTAAAGCATCGAATGCTTATATGTCGCCGGAATAATCATATCAATGACTTTAAATGA	23544
QY	1571	rgInValSerAlaTYrProAspSerLeuAlaValAspSerSerCysArgLeuThrTY	1591
Db	23546	AGTTGTCTCAAGCAACGATATCATGTTGGCTAGTCATGAATGATTTGACAAATGACGTA	23487
QY	1591	rThGluLeuAspArgInSerAspLLeuAlaGlyTYrPheuArgArgSerMetCr	1611
Db	23486	TGAACACATTCGCAACATATGTGTGATGTCATGGCAGCATGCTCTATCAATGCTGTGG	23427
QY	1611	oAlaGluThrLeuValAlaValPheAlaProAGSerCysGluThrTlLeuAlaPheH	1631
Db	23426	CAATGCTCAACGGGTTCCTTGTTTACAGAACGTAGTTTGAATGATTTGCGCGCATGTT	23367
QY	1631	egIValLeuYsAlaAsnLeuAlaTYrLeuProLeuAspValArgSerProSerAlaAr	1651
Db	23366	GGCAGACAGTTAAAGTAGTCGATCTTATATACCATGATGATTTGATTTCCGATTAAG	23307
QY	1651	gValGlnAspLLeuSerGlyLeuSerGlyProThrTlLeuAlleuLlGlyI----	Hi 1669
Db	23306	ACAGGTGCATATTTTGAGAGATGCTAAAGTAACTGCAGCATGCTTACCGCGCTGMAAT	23247
QY	1669	sAspThrAlaProProAspLlGluValThrAsnValGlu---PheValArgLLeArg--	1687
Db	23346	TGAACACATTCACAGTCATTCATATGGAATAATGCTAAAGGCTTTGTTGATCAAGA	23187
QY	1688	-----AspAlaLeuAsnAspSerAsnAlAspGlyPheGluValLlGluLHl	1703
Db	23186	AAATGAACATATGATGATTTTACATGCGCATCAACTGAAACACAGCATGTTAATGA	23127
QY	1703	sAspSerThLYeProSerAlaThrSerLeuAlaTYrValLeuTYrThSerGlySerTh	1723
Db	23126	TGAG-----ANGTATGCTATTTTACATCATCTGTGTGCGAC	23094
QY	1723	rgIArgProLYeGlyValMetLlGluHlAspValLlLeuArgThValThSerG	1743
Db	23093	CGGATGCTTAAGAGGGGTGTCACACACACAAATTTGTAATTTAGTGCATGCA--	23038
QY	1743	yCysAlaProAsnTYrProSerGluThrArgMetAla-----HisMe	1757
Db	23035	-----TGCTCACTGAATTTGCAATTAGCGGACAAATGAAGTATTTTGCAGCA	22988
QY	1757	lAlaThrLlLeaLAspLysAlaSerTYrGluLlTYrSerAlaLeuLeuPheGlyAr	1777
Db	22988	TGCAAAATATTTGTTTTTATGCATCAGATTATGAGATTATTTGTTTGTAAATGCTCA	22929
QY	1777	gThLeuValCysValAspTYrMetThrThrLeuAspAlaArgAlaLeuLYeAspValH	1797
Db	22928	TACCTTGTAATTCACATGATGAGAGAAACGTGTAATCCAGAACATTCACAACTCAT	22863
QY	1797	ePheArgLHlHlValAsnAlaLAspSerHlValThrSerSerGlnAspValProLe	1817
Db	22868	TAAATACATCGTGTGACGGTTCGTG-----	22841
QY	1817	uArgValProArgThrLeuSerArgThrLeuMetPhePhePheLeu-----ValAlaTh	1835
Db	22840	-----ATTCGGTACAGATGTGTAGTGTATGGAAGACTTTTATTTGAAAAGTTGATTAC	22785
QY	1835	rAspSerThAlaProAspAlaLeuAspAlaGln-----GlyLeuTY	1849
Db	22784	AGCGGGGCAACTAGTACGCGATCTTTGTTAAATATTTGAGAACATGTTGGACGTA	22725
QY	1849	rgInGlyValGlnCysTYrAsnGlyTYrGlyProThrGluAsnGlyValMetSerThrTl	1869
Db	22724	T-----TTCAATGCTATGACATCTGAGTCAACGATATCATCATCGTA	22688
QY	1869	eTYrProLlAspSerThrGluSerPheLlAsnGlyValProLlGlyArgAlaLeuAs	1889

Dd	22679	TTGGTGCATCATTTGGTGGTATTTGATACCTGAGACGATTCCTCAATGGCAAAACCTTATC	22622
Qy	1889	naasnserglYalatyValValAspProglunglnleuValglYleglYValmetgl	1909
Dd	22619	TAAATCCAAAGTGATATATATGCA---GATGGTGTGTTATGCGGATTTGGATGCGAG	22565
Qy	1909	YgluleuValValThrglYAspglYleuValatgglYTYT-----	1922
Dd	22562	CGAGTTTGATGATGCAAGTGATAGTTTGAAGATAGATATATTAACTGTCGCAATTAAT	22503
Qy	1923	-SerAspLysAlaLeuAspGluAsnArgPreValHsileThrValAsnAspGlnThrVa	1942
Dd	22502	GGCGATPAA---TGCCAAAATATACATT-----GCTAAAG	22467
Qy	1942	llyValatyArgThrglYAspArgValArgTYArgglleglYAspglYleuilegluPh	1962
Dd	22466	AAATTTGATTCATAGTGGTATTTAGACGCTTAT---ACATCGATGGTCAATTGAAAT	22410
Qy	1962	ePheglYArgmetAspThrGlnPheYsileArgglYAsnArgllegluSerAlaGluI	1982
Dd	22409	TTTGTGAAGATATGATTAACAAGTAAAGTTAACCGGTACCGGTATGAACCTTGATGAAT	22355
Qy	1982	egluAlaAlaLeuLeuArgAspSerSerValArgAspAlaAlaValLeuclnlns	2002
Dd	22349	TGAANAATGCAATATTACTATTCGTGGTAAATGATGTGTTGTAAACGTAACTGACTT	22290
Qy	2002	nglAspArgAlaAspGluIleuclnYleuclnYPheValAlaAspHsileAspHsileAsp	2022
Dd	22289	TGATACCGAT-----GATATATGTAAGTGTATTATGTCGAGACCAACAAGTGAACA	22236
Qy	2022	naAspLysglYgluSerAlaAsn-----GlnValgluclnYTrpGlnAs	2036
Dd	22235	GGATTTGAACCAATATTATTAATGATGACGCTCTAAGTATATGATTCCTAAGACTATAAC	22176
Qy	2036	philePhegluSerclYmetYrserAspHsileglYgluIleAsp-----	2050
Dd	22175	GCAATTCGATTTGATGCCATTAAACCAAGATGACAGGTGAATCTACGCTTGCCAAA	22118
Qy	2051	-ProserThrleglYserAspPheYsileglYTrpHsermetYAspglYserGlnI	2070
Dd	22115	TTCATTCACCTATACACAGCTCTAATAAGGTATAGCGAACCTCTAATGAATTGACA	22055
Qy	2070	eAspPhe---AspGluMetHsilegluTrpLeuclnYgluThrThrArgThrLeuHsileAspAs	2089
Dd	22055	GACATTTGTGTGATGATTTGGAGAGGATTAAGAAACAATAATGATGTCGGTTCGACGAT--	21998
Qy	2089	naYrSerleuclYAsnValleuclnuleglYThrglYser-----GlymetlleuAspH	2107
Dd	21997	-----GATTTCTTAAACTGGTGTAACTATTAAGACGCGATGTAACTTGT	21951
Qy	2107	eAsnLeuAspSerArgleuclnYserYrValglYleuclnY-----ProserArgse	2124
Dd	21950	CTCCGACTTTAAACGATTTGGCCATCATATTTCAATGACGACATTTATACCAATATTAAC	21891
Qy	2124	TAlaAlaAlaPheValAsnLysAlaThrGluSerIleProserLeuAlaGlYlysAlaY	2144
Dd	21890	CGTCCGACAGATTTTATATATATGTAACCAATTCACAATCATTA-----	21845
Qy	2144	sValGlnValglYThrAlaThrAspHsileglYGlnValAspAspLeuHsileProAspLeuVa	2164
Dd	21844	-----GTGCATTAACCGGATTAATCTT-----	21822
Qy	2164	lValleuAsnSerValileGlnYrPheProserSerGluTYr---LeuAlaGluIleAl	2183
Dd	21823	-----TCGAAATTCAAAAGATTTGATGTCTCGTTAACTTGGGATTTTAA	21774
Qy	2183	AspThrleuIleHsileuProAsnValGlnArgIlePhePheglYAspValArgsergl	2203
Dd	21773	GGATAGCTTAAGTCACTGACCTCTAGGAATAACATATGACGCGC-----	21728
Qy	2203	naIleThrAsnGluHsilePheLeuAlaAlaArgAlaIleHsileThrleuclnYlysAsnAlaTh	2223

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Db 21277 -GGCAGAGGT-----TTTTAGGTGCTTATCTGATTGAAGTACTA----- 21689
Qy 2223 rlyAspAspValArgGlnySMeCAlaGluLeuGluAspMeGlnGluLeuLeuVa 2243
Db 21688 -----CAAGATACGATCGATTCGATTTTGTTCATACGTCGATATATAGCAAAATAGC 21633
Qy 2243 lGluProAlaPhePheThrSerLeuLysAspArgPheProGlyLeuValGluHisValG1 2263
Db 21632 ATGGTAAAGTTGATGACGAATTTAAATGATTATTATTCA-----CAAGACGCGTTGA 21579
Qy 2263 uilleuProLysAspMeGlnAlaValaAsnGluLeuSerAlaTyrArgGlyrAlaAlaVa 2283
Db 21578 AAATAATTGATCAAAACATTAAGTCAAT----- 21551
Qy 2283 lValHisValArgGlySerLeuGly-----AspGluLeuValLeuProVa 2298
Db 21550 -----GTGGTGATTTCGAGTGTATGATGATGATGTTTTCACAGA 21510
Qy 2298 lGluLysAspAspTrpIle-----AspPheG1 2307
Db 21509 AAACATGATACGATTCATTCATGTCAGAGTCTCTACACATCATTGTGATGATGATGA 21450
Qy 2307 nAlaAsnGluLeuAsnGlnySerLeuGlyAspLeuLeuLysSerSerAsp----- 2324
Db 21449 ATTTGAAAAAGTAAATGTTCAAGGTACTGTTGATGTCATACGTTTGGCACAACAACATCA 21390
Qy 2325 -AlaAlaIleMeCAlaValaSerLysIle----- 2333
Db 21389 TGCAGGTAAATATATATGTCGTCTACGATTAAGTGGAACTTATTGATTAAGACAGAA 21330
Qy 2334 -----ProPheG1 2336
Db 21329 AGATGTGACATTTTCASAGCGGATGCTTAAAGGCAACTACTAAATCATCACAATATAC 21270
Qy 2336 uilleThrAlaPhe-----GluArgGlnValAlaSerLeuAsnSerAlaAsp-- 2353
Db 21269 ACGAGCAAAATTTATAGTAATTAAGATTAAGAACTGTAATTAATGAGCTTAAGATGG 21210
Qy 2354 -----GluTrpGlnLeuSerTh 2359
Db 21209 TCGGATTCGACGTCTGTTGTAATTTGACGAATCCTTACATGAGAAATGCGCATATGAAATA 21150
Qy 2359 rIleAspSerSerAlaGluGlyAspSerSerLeuSerValProAspIlePheArgIleAl 2379
Db 21149 TATATAAACTAAACCGT-----TTTCAATGATGATGATGATTGTTACAA----- 21104
Qy 2379 aGlyGluAlaGlyPheArgValGluValSerSerAlaArgGlnTrpSerGlnAsnGlyAl 2399
Db 21104 ----- 21104
Qy 2399 aLeuAspAlaValPheHisHisCysSerGlnGlyArgThrLeuValAsnPheProTh 2419
Db 21103 -CTGGATTGATC-----GGGGTTAGCATGGCTGAAATGCCCTGT 21066
Qy 2419 rAspHisHisLeuArgGlySerAspLeuLeuThrAsn-ArgProLeuGlnArgLeuGlnA 2439
Db 21065 AGATTTTCTTTCTTGT-CGATACGACCTGCAAGACAAATTTGCGCATAGCAGGTCAACA 21007
Qy 2439 sMArgAlaGluIleAlaIleGluValaArgGluArgLeuAspSerLeuLeuProSerTyrMet 2459
Db 21006 CACCACAAATCATTTTACCATGTG-----CTATCACT----- 20975
Qy 2459 lProSerAsnIleValaValLeuAspLysMetProLeuAsnAlaAsnGlyLys---ValA 2478
Db 20974 -----AATTAATGCCGGGGAATCTTTGTAGAAAGCGTTA 20938
Qy 2478 sPArgGlyGluLeuSerArgThrAlaLysValaValProLysGlnGlnThrAlaAlaProL 2498
Db 20937 ACGCGCAAA----- 20930
Qy 2498 eupProThrPheProLysSerGluValaGluValIleLeuCysGluGluAlaThrGluValP 2518
Db 20929 -----GAAATTGAACCTGTCACGCAATTAATTAATAAATTT 20890

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Qy 2518 heGlyMetLysValaAspIleThrAspHisPhePheAsnLeuGlyGlnHisSerLeuLeuA 2538
Db 20889 TACAGAAACAA-----GACATGTACAAAGATGGATTAATCAATGATTGACC 20842
Qy 2538 lathTrpLysLeuIleSerArgGlyIleAspGlnArgLeuLysValaGlnIleThr----- 2554
Db 20841 GTGACACAAACATGACATGATGATGATCAACATTAATTAATAAATTAATGATACATCA 20782
Qy 2555 -----ValLysVa 2557
Db 20781 GTGAAAAATGGCCAGATTAACATTAATGCTGTATCATTTGGCACAATATATACAAA 20722
Qy 2557 sPValPheAspHisProValaPheAlaAspLeuAlaSerValIleArgGlnGlyLeuGlyL 2577
Db 20721 CAATATTCAATTAAGTAAGTGGGAAAGTTATGACAGATTTGTAATGCAATTAACAGATA 20662
Qy 2577 euGlnGlnProValaSerAspGlyGlnGlyGlnAspArgSerAlaHisMeCAlaProArgT 2597
Db 20661 ACTTGAAAAGTATGAAGAATTAATATCAACAAAGTGGTGTGATTAATAAACCCTGA 20602
Qy 2597 hArgIleThrGluAlaIleLeuCysAspGluPheAlaLysValaLeuGly-----PheG 2614
Db 20601 CAGTCAACTATATATATCAATCAAGATTAATCACTGACACAGATTGGAGATATTATAGTC 20542
Qy 2614 lValaGlyIleThrAspAsnPhe----- 2621
Db 20541 AATATGAAATTTCAATGACACAGAGTTTATACCATGAAATGSCATTATACATTTCCG 20482
Qy 2622 -----PheAspLeuGlyLysIleSerLeuMetAlaThrLysLeuAlaValArgI 2638
Db 20481 CACGAGTAAAGGCAATATTTGTTCAACAAATGTGATGAGCAGCCCATTTATGAGCT 20422
Qy 2638 lGluHisArgLeuAspThrThrValaSerValLysAspValPheAsnHisProValaLeuP 2658
Db 20421 TATCATATATATATCTTATATGTCGTGTCGTGAT-----AAAGAACAGTT----- 20372
Qy 2658 heGlnLeuAlaIleAlaLeuAspAsnLeuValGlnSer----- 2670
Db 20371 -----GGTATGATATGAAAGATATCAACAGTTTATGACGTGCGGTACGTGATGA 20320
Qy 2671 -----LysThrAsnGlnIleValaGlyLysArgLeuMetAlaGlyLysSerProPheG 2688
Db 20319 CGTGTCTCTCTCAAAACGAA-----GCACATCAAAATATGATTTTAAATGATTTT 20269
Qy 2688 lLeuLeuPheThr-----GluAspProGluLysPheMetAlaSerGluIleLysProG 2706
Db 20268 ATCAAAATATGACACAAAAGAAAGTTTACAAATTTGATGTTGTAAGTTTAACAAAG 20209
Qy 2706 lLeuGluLeuGlnGlnIleIleGlnAsp---IleTyrProSerThrGlnMetGln---L 2724
Db 20208 GATTGCAATTTATGATATGATGACACAAATCACTTTATCAATCAGCGAAAGTGAATGCA 20149
Qy 2724 yAlaLysPheLeuPheAsp 2729
Db 20148 AACAAATTAATTTTGTAT 20132

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RESULT 11
 US-09-134-001C-627
 Sequence 627, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 PRIOR FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 627
 LENGTH: 7215
 TYPE: DNA
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-627

Alignment Scores:

Pred. No.:	3,546-139	Length:	7215
Score:	1425.50	Matches:	581
Percent Similarity:	41.42%	Conservative:	459
Best Local Similarity:	23.14%	Mismatches:	1040
Query Match:	8.84%	Indels:	431
DB:	3	Gaps:	94

US-09-482-788-2 (1-3129) x US-09-134-001C-627 (1-7215)

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QY 68 GlnSerAlaIleGlyHisAlaVal-----TyrAspValProThrAspIleAspIle 84
DB 106 CATCAAGTTCAGAAACAGCGGTGACATCTGGTAAAGTTAAGTCGCCGACATTGAGTTA 165
QY 85 SerArgPheAlaLeuAlaTrpLysGluIleValAsnGlnThrProAlaLeuArgAlaPhe 104
DB 166 CGTAGTAAATGATGATGATTTAGATGTCGTTCAAGTCAACCTGTTGCGTACA--- 222
QY 105 AlaPheThrSerAspSerGlyLysThrSerGlnValIleLeuLysAspSerPheValPhe 124
DB 223 CAGTTTGTCAGATGATTTTATCAACTCAAGATAAATTTAAGAGATTTTTCATT 282
QY 125 SerTrpMetCysTrpSerSerSerSerProAspGluValAlaArgAspGluAla 144
DB 283 -----ATTGAAATTTAAAGAAAGTTAAATGAAATGTCGAAACATAGATT 327
QY 145 AlaAlaAlaSerGlyProArgCysAsn-----Arg 154
DB 328 GAGCACTTCTTACACGTAATTTAAATCTCTACATTCAATCAATTAACCTGTTAAT 387
QY 155 PheValLeuLeuGluAspMetGlnThrLysCysGlnLeuValTrpThrPheSerHis 174
DB 388 TTTAACATTTTCAATTTCTGAT-----GAAGCCTACTACTTTAAGATTTTCAAGCT 441
QY 175 AlaLeuValAspValThrPheGlnAlaArgValLeuSerArgValPheAlaAlaTyrLys 194
DB 442 ACTATTTTTAAAGAAAGTCAATTAACCTCATTTTTCACAAATTAATATCGCTTAAC 501
QY 195 His----- 195
DB 502 CACTCTTTAAAGAAAGTAAATAGTATCTCGATTTTAAATGATGATTAAGAAATGAAT 561
QY 196 ---GluLysAspThrHisArgProGluThrProGluSerSerAsp-----AlaThr 211
DB 562 CAAACATGATCAAAATCAAGTGTGTCTCCATCAAGCATTCACACGATTTGAATGCA 621
QY 212 AspThrAspSerGlnSerValSerValSerMetSerCysGluAspAsnAlaValSer 231
DB 622 GACGGGATGATTAATACCTTACATCTGTTAAGAAATATCATGTGAAAAAAGAAATGTGT 681
QY 232 AlaThrHisPheTrpGlnThrHisLeuAsnAspLeuAsnAlaSerValPhe----- 248
DB 682 TCTTTGCAT-----GCAGAACTAACCATCTTTAGACATGTGATGTGATTTAAGT 732
QY 249 ProHisLeuSerAspHisLeuMetValProAsnProThrThrThrAlaGluHisArgIle 268
DB 733 ATTACTTTGCGCATATTTTATAGTCAGCTTTTCATGTGACGTTA-----GGCATC 786
QY 269 ThrPheProLeuSerGlnLysAlaLeuSerAsnSerAlaIleCysArgThrAlaLeuSer 288
DB 787 CATTTTTCATGATATATAAAATATCTGAGAAATATGATGTTTAAACACAGACATTTGCC 846
QY 289 IleLeuLeuSerArgTrpThrHisSerAspGluAlaLeuPheGluAlaValThrGluGln 308
DB 847 CCACTTAATTTTAAGATTAATGTCAAAGTGAC--GTGCTAAAGATATGTGATGAGTGT 903
QY 309 SerLeuProPheAspLysHisTyrLeuAlaAspGlyThrTyrGlnThrValAlaPro-- 327

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DB 904 TCCGCTCTACTTGAAGAGCTTCAAAATGTGTGTCGCTCTTT---GTTGTTCACCTTAA 960
QY 328 ---LeuArgValHisCysGlnSerAsnLeuArgAlaSerAspValMetAspAlaIleSer 346
DB 961 GCAGTACAAATTAATAGTATGAAACAGATGATTCATATTGAAAAAGTACAGAAACAATTT-- 1017
QY 347 SerTyrAspArgLeuGluHisLeuAlaProPheGlyLeuArgAspIleArgAsnThr 366
DB 1018 -----GAGCTTAATCATATATGT-----CATCATATATATCGCTTA 1053
QY 367 GlyAspAsnGlySerAlaAlaCysAspPheGlnThrValLeuLeuValThrAspGlySer 386
DB 1054 TACAAATGAGCATCATCATTCGCGGATTTAGAGTTTATTCCTCATGTGCGAGATGTTT 1113
QY 387 HisVal-----AspAsnGly----- 391
DB 1114 GATATAGTATTATATATGACAAAGTTTATGATGATTTAATCTGTATACATGCTTAATTA 1173
QY 392 IleAsnGlyPheLeuGlnGlnIleThrGluSerSerHisPheMetProCysAsnAsnArg 411
DB 1174 ATTATATGCGATTTATATGCAATTTACAA-----ATATCA 1209
QY 412 AlaLeuLeuLeuHisCysGlnMetGluSerSerGlyAlaLeuLeuValAlaTyrTrpAsp 431
DB 1210 TCATTTATTAATTAAGATATTAAGTAAAGTCAAGTATCGCTCAGATTTTATGCTTAATTAATGAC 1269
QY 432 HisAsnValIleAspSerLeuGlnThrThrArgLeuLeuGlnGlnPheGlyHisLeuIle 451
DB 1270 ATCAAT-----CTTCAAAACAAATGACATT----- 1293
QY 452 LysCysLeuGlnSerProLeuAspLeuSerSerMetAlaGluValAsnLeuMetThrGlu 471
DB 1294 -----AATTATATGATGCTACTTATAAACCGCTG 1323
QY 472 TyrAspArgAlaGluIleGluSerTrpAsnSerGlnProLeuGluValGlnAspThrLeu 491
DB 1324 GTTGAAAGATTCGA----- 1338
QY 492 IleHisIleGluMetLeuLysAlaValSerHisSerProThrLysThrAlaIleGlnAla 511
DB 1339 -----CGTCAAGTGCACCAACATCCCATGATGATTTGGGTGCATATAT 1380
QY 512 TrpAspGlyAspTrpThrTyrSerGluLeuAspAsnValSerSerArgLeuAlaValHis 531
DB 1381 GAAACAAGATCGATGACATATCATCATTTAAATCAATGTCGCAATCTTTTACGATATGCA 1440
QY 532 IleLysSerLeuGlyLeuArgAlaGlnAlaIleIleProValTyrPheGluLysSer 551
DB 1441 TTGCGTTTAAATCATGACATGAAACCTAATGATATGCTGSCATTTATAGCAGAACGAGC 1500
QY 552 LysTrpValIleAlaSerMetLeuAlaValLeuLysSerGlyAsnAlaPheThrLeuIle 571
DB 1501 TTGAAGATGATTTTGAATGATTTGAGGATCTTGAAGACGTGTCAGAGCTTACATCAAT 1560
QY 572 AspProAsnAspProProAlaArgThrAlaGlnValValThrGlnThrArgAlaThrVal 591
DB 1561 GATCCGATATATCTGAAAGAAAGATGATTAATTAATTTGAGACCGCAAAACCTTAAAGCG 1620
QY 592 AlaLeuSerLysLysHisArgGluThrValGlnLysLeuValGlyArgCysValVal 611
DB 1621 GTTGTAAACA-----TATGCTACATCATTTCAATCAAGCTTTAATCTCAAA----- 1662
QY 612 ValAspAspGluLeuLeuGlnSerValSerAlaSerAspAspPheSerSer----- 628
DB 1663 ATGATATATGATATGATTTAGTTGAT--TCAGAGAAACATATATTTGATATACCCGAGAGGC 1719
QY 629 LeuThrLysSerGlnAspLeuAlaTyrValIlePheThrSerGlySerThrGlyAspPro 648
DB 1720 ATTAAATTTTCAAGAGATATCGCTTATGTCATATATATATATATATATATATATATATAT 1779
QY 649 LysGlyIleMetIleGluHisArgAlaPheSerSerCysAlaLeuAspPheGlyAlaSer 668

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Db 1780 AAMGGCACTGGTGGCCATAGAGAAATGATCGC---TTAGTACAACAATCCAAATTAT 1836
Qy LeuGlyIleAsnSerAspThrArgAlaLeuGlnPheGlyThrHisAlaPheGlyAlaCys 688
Db 1837 GTGGAATTGACCAAAATATACACCGCTTATTATCAGAAACAGTAGCTTTGATGCGCA 1896
Qy LeuLeuGlnIleMetThrThrIleLeuIleAsnGlyCysValCysIleProSerAsp 708
Db 1897 ACCTTGAAATATATAGTCATATTGATGAGCGGTAGCATTAATCATCATCAAGAT 1956
Qy AspArgMetCAsnSer-----IleProSerPheIleAsnArgIleAsnValLeuIlePheMet 726
Db 1957 ACCTTGTAATTCCTCAATTGATGATCAAGCTATTACTGAAATAAAGTCAACACCATG 2016
Qy MetAlaThrProSerTyMetGlyThrPheSerProGluAspValProGlyLeuAlaThr 746
Db 2017 TGGTTAACGTCATTTTATTATCAAAATGTCAGCAACGTAACGACGACCTAGATCT 2076
Qy Leu-----ValLeuValGlyGlnIleMetSerSerSerValAsnAlaIleTProAlaPro 764
Db 2077 TTAACTTATTTGCTTATTTGGTGGGAAGT-----TTAAATGCTAAATGGGTTTAC 2127
Qy LysLeu-----GlnLeuLeuAsnGlyTyrgIleGlnSerGlnSer 777
Db 2128 TTATTAATTCGGCGTAGTGTCACTCTCAAAATATCATAGTTATGACCGACAGAGAAT 2187
Qy SerSerIleCysPheAlaSerAsnMetSerThrGluProAsnAsnMetGlyArgAlaVal 797
Db 2188 ACAACA-----TTTACTACACTTTTGGCAT---CCACAAGAGATCGCTTACAGATA 2238
Qy 798 -----GlyAlaHisSerTrpValIleAspProAsnAspIleAsn 810
Db 2239 CCTATTGGTTTACCTATTAGTGAACAGAGTTTATGTCATGCAAGGT-----GAT 2289
Qy ArgLeuValProIleGlyAlaValGlyLeuValIleGlnSerProGlyIleAlaArg 830
Db 2290 CGATTATTTGGCGTAGTGTTCAGAGTGAATTTGCGATTTGGTGGCGAGTTTGAAGAAA 2349
Qy AspTrpIleValProProProGlu-----LysSerProPhePheThr 845
Db 2350 GGTATTATTAATCAACCTTAACCTTACGTCGAACGTTTATTCAGTACCTTTTAATAT 2409
Qy AspIleProSerTrpTyProAlaAsnThrPheProAspGlyAlaLysLeuTyArgThr 865
Db 2410 GAATAG-----CTTATTCGAAGC 2427
Qy 866 GlyAspLeuAlaArgTyArgAlaSerAspGlySerIleValCysLeuGlyAlaGlnSer 885
Db 2428 GGTGATTTTACTGCTTCAAGAGAGTGGCTATATGATTATTAATGCTGATTCGATTAAG 2487
Qy GlnValLysIleArgGlyGlnArgValGlnLeuGlyAlaIleGluThrHisLeuArgGln 905
Db 2488 CAAATTAAATACGTGGTTTAAATGAAATTAATCAGAAATTTGAAAAGCATTA---GAA 2544
Qy GlnMetProAspAspLeuThrIleValAlaGlnAlaThrLysArgSerGlnSerAlaAsn 925
Db 2545 GCTATACGTGATTTAAATAAGCTGTAGTCATGCTGAGAGCAAGCAACA----- 2595
Qy SerThrSerIleuIleAlaPheLeuIleGlySerSerTyPheGlyAsnArgProSerAsp 945
Db 2596 GATTAACAATATAGTGGCATTTATGAAGCATCGCAATTA----- 2634
Qy 946 AlaHisIleLeuAspHisAspAlaThrLysAlaIleAsnIleLysLeuGlnGlnValLeu 965
Db 2635 -----AATCAACAGTCAATTAAGAATATTTTAACTGAACATTA 2676
Qy ProArgHisSerIleProSerPheTyIleCysMetLeuGlnLeuProArgThrAlaThr 985
Db 2677 CCGAATATATGATACCTGTACATTTTATGAAGTATAGTATACCTATCACAGATGAAT 2736
Qy GlnLysIleAspArgAlaGlyLeuArgIleMetCysLysAspIleLeuAspLysGlnThr 1005
Db 2737 GGGAAATTTAGATGTGCGTGAATTA-----CCTGAATTAATCTTAAGAAATTAAT 2784

Qy GlnGlyAlaIleValGlnGlnAlaProAlaProIleProValPheAlaAspThrAlaAla 1025
Db 2785 AGAATTAATGATCAACACAGT-----AACGATATTGAACCG 2820
Qy 1026 LysLeuHisSerIleTrpValGlnSerLeuGlyIleAspProAlaThrValAsnValGly 1045
Db 2821 ACCTTTGGCGTATTTTTCGAAGAGATTTTACATGGTGAAT-----CAAGTAGGTGTTAA 2874
Qy 1046 AlaThrPhePheGlnLeuGlyGlyAsnSerIleThrAlaIleLysMetValAsn---Met 1064
Db 2875 GATTAATTTCTTTTAACTTAGGTGACACCTCTTTCAGACACATTAAGTTGTAACCGTATT 2934
Qy 1065 AlaArgSerValGlyMetAspLeuLysValSerAsnIleTyGlnHisProThrLeuAla 1084
Db 2935 GAAGAAAGGTTAAAAAACGTTAAAGTAGAGATTATTAAGAAATCGCTACTGTAGAG 2994
Qy 1085 GlyIleSerAlaValVal-----LysGlyAspProLeuSerTyThrLeuIlePro 1101
Db 2995 CAACCTGGACAAACAATGGAAGATCGCAAAATGAT-----GTCATGAAGTAGATTTCC 3048
Qy 1102 LysSerThrHisGlnGlyProValGlnGlnSerTySerGlnGlyArgLeuTrpPheLeu 1121
Db 3049 AAMGCAATGAATCGATATCATATGATTTTAAGTCGCTCAAAAAGTATGATCTTTTA 3108
Qy 3109 TGAAGGTCAATCGTAAAGACACAGTGTATTAACATTCATCTTATGAGATATATCTTCT 3168
Qy 1122 AspGlnLeuAspValGlySerLeuTrpTyLeuIleProTyArgAlaArgMetArgGly 1141
Db 3169 GAACTTAATGTTTGAATTTGCAATTTGCAACGTCATTTCAAGTTGATTAACGTCATGAATA 3228
Qy 1162 LeuArgThrThrPheGlnLeuAspGlyValGlyValGlnIleValHisGlyLysLeu 1181
Db 3229 TTACGACACAAATATGTAATGATGACATGAAGTTAAACAGCTATGCGACACATGTT 3288
Qy 1182 SerGlnLeuMetLysValIleAspLeuCysGlySerAspLeuAspProPheGlnValLeu 1201
Db 3289 TCGCGATTTTGAAGGTAAGC-----ACATCTTAAAGCAAGCAAGATATT 3339
Qy 1202 AsnGlnGlnIleThrThrProPheAsnLeuSerSerGlnAlaGlyTrpArgAlaThrLeu 1221
Db 3340 ATTCAAATCATTTATGAAACCGTTTGAATTTAGAACCAACAAAGTCAGATGCAATTAATAT 3399
Qy 1222 LeuArgLeuGlyGlnAspAspHisIleLeuThrIleValMetHisIleIleSerAsp 1241
Db 3400 ATTCATGAGACCAACAACAGTTAT---TTATTTATGATATCTCATATGATTAATGAT 3456
Qy 1242 GlyTrpSerIleAspValLeuArgArgAspLeuAsnGlnLeuTyrgSerAlaAlaLeuLys 1261
Db 3457 GGTATGAGTAACACGATTTTATCATATGATTTGAACGCTTATACCAAGAT----- 3507
Qy 1262 AspSerLysAspProLeuSerAlaLeuThrProLeuProIleGlnTyrgSerAspPheAla 1281
Db 3508 -----AATCATTAACCTGAACCTTAAGCTTATGATTAAGTTTATAGT 3549
Qy 1282 LysTrpGlnLysAspGlnPheIleGlnGlnLysGlnLeuAsnTyrgTrpLysGln 1301
Db 3550 GAGTGGATGGTGCACAA-----GACTTATCTTAACCAACAGTCACTTTGGTTACGCAA 3603
Qy 1302 LeuLysAspSerSerPro---AlaLysIleProThrAspPheAlaArgProAlaLeu 1320
Db 3604 TTGGAATATCAGGTTCCAAATTAATTAATATGCGTACAGATTAATCTGACCAATATTAA 3663
Qy 1321 SerGlyAspAlaGlyCysValHisValThrIleAspGlyGlnLeuTyrgIleSerLeuArg 1340
Db 3664 ACAACCAACGCTATATGTTAGCGTTTCATTAACATCGTCAAAATCAACAGCATTAAGAA 3723
Qy 1341 AlaPheCysAsnGlnLysAsnThrThrSerPheValValLeuLeuAlaIlePheArgAla 1360
Db 3724 TCTTATGTAGAACAAACATCAAGTACAGACATTAATGTTCTTTCGTAGTCAATCATGCTA 3783

QY 1361 AlaHisTyrArgLeuThrAlaValGluAspAlaValIleGlyThrProIleAlaAsnArg 1380
 Db 3784 TATTTCGCAAAATATACAGCTCAGACGATATGCTATTGCTGTAATCAGTGGCGT 3843
 QY 1381 AsnArgProGluLeuGluAspIleIleGlyCysPheValAsnThrGlnCysMetArgIle 1400
 Db 3844 ACTCATCGCGATCTGTAATAATATGATGATGTTGCTAATACACTTGATATCGGT 3903
 QY 1401 AsnIleAspHisIleAspThrPheGlyThrLeuIleAsnGlnValValAlaThrThr 1420
 Db 3904 CGACCATCATGATGAAAAGACATGATCAATTAATGCTGATGAAAGAGATGCTCTA 3963
 QY 1421 AlaAlaPheGluAsnGluAspIleProPheGluArgValValSerAlaLeuGlnProGly 1440
 Db 3964 GGGGCAATGAGATCAAGATATCCCTTTGAAAGCTACTCATATGATCTT---GTTGAT 4020
 QY 1441 SerArgAspLeuSerSerThrProLeuAlaGlnLeuIlePheAlaVal---HisSerGln 1459
 Db 4021 GAAAGAGATGCTTCCATATATCCGTTATTTGATGTGATGCTGCTACTTCAAAATATGAA 4080
 QY 1460 LysAspLeuGlnLysArgPheLysPheGlnGlyLeuGlnSerValProValProSerLysAla 1479
 Db 4081 ACAATATCATGCGAATTTTGACATAGTCAATTAACATATTCGA---CCTCAGTCAACA 4137
 QY 1480 TyrThrArgPheAspMetGluPheHisLeuPheGlnGluThrAspSerLeuLysGlySer 1499
 Db 4138 ACAGCTAAATTTGATTTGATTTATTTATGAAAGATGCAATGATGCTATGCTCAT 4197
 QY 1500 ValAsnPheAlaAspGluLeuPheLysMetGluThrValGluAsnValValArgValPhe 1519
 Db 4198 ATTGAATATATATACATTTATATATTAACAAGACCATTCATCATATGCTGAAACATT 4257
 QY 1520 PheGlnIleLeuArgAsnGlyLeuGlnSerSerArgThrProValSerIleLeuProLeu 1539
 Db 4258 CAATGATATATTAACATGTAATATCTACCGAAACCTAAATTCAGATATTGATGAA 4317
 QY 1540 ThrAspGlyIleValThrLeuGluLysLeuAspValLeuAsnValLysHisVal----- 1557
 Db 4318 AATGATGACTTA-----TTAATTGGTTGAC-----AAGCATGAGATGAT 4359
 QY 1558 -----AspTyrProArgGlnSerSerLeuAlaAspValPheGlnThrGlnValSer 1574
 Db 4360 TGTCTTTTGAAGCTTCCAAATAATTAAGTCATATCAGACCATTTTACATGATGATGAAA 4419
 QY 1575 AlaTyrProAspSerLeuAlaValAlaAspSerSerCysArgLeuThrTyrThrGlnLeu 1594
 Db 4420 GCGAAACAGATGATGATGATGATTAATAATGAATGACATGATGATGATGATGATGAT 4479
 QY 1595 AspArgGlnSerAspIleLeuAlaGlyTyrPheArgArgArgSerMetProAlaGluThr 1614
 Db 4480 GATGATTTATTTCTAATAGTATGCTCAAAACATTCATACAAATGCGATTTCAAAAGGGAA 4539
 QY 1615 LeuValAlaValPheAlaProArgSerCysGluThrIleValAlaPhePheGlyValLeu 1634
 Db 4540 CGGTGACCTCTTTAAGTGAAGAGATTTGAAATGTTGCTGATGATGATGATGATGATGAT 4599
 QY 1635 LysValAsnLeuAlaTyrLeuProLeuAspValArgSerProSerAlaArgValGlnAsp 1654
 Db 4600 AAGGTGAGAGTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4659
 QY 1655 IleLeuSerGlyLeuSerGlyProThrIleValLeuIleGlyHisAspThrAlaProPro 1674
 Db 4660 ATTATTTGAGACCGCTGAGTGCAGCGAGCTCTCATATGAGAAAGCAATATTC----- 4713
 QY 1675 AspIleGluValThrAsnValGluPheValArgIleArgAspAlaLeuAsnAspSerAsn 1694
 Db 4714 -----TCACATATACAGTATATTAATTAATTAATTAATTAATTAATTAATTAAT 4761
 QY 1695 AlaAspGlyPheGluVal-----IleGluHisAspSerThrLysProSer 1709
 Db 4762 AATTAAGAGTTAAATATGATATGACGAGAAATTTGAGAGATGAT----- 4806
 QY 1710 AlaThrSerLeuAlaTyrValLeuTyrThrSerGlySerThrGlyArgProLysGlyVal 1729

Db 4807 -----ATGATCATATTTATATACATCTGGAACAACAGAAAGCTTAAGCAGTA 4854
 QY 1730 MetIleGluHisArgValIleIleArgThrValThrSerGlyLysIle----- 1745
 Db 4855 TCAGTAAACACAGATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1765
 QY 1746 ProAsnTyrProSerGluThrArgMetAlaHisMetAlaThrIleAlaPheAspGlyAla 1765
 Db 4906 CTCAATTTATCCAGATGATGAGTCTATCTGCATAGCTTAATTAATGATGATGATGATGAT 4965
 QY 1766 SerTyrGluIleTyrSerAlaLeuLeuPheGlyArgThrLeuValCysValAspTyrMet 1785
 Db 4966 GCAATGATTTCTAGTGTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5025
 QY 1786 ThrThrLeuAspAlaArgAlaLeuLysAspValPhePheArgGluHisIleValAlaAla 1805
 Db 5026 GACCGGACCAATACAGATTTATTAAGAAAGTAAATTTACAAAGAAATATCACCATCGCA 5085
 QY 1806 SerHisValThrSerSerSerGlnAspValProLeuArgValProArgArgLeuSerArg 1825
 Db 5086 TCT-----ATTCACATCAGTATATAT 5109
 QY 1826 ThrLeuMetPhePheLeu-----ValValThrAspSerThrAlaProAspAlaLeu 1843
 Db 5110 GTGATGATCATTTCTATATCTTAAGTATTAAGATTAACAGAGTGCAGCAATCTCCAGCA 5169
 QY 1844 AspAlaGlnGlyLeuTyrGlnGlyValGlnCysTyr---AsnGlyTyrGlyProThrGln 1862
 Db 5170 TTGTTCACATATTTCTTAAGCATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5229
 QY 1863 AsnGlyValMetSerThrIleTyrProIleAspSerThrGlnSerPheIleAsnGlyVal 1882
 Db 5230 AATACAGTTATCATCTTCTTGATATACGAAAGTGAACCCATCAGTATGATGAT 5289
 QY 1883 ProIleGlyArgAlaLeuAsnAsnSerGlyAlaTyrValValAlaAspProGlnGlnLeu 1902
 Db 5290 CCGATGCGGAACCGTTAGCTAATGTTGATTTATTTATTTATTTATTTATTTATTTATTTAT 5346
 QY 1903 ValGlyIleGlyValMetGlyLeuLeuValValThrGlyAspGlyLeuAlaArgGlyTyr 1922
 Db 5347 TGTGGCTGTGATTTCCAGGTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 5406
 QY 1923 SerAspLys---AlaLeuAspGluAsnArgPheValHisIleThrValAlaAspGlnThr 1941
 Db 5407 TTAAACGACCCGAACTTTCTGCTGAAATAATTAATAATATCTTTGGCCAGCA--- 5463
 QY 1942 ValLysAlaTyrArgThrArgThrArgValArgTyrArgIleGlyAspGlyLeuIleGlu 1961
 Db 5464 ---CACTTATGAGAGTGTGATTTAGCAGATG---ATGCCAGATGGCAATTTGAA 5517
 QY 1962 PhePheGlyArgMetAspThrGlnPheLysIleArgGlyAsnArgIleGlnSerAlaGlu 1981
 Db 5518 TTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5577
 QY 1982 IleGluAlaAlaLeuLeuArgAspSerSerValArgAspAlaAlaValValLeuGlnGln 2001
 Db 5578 ATTGAATAATATCATTAATTCATGATGATGATGATGATGATGATGATGATGATGATGAT 5637
 QY 2002 AsnGluAspGlnAlaProGluIleLeuGlyPheValValAlaAspHisAspHisSerGln 2021
 Db 5638 CAGGTGAGCGT-----GAGAGTCTGCATGCTTATATGTTGGAAGTCAAGAAATGAA 5691
 QY 2022 AsnAspLysGlyGlnSerAlaAsnGlnValGlnGlyTyrGlnAspHisPheGlnSerGly 2041
 Db 5692 AATCATATTTCAACAATTTAAATCAATAT-----TTGCCCTAAATCAATGATTCCTAAC 5745
 QY 2042 MetTyrSerAspIleGlyGluIleAspProSerThrIleGlySerAspPheLysGlyTyr 2061
 Db 5746 ACATTAACAGCTATTAAGCAATTT---CAATTAAAC---GGAATAGAT----- 5787
 QY 2062 ThrSerMetTyrAspGlySerGlnIleAspPheAspGluMetHisGluTyrLeuGlyGlu 2081

Db 5788 -----AAGGTGATGATGACAGATTACCTGATCTTATGATGACAAATAATTTGTT 5841
 Qy 2082 ThrThrArgThrLeuHisAspAsnArgSerLeuGlnValLeuGluIleGlyThrGly 2101
 Db 5842 GCACCAACGTTAT---AATATGCAACGAGAAATAGCAAAATCGT----- 5883
 Qy 2102 SerGlyMetIle-----LeuPheAsnLeuAspSerArgLeuGlnSerTyrValGly 2118
 Db 5884 AGCGGAGTGTGGACGATGCTGATGATGATGATGAT----- 5922
 Qy 2119 LeuGluProSerArgSerAlaAlaPheValAsnLysValAlaThrGluSerIleProSer 2138
 Db 5923 -----GACTTCTTGAATGGGTGCTATCATCATGATGCT 5958
 Qy 2139 LeuAlaGlyLysAlaLysValGlnValGlyThrAlaThrAspIleGlyGlnValAspAsp 2158
 Db 5959 ATGGTGTGATATCAAAACTA-----AATCAAAATGCG 5991
 Qy 2159 LeuHisProAspLeuValValLeuAsnSerValIleGlnTyrPheProSerSerGluTyr 2178
 Db 5992 ATACAC-----ATTACAAATGCAAGATGATATCA---TTTAAACGTTCGTTAT 6039
 Qy 2179 LeuAlaGlu-----IleAlaAspThrLeuIle-----HisLeu 2189
 Db 6040 ATAGCTATATCACACAGAAAAACCCCAACACACTACAGAGAGTATTACAGATCATCTA 6099
 Qy 2190 ProAsnValGlnArgIlePhePheGlyAspValArgSerGlnAlaThrAsnGluHisPhe 2209
 Db 6100 CCACATATTAACATCTTGTT-----GAAAGACGATACCAAAATCAACACACCTA 6153
 Qy 2210 LeuAlaAlaArgAlaIleHisThrLeuGlyLysAsnAlaThr----- 2223
 Db 6154 ACCCAATCATCTCTAGCTCATGTATCTTAACCTGTCACACAGGCTTCAGGCGCATAT 6213
 Qy 2224 -----LysAspAsp 2226
 Db 6214 TTAAATGATAAATGCAAGATGATGATGATCAAAATTCATGATTCGACAGGTCATGAT 6273
 Qy 2227 ValArgGlnLysMetAlaGluLeuGluAspMetGluGluLeuValGluProAla 2246
 Db 6274 ATCAATCAACCTAAACTACTGGAATAATAT-----TTAAATGTTAT 6318
 Qy 2247 PhePheThrSerLeuLysAspArgPheProGlyLeuValGluHisValGluIleLeuPro 2266
 Db 6319 TTGATATACGCTCATGTGATTA---TTAATGAGCAGCATGATATATTTTA 6369
 Qy 2267 LysAsnMetGluValAlaGluLeu-----SerAlaTyrArgTyrAlaAlaVal 2283
 Db 6370 GCGGATTTATCAGAACTTGACCATTTATATTCGATTCAGCC-----ATTGATCAAT 6423
 Qy 2284 ValHisValArgGlySerLeuGlyAspGluLeuValLeuProValGluLysAspAspTyr 2303
 Db 6424 ATTCATGCT---GGAGCTCGTACAGATCAGCTT-----GGCGATGATGAA 6465
 Qy 2304 IleAspPheGlnAlaAsnGlnLeuAsnGlnLysSerLeuGlyAspLeuLeuLysSerSer 2323
 Db 6466 ACATTTTTCATGTCATGATGATGAGAGATACACAGCATTAATGATTAGCTAAGAAATAA 6525
 Qy 2324 AspAlaAlaIleMetAlaValSerLysIleProPheGluIleThrAlaPheGluArgGln 2343
 Db 6526 AAAGCGAAATTAATCTATATACAGATA----- 6555
 Qy 2344 ValValAlaSerLeuAsnSerAsnIleAspGluTyrGlnLeuSerThrIleArgSerSer 2363
 Db 6556 -----AGTGGGTACGGATTTGAGTA 6579
 Qy 2364 AlaGluGlyLysPheSerLeuSerValProAspIlePheArgIleAlaGlyGluAlaGly 2383
 Db 6580 CATCAAGACCATTTTATCTTTCGAAAGATTAATAA-----GGCCAGTTA--- 6630
 Qy 2384 PheArgValGluValSerSerAlaArgGlnTyrSerGlnAsnGlyAlaLeuAspAlaVal 2403
 Db 6631 TTATCATCACCATTAATAAAGTAAAGTTTATATGCGAATTAAGTTAAAGTTCGAGCGGTT 6690

Qy 2404 PheHisIleCysCysSerGlnGlyArgThrLeuValAsnPhe-----ProThrAspHis 2421
 Db 6691 AATGAAGTTTACACACTCATGATTATAGATTAGAAATCTGCAAGATGCTTCTACTGCA 6750
 Qy 2422 HisLeuArgGlySerAspLeuLeuThrAsnArg 2432
 Db 6751 CCAATTAATATGAAATAATTTAACACTTAATCGT 6783
 RESULT 12
 US-08-471-119A-4
 ? Sequence 4, Application US/08471119A
 ? Patent No. 5827706
 ? GENERAL INFORMATION:
 ? APPLICANT: Leitner, Ernst
 ? APPLICANT: Schneider, Elisabeth
 ? APPLICANT: Schoengendorfer, Kurt
 ? APPLICANT: Weber, Gerhard
 ? TITLE OF INVENTION: Cyclosporin Synthetase
 ? NUMBER OF SEQUENCES: 8
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: No. 5827706artis Corporation
 ? STREET: 59 Route 10
 ? CITY: East Hanover
 ? STATE: New Jersey
 ? COUNTRY: USA
 ? ZIP: 07936
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? OPERATING SYSTEM: IBM PC compatible
 ? SOFTWARE: PC-DOS/MS-DOS
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/471,119A
 ? FILING DATE: 06-JUN-1995
 ? CLASSIFICATION: 435
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Kaszenoff, Melvyn
 ? REGISTRATION NUMBER: 26,389
 ? REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 201 503 8474
 ? TELEFAX: 201 503 8807
 ? INFORMATION FOR SEQ ID NO: 4:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 1713 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: unknown
 ? MOLECULE TYPE: DNA (genomic)
 ? HYPOTHEICAL: NO
 ? ANTI-SENSE: NO
 ? ORIGINAL SOURCE:
 ? ORGANISM: Necosmospora vasinfecta
 ? US-08-471-119A-4
 Alignment Scores:
 Pred. No.: 7,21e-136 Length: 1713
 Score: 1383.00 Matches: 299
 Percent Similarity: 68.64% Conservative: 84
 Best Local Similarity: 53.58% Mismatches: 142
 Query Match: 8.58% Indels: 33
 DB: 1 Gaps: 8
 US-09-482-788-2 (1-3129) x US-08-471-119A-4 (1-1713)
 Qy 2046 IleGlyGluIleAspProSerThrIleGlySerAspPheLysGlyTyrThrSerMetTyr 2065
 Db 3 ATGGGGGTATTTGATGCGCATGCGCTCGACAGAGACTTCTTATCTCGACATCATGATAC 62
 Qy 2066 AspGlySerGlnIleAspPheAspGluMetHisGluTyrLeuGluGluTyrThrArgThr 2085
 Db 63 GACGGCTCATGATTTCCCGGAGAGATGACAGAAATGCTCAGCGACATATGCACTCA 122

QY 2086 LeuH1ASPAspArgSerLeuGlyAenValLeuGlu11leGlyThrGlySerGlyMetCile 2105
 DB 123 CTCTCGACACACCGACCCCGAAGAGTCTCGAGATCGAACTGCTGACCGGTATGGTG 182
 QY 2106 LeuPheAsnLeuAsp-----SerArgLeuGlySerTyArg1GlyLeuGluProSerArg 2123
 DB 183 CTTTCAATCTGGCGCAAGGTGAGGAGCTACAGAGCTATCGCGTCTTGAGCCCTGGCG 242
 QY 2124 SerAlaAlaAlaPheValAsnValAsnValAsnValAsnValAsnValAsnValAsnVal 2143
 DB 243 TCCGTCACCTGCGCGGTAAACAAGCAATCTTCCCAAGCCTGCGAGGAGAGCGCC 302
 QY 2144 LysValGlnValGlyThrAlaThrAsp11leGlyGlnValAspAspLeu1SProAspLeu 2163
 DB 303 CAGATCAGCTGAGAACCGCCGAGAGTGAAGTCACTCAATGAGTGAAGTGAAGTGAAGTGA 362
 QY 2164 ValValLeuAsnSerVal11leGlnTyPheProSerSerGlyTyPheValAsnValAsnVal 2183
 DB 363 GTTGATATCACTCGCTCGCCCAATCTTCCCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 422
 QY 2184 AspThrLeu11leHisLeuProAsnValGlnArg11lePhePheGlyAspValArgSerGln 2203
 DB 423 GCCAATCTGATTCGACCTGCGCGCGTCAAGCGTATTTCTTCCGCGCATGAGAACCTAT 482
 QY 2204 AlaThrAsnGlnHisPheLeuAlaAlaArgAla11leHisPheLeuGlyTyAsnValAsnVal 2223
 DB 483 GCACCAATTAAGGACTCTTGTGGGACGAGCACTCAATCCCTAGGCTCAATGACATCT 542
 QY 2224 LysAspAspValArgGlnTySmetAlaGluLeuGluAspMetGluGluGluLeuVal 2243
 DB 543 AAGGCAATGTTGACACACAGTGGCCCAAGCTTGAAGTACAGAGAGAGTTCCTTGT 602
 QY 2244 GluProAlaPhePheThrSerLeuLysAspArgPheProGlyLeuValGluHisValGlu 2263
 DB 603 GACCCGCTCTTCTTCAACGAGCTGAGCAGCACTTCCCTGACCAATCAAGCAGCTGAG 662
 QY 2264 11leLeuProLysAsnMetGluAlaValAsnGluLeuSerAlaTyArgTyArgAlaVal 2283
 DB 663 ATTCTGCCAAGAGGATGCGCGGACCAACGAACTCACTTACCGATATGCTGCTGT 722
 QY 2284 ValHisValArgGly-----SerLeuGlyAspGly-----LeuVal 2295
 DB 723 ATTCACTGGGAGGACCAAGATGCCGAATGGGAGATAGATAGATAGATAGATAGATAGATAG 782
 QY 2296 LeuProValGluLysAspAspTrp11leAspPheGlnAlaAsnGluLeuAsnGlnLysSer 2315
 DB 783 AAGGATATCGATCGAAGGCTGGGTGACTTCCGCGGACAGAGATGACCGTCAAGCT 842
 QY 2316 LeuGlyAspLeuLeuLysSerSerAspAlaAla-----11leMetAlaValSerLys11le 2333
 DB 843 CTCTTCAGCTCTCTCGACGACCGCCCAACGTGGCGATGACCTTGTGCGCTGATTAACATC 902
 QY 2334 ProPheGlu11leThrAlaPheGluArgGlnValAla11leSerLeuAsnSerAsn11leAsp 2353
 DB 903 CCATACAGCAAGACCATGAGAGCCCATCTGCTCACTTGAACGATGACGAGGAC 962
 QY 2354 -----GluTrpGlnLeuSerThr11leArgSerSerAlaGlu 2365
 DB 963 GGCACTTCAGATGACAGCGAGCGGCTG---ATATCGGCACTCAATCAAGGCGGAG 1019
 QY 2366 GlyAspSerSerLeuSerVal1ProAsp11lePheArg11leAlaGlyAlaGlyPheArg 2385
 DB 1020 GAATGCCCTGCTCTTCAGTGGCGGATGAGATTTGAGATTTGAGATTTGAGATTTGAGATTT 1079
 QY 2386 ValGluValSerSerAlaArgGlnTyPheSerGlnAsnValAlaLeuAspAlaValAlaPheHis 2405
 DB 1080 GTTGAACACAGCTGGGCTGACCAACACTCCCAAGCGGCGGATCTGATCTGTTTCCAC 1139
 QY 2406 -----HisCysCysSerGlnGlyArgThrLeuValAsnPheProThr 2419
 DB 1140 CGATCGAAGAACCAAGACAC-----TCGGGTGATGTCATGTTCCAGTTCCTCACT 1190

QY 2420 AspHis-HisLeuArgGlySerAspLeuLeuThrAsnArgProLeuGlnArgLeuGlnAs 2439
 DB 1191 GAAACACAGGGGCGGCTCTTCAGAGCTCTCAAGATCCGCGCTACACTGGTTAGAG 1250
 QY 2439 nArgArg11leAla11leGluValArgGluArgLeuArgSerLeuLeuProSerTyMetCil 2459
 DB 1251 CCGCGGCTGAGAGGCAAGGTCGCGAGCGGCTGATCGCTGCTTCCATCGTACATGAT 1310
 QY 2459 eProSerAsn11leValLeuAspLysMetProLeuAsnAlaAsnGlyLysValAspArg 2479
 DB 1311 TCCCTCTCGATCATTTGCTGATCAAGATGCTCTCACTCAAGCGGCAAGGTGGATCG 1370
 QY 2479 GlyGluLeuSerArgArgAlaLysValValPro-LysGlnGlnThrAlaAlaProLeuP 2499
 DB 1371 CAAGAGCTCGCTCGACAGCCCGGCTCATCCCAAGATTCGCGCAAGCAGTGGACTT 1430
 QY 2499 roThrPhePro11leSerGluValGlnVal-11leLeuGlyGluGluAlaThrGluValPhe 2518
 DB 1431 TGTGGCGCGCAGCAGCAAGATGAGGTGCTTCTGCGAAGAAATTAACCGATCTACTA 1490
 QY 2519 GlyMetLysValAsp11leThrAspHisPhePheAsnLeuGlyGlyHisSerLeuLeuAla 2538
 DB 1491 GGGGTCAAGTCCGACTTACAGCAACCTTCTGAGTGGCGGCAATTCGCTGGCGCC 1550
 QY 2539 ThrLysLeu11leSerArg11leAspGlnArgLeuLysValArg11leThrValLysAspVal 2558
 DB 1551 ACAGAACTGAGCGCAGCTCTTAAGTCCAGACTGAGCGCGGTCTCACTGGAAGCAGATC 1610
 QY 2559 PheAspHisProValPheAlaAspLeuAlaSerVal11leArgGlnGly 2574
 DB 1611 TTGAGCAGCAGTACTTGTGCTGATCTTGTGCTTCTTATTTGTCAGAGC 1658

RESULT 13
 US-08-222-617A-26
 ; Sequence 26, Application US/08222617A
 ; Patent No. 5882879
 ; GENERAL INFORMATION:
 ; APPLICANT: Veenstra, Annemarie E.
 ; APPLICANT: Martin, Juan F.
 ; APPLICANT: Garcia, Bruno D.
 ; APPLICANT: Gutierrez, Santiago
 ; APPLICANT: Barrero, Jose L.
 ; APPLICANT: Von Doehren, Hans
 ; APPLICANT: Palises, Harriet
 ; APPLICANT: Van Lempt, Henk
 ; APPLICANT: Montenegro, Eduardo P.
 ; TITLE OF INVENTION: A Method for Influencing Beta-Lactam
 ; TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
 ; NUMBER OF SEQUENCES: 27
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: McDonnell Boehnen Hulbert & Berghoff
 ; STREET: 300 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/222,617A
 ; FILING DATE: 04-APR-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; REFERENCE/DOCKET NUMBER: 97,157
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1144 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single

QY 858 AaSGlYAlaLysLeuTYrArgThrGlyAspLeuAlaArgTYrAlaSerAspGlySerIle 877
 DB 2400 -----ATGTAACAAGACCGGATGACCTGGCCGCTGGCTCCGAACGGCAGAGTT 2447
 QY 878 ValCysLeuGlyValArgIleAspSerGlnValLysIleArgGlyGlnArgValGluLeuGly 897
 DB 2448 GAGTATCTCGAGACCGCCAGATTTCACAGATCAAACTCGAGGTATTCGAATTGAACTCGGT 2507
 QY 898 AlaIleGluThrHisLeuArgGlnGlnMetProAspAspLeuThrIleValIleGluAla 917
 DB 2508 GAATTGAGAACATGCTGGCTATGTAACCTAGGGTCCGACCGATTAGGTGTCACAA 2567
 QY 918 ThrLysArgSerGlnSerIleAsnSerThrSer-----LeuIleAlaPheLeuIleGly 935
 DB 2568 AAGCTCCGACCGCTCCAGAGAACTACCAACGACGACTCGGGGTATTTAGTTGT 2627
 QY 936 SerSerTYrPheGlyAsnArgProSerAspAlaHisIleLeuAspHisAspAlaThrLys 955
 DB 2628 GATAGC-----GCCTCAGTGTCCGAGGACAGCTCGTCTCATTT----- 2666
 QY 956 AlaIleAsnIleLysLeuGlnValLeuProArgHisSerIleProSerPheTYrIle 975
 DB 2667 -----TTAGAGAGAAACCTGCTCGATACATGATTCACAGCGGTTGGTA 2711
 QY 976 CysMetLeuGlnLeuProArgThrAlaThrGlyLysIleAspArgArgArgLeuArgIle 995
 DB 2712 CAGCTTCGCAATCCCAAGTAATGGAACGGGAGCGGACCTACGGCGCTTGGCCGCC 2771
 QY 996 MetGlyLysAspIleLeuAspLysGlnThrGlnValAlaIleValGlnGlnAlaProAla 1015
 DB 2772 GTCGAT-----ATCTCAATTCCACGAGAGTG 2798
 QY 1016 ProIleProValPheAlaAspThrAlaAlaLysLeuHisSerIleTYrValGlnSerLeu 1035
 DB 2799 CGTTCGACCTTCGAGCGGATCGGAATCGCCCTGGGGAATCTGGGCGGACGTGTTG 2858
 QY 1036 GlyIleAspProAlaThrValAsnValGlyAlaThrPhePheGluLeuGlyLysSer 1055
 DB 2859 GAGAGCCGCGAGAGATCCGCTCTCCGACAGACAACTTCTCCGCTCAGAGGGGACACGC 2918
 QY 1056 IleThrAlaIleLysMetValAsnMetValArgSer-----ValGlyMetAspLeu 1072
 DB 2919 ATCACTGCATCCAACTGATCGCTCCGATCCGACAAACAGACAACTCGTCGACAGATC 2978
 QY 1073 LysValSerAsnIleTYrGlnHisProThrLeuAlaGlyIleSerAlaValLysGly 1092
 DB 2979 TCCGTGAAGATGTTTTGCAACAAGGACCTTGAGCGCATGGCAGACCTTCTACAGAAC 3038
 QY 1093 AspProLeuSerTYrThrLeuIleProLysSerThrHisGlnGlyPro-----Val 1109
 DB 3039 AAGCAGACGAGAAATGCCAACAACCC-----CATAGGCGCCGACAGAGCTGCTT 3089
 QY 1110 GlnGlnSerTYrSerGlnGlyArgLysLeuTYrPheLeuAspGlnLeuAspValGlySerLeu 1129
 DB 3090 GAGGAGAAATCCAGACAGCAACATATCTATCTGCAGAAACAGTCTTCAGAGGCGCTTCGTC 3149
 QY 1130 Tyr-----TyrLeuIleProTYrAlaValArg 1138
 DB 3150 TACCATTAACCTCAAGACATGAAACAATCCGACGCGCTATGTAATGACGCTCGTCTTCGG 3209
 QY 1139 MetArgGlyProValAsnValAspAlaLeuArgArgAlaLeuAlaIleLeuGlnGlnArg 1158
 DB 3210 TACAAACACCAATGCTCCAGATCTGTTTCAAGAGACCTGGAAGCATGCACAGCACTCC 3269
 QY 1159 HisGluThrLeuArgThrThrPheGlu-----AspGln 1169
 DB 3270 TTTCAGCGCTGGCGGTCTCTCATGAGAAAGAGGTTTCCAACTGCTCGATCAG 3329
 QY 1170 Asp-----GlyValGlyValGlnIleValHis 1178
 DB 3330 GATCCACCATTTGACGTGGCGTTCCTTACTTACCAACGACGTTCCGCGGGGTGCTGTGAG 3389
 QY 1179 GluTYrLeuSerGlnGluMetLysValIleAspLeuCysGlySerAspLeuAspProPhe 1198

DB 3390 GACCGGAAATTGAGACATTCGCG----- 3413
 QY 1199 GluValLeuAsnGlnGluGlnThrThrProPheAsnLeuSerSerGlnAlaGlyTYrParg 1218
 DB 3414 -----CGCCAAACCTTACGAGAGATTCAACCTGAGATTGGCAGACTGTTCCGC 3464
 QY 1219 AlaThrLeuLeuArgLeuGlyGluAspAspHisIleLeuThrIleValMetHisIle 1238
 DB 3465 GTCTATCTGATTAAACACAGCGGAATCGCTTACCGTCTTTTACAGTCCATCATGCA 3524
 QY 1239 IleSerAspGlyTYrPheSerIleAspValLeuArgArgAspLeuAsnGlnLeuTYrSerAla 1258
 DB 3525 ATCTCGATGATGTGAGTCTGACACTCTTGTGAAAAGGTTCACAGACCTTCACTGCA 3584
 QY 1259 AlaLeuLysAspSerLysAspProLysSerAlaLeuThrProLeuProIleGlnTYrSer 1278
 DB 3585 CTGCTCATGG-----GACAACTTCATCTGCTCATGATGATACCT----- 3626
 QY 1279 AspPheAlaLysTYrGlnLysAspGlnPheIleGlnGlnLysGlnLeuAsnTYrTYr 1298
 DB 3627 ---TACACTGCACCCAGCGGATCTCCACGCTCACCGTGAAGATCACCTTCGACTTTGG 3683
 QY 1299 LysLeuGlnLeuLysAspSerSerProAlaLysIleProThrAspPheAlaArgProAla 1318
 DB 3684 GCCGATGTGATCA-----AAGATCAACGACGCGTGATATGAACGCC 3728
 QY 1319 LeuLeuSer-----GlyAspAlaGlyCysVal----- 1327
 DB 3729 TTGTGTAACGAGCGAGCTGTTACAAAGTCCAGCTGCGACACTATGACGAGTGACGAG 3788
 QY 1328 -----HisValThrIle-----AspGlyGluLeuTYr-----GlnSerLeuArgAlaPhe 1342
 DB 3789 CAGCGACAGCTGCATTTGCTCTCTGAGAGACGCTGACAGACCTTACAGACCTTCTGACAGC 3848
 QY 1343 CysAsnGlnHisAsnThrThrSerPheValValLeuLeuAlaAlaPheArgAlaAlaHis 1362
 DB 3849 TGCTCGCCAGAGGATTAACCTTAACAATGATTCCTCAATTTGTTGGACGCGTGTG 3908
 QY 1363 TyrArgLeuThrAlaValGluAspAlaValIleGlyTYrProIleAlaAsnArgAsnArg 1382
 DB 3909 CAGCGTTATGCGCGTGGACCCACACACTTAACCGGACGCACTTCTTGGACAGACCTG 3968
 QY 1383 ProGluLeu-----GluAspIleIleGlyCysPheValAsnThrGlnCysMetArgIle 1400
 DB 3969 CCGATCTGGGAATTGAACAGCATGTTGTCGTATATCAACT-----CTACCGCTG 4022
 QY 1401 AsnIleAspHis-----HisAspThrPheGlyThrLeuIleAsnGlnValLys 1416
 DB 4023 GTACTGATCATTCGACGTTCAAGATTAAGACAATCATGAGGCCATCGAGATGTGACG 4082
 QY 1417 AlaThrThrThrAlaAlaPheGluAsnGluAspIleProPheGluArgVal---ValSer 1435
 DB 4083 GCCAAGGTAAACGTCAAGAACCGCGGCAATGTGGAACTGGCGGTTTGCACAAAAC 4142
 QY 1436 AlaLeuGlnProGlySerArgAsp-----LeuSerSerThrProLeuAlaGln 1451
 DB 4143 GACTTAAAGCAGGATTAATTCGATTTCTTAATTCGTGCTGTAACCAACCGAATTGGAC 4202
 QY 1452 LeuIlePheAlaValHisSerGlnLysAspLeuGlyArgPheLysPheGlnIleLeuGln 1471
 DB 4203 AAATCGGAACATTTAGACACAGACTGAACCTGGGGATTCGATTGAAGCGGACATGAG 4262
 QY 1472 SerValProValProSerLysAlaTYrThrArgPheAspMetGluPheHisLeuPheGln 1491
 DB 4263 AAGCTGAATTATCACTGGCTGTCAATCGCGCG----- 4295
 QY 1492 GluThrAspSerLeuLysGly-----SerValAsnPheAlaAspGluLeuPheLys 1508
 DB 4296 GAAGTCAGACGACTGGCGGATTCACAGTATTCATCTGCTACAGCCAGTGAAGCTATTTGAG 4355
 QY 1509 MetGluThrValGluAsnValAlaArgValPhePheGluIleLeuArgAsnGlyLeuGln 1528

QY 2095 -----ValLeuGluIleGlyThrGly 2101
DB 6516 CTGTGCAAGGATCAGCAACCGGAGCTATCTTCAGAAAGTATTGATCCCGATGAAGCC 6575
QY 2102 SerGlyMetIleLeuPheAsnLeuAspSer----- 2111
DB 6576 CAGGGATGTTCTCCGTCACGTCAGACAGCAAGAGGTGAGCGGCTGACCAAGAG 6635
QY 2111 ----- 2111
DB 6636 ATAGCCAGTCTATCCAGCATGTTTCCGCTCGATGATGAACTGCTTGGAGGCCCGC 6695
QY 2112 -----ArgLeuGluSer----- 2115
DB 6696 ATCTTAACCTCAATCCGGCGGCTGATCTCATTTGGCGTTCCACCATTCCTGCTTC 6755
QY 2116 -----TyrValGlyLeuGlu 2120
DB 6756 GATGCAATGTCATTGAAAGTCTTCGAGCAAGAGCTTCGGGCTTGTACGAGCGCTCCAG 6815
QY 2121 ProSerArgSerAlaIle----- 2126
DB 6816 AAAACCAAAAGTCAGCGAACTTACCAAGCCCTCAAGCGCATGACAAAGAAATACGGGCTC 6875
QY 2126 ----- 2126
DB 6876 TACCATGCGCGGAGCTGTGCGCATGCGATGCGCAACCTGTACAGCTTTGGCTGGC 6935
QY 2126 ----- 2126
DB 6936 AAATCATTTGGCTTGGAAACCATTTGACGTGATCAGGACCGCCACGCTCTGTGCAATTC 6995
QY 2127 -----AlaPheValAsnLysAlaThrGluSerIlePro 2137
DB 6996 AAATGACGCGTACGACCTCACTGATGAACTGACAGAAAGAAACGGAACCTGAGG 7055
QY 2138 SerLeuAlaGlyLysAlaLysValGln-----Val 2147
DB 7056 GGGGTGGCCAAAGTTGGCAAGTCGAGTCTGAGTGTGTTGGTTTCGTTATTTGGGTT 7115
QY 2148 GlyThrAlaThrAspIleGlyGlnValAsp-----Asp 2158
DB 7116 ATGCTGAGCTCTGTACGCGAAACGATCCGATGTTTCCGTGGGTATCCAGTCAAGCCAGA 7175
QY 2159 LeuHisProAspLeuValIleLeuAsnSerValIleGlnTyrPheProSer----- 2175
DB 7176 AGCGATCTCTAG-----TTCCAAATCGGTCAATGATTTCTGTCAACTTGTGGTG 7226
QY 2176 -----SerGluTyrLeuAlaGlu 2181
DB 7227 CTAAAGGTGATATTCTCACTCAAGCATTTGGCGGCTCATCAGAAAGGTATATGAAGAG 7286
QY 2182 IleAlaAspThrLeuIleHisLeu----- 2189
DB 7287 CTGCTGAGCGCCCACTGACACAAAGACATCCGTTCCAGAGAGTGAAGAGTGTGACG 7346
QY 2190 -----ProAsnValGlnArgIlePhePheGlyAspValArg 2201
DB 7347 GTGGATATATGACCCAGCCGCGCATCCGCTGTACAGAACGTGTTCC-----AACTTCGAA 7400
QY 2202 SerGlnAlaThrAsnGluHisPheLeuAlaIleArgAlaIleHisThrLeuGlyLysAsn 2221
DB 7401 TCCCGTCGCAACGAGAACACGATGCGAGGTCCGAGATGAAGATGCTTGCTTCAT 7460
QY 2222 -----AlaThrLysAspAspValArgGlnLysMet 2231
DB 7461 CAATACCGCGCGGTTCAGCCCGTGAATTCGTTGCGAAAGTTTCATCTGAACGCAACGCTC 7520
QY 2232 AlaGlnLeuGlnLysPheMetGluGluLeuLeuValGluProAlaPhePheThrSerLeu 2251
DB 7521 ACGGAATTTG-----GAGTCGGAGTTGAGAGTCAACTTCAACTATGCGACCGCTTA 7571
QY 2252 -----LysAspArgPheProGlyLeuValGluIleValLeuProLysAsnMet 2269

DB 7572 TTCACAAAAGCAGATCCAGGCGTTTTCATACCTATGATGATCTC-----CTG 7622
QY 2270 GluAlaValAsnGluLeuSerAlaTyrArg-----TyrAlaAlaValHis 2285
DB 7623 CGCCAGCTGTCCCACTGAGTCGAG-AGGATCAATGAGATTAAGATGCGAGCTGTGTTA-- 7679
QY 2286 ValArgGlySerLeuGlyAspGluLeuValLeuPro----- 2297
DB 7680 GTTCGCCGACACAGATGGCGATCTGCACTTGCACTTGGCACAGTCCCGCTTGGAGC 7739
QY 2297 ----- 2297
DB 7740 ACTGTGAGAGCAGAAAGTAGCGTGTGTAACCAAGCCCTTTGAGCGCGAGCTTCTT 7799
QY 2298 -----ValGluLysAspAspTyrIleAspPhe----- 2306
DB 7800 GCCGACAGAGAAAGTCCGTCGTGACGAGATGAGCACTTATGTCTGATCTTAAAC 7859
QY 2307 -----GlnAlaAsnGlnLeuAsn----- 2312
DB 7860 GGGCAGGCTTACCAAGCTCGCCCGGTACATACAGTCCGTGTCTATTTGGGGCAGAC 7919
QY 2313 -----GlnLysSerLeuGlyAspLeuLysSerSerAspAlaIle 2326
DB 7920 GGAATAGCTTTGATGCTGGAAGAGATATCAGACATTTAT-----TGC 7964
QY 2327 IleMetAlaValSerLys-----IleProPheGluIleThr----- 2338
DB 7965 ATTCTGCGATTTGGAAGCGTGTGACAGATACATGCTGCTTGGATCGACTTACCAACC 8024
QY 2339 -----AlaPheGluArgGlnValAlaIleSerLeuAsnSer 2350
DB 8025 GAGCGGCTCAGCTGATTTCTGAGAGATTAAGCGAAGCTCTCTTGTGCACTCCAGT 8084
QY 2351 AsnIleAspGluTyrGln-----LeuSerThrTyrIle 2360
DB 8085 CATGCTTCGAAATGTGAACGCCATGCGCGGAAGTATTGACATGCACTGCGCCGCGATC 8144
QY 2361 ArgSerSerAlaGluIleLysPheSerLeuSerValProAspIlePheArgIleAlaGly 2380
DB 8145 GAGACGCGGCTGACCCAAACGATGCTGACCTGCCCAATTTCTGACCTCGGCAAT 8204
QY 2381 GluAlaGlyPheArgValGluValSerSerAlaArgGlnTyrSerGlnAsnGlyAlaLeu 2400
DB 8205 CTAGCG-----TATATATCTTACTTACAGCACTTCGCGTAAAGCCAAAGGAGTCTTA 8258
QY 2400 ----- 2400
DB 8259 GTTGAGCAAAAGCAGTTCTTCTTACCGCATGCCCTCCGGAGGGATATTCCGTCGA 8318
QY 2401 AspAlaValPheHisHis----- 2406
DB 8319 GACTGTACCAAGCATGAGCGTCTGTCTCTGTCACATGCTTTCGATCTTCGCTC 8378
QY 2407 -----CysCysSerGlnLysArgThrLeuValAsnPheProThrAsp-- 2420
DB 8379 GAAACAATTGTGTTCGGGTCTCAGGGGACACAGACTGATGTTCTTCCCACTGAGTTC 8438
QY 2421 -----HisIleLeuArgGly 2425
DB 8439 GTGCGAGATGATGATTTTACAGATGGCCAGACGACGAGTCTTCCTTATCTCAGCGGC 8498
QY 2426 Ser--AspLeuLeuThrAsnArgProLeuGlnArgLeuGlnAsnArgAlaIle 2444
DB 8499 ACACCATCTTACTGACAGAAAGATGATCTGGCAGCATGCAACCATCTGCGAGTTTACC 8558
QY 2445 -----GluValArgGluArg----- 2449
DB 8559 GCCCGGGGAGAGAGCTTACGCCACCCAGTACGAAAGATGCGCGCGCATTCACAGGT 8618
QY 2449 ----- 2449

Db 8619 CCCATCTACATGCTTATGCTGTCACCGAGACACGGGTGTAACAATTATCGCGAATTC 8678
 QY 2450 -----LeuArgSerLeuLeuPro-----SerTyr 2457
 Db 8679 ACAAGCAATTCGATATTGGAATGCTCTTCGGGAATGCTCCCTGGTACCGACGCTAT 8738
 QY 2458 MetIleProSerAsnIleValIleuAspIleMetProLeuAsnIleAsnGlyVal 2477
 Db 8739 GTGCTGACCGCG-----GCACCTTCAGCCCTCCCTTCGATGCTGTGCGA----- 8783
 QY 2478 AspArgIleGlyLeuSerArgArgAlaValAlaProIleGlnIleThrAlaAlaPro 2497
 Db 8784 -----GACCTATCTTCCCGCGACACGGTACCGGTGTTCACAACT 8834
 QY 2498 LeuProThr-----PheProIleSerGluValGluValIleLeuCys 2511
 Db 8835 CTTCCTAACGATCAGCGATTCATTCACACCTTTCGCAAGAGAGACATCGCTATG 8894
 QY 2512 GluGluAlaThrGluValPhe----- 2518
 Db 8895 GGGCGCTTCGCGCGCTCTACAGACCGGACCTGTGCTGATCGCTTCAACCTCAG 8954
 QY 2519 -----GlyMet 2520
 Db 8955 CACAGCCGAGCTGGAATACCTAGAGAGCGATCTGCATCAAGATGAGGGGATAC 9014
 QY 2521 LysValAspIleThrAsp----- 2526
 Db 9015 CGGATCGAAGTTTCTGAAGTTCAAGAGCTCCTCAAGTCCCGGTCCGGAGGCT 9074
 QY 2527 -----HisPheAsnLeuGlyHisSerLeu 2537
 Db 9075 GCAGTCGTTGCCAAGTATGAGAACAGATACCTATTCGCGACCGCTCTCTGTCTC 9134
 QY 2538 Ala-----ThrIleLeuIleSerArgIleAsp-----GlnArgLeuIle 2550
 Db 9135 GGTTCATATACACGCAATGAAACAGTATCGAAGCCGATATTCATCTTCATATAA 9194
 QY 2551 ValArgIleThrValIleAspValPheAspHis-----Pro 2562
 Db 9195 GCAAGGTTCCACAGTCATGATGCCAAGCACCTGTGTGTGAGAGCGACCTGCT 9254
 QY 2563 ValPheAlaAspLeuAlaSerValIleArgGlnIleGlyLeuGlnIleProValSer 2582
 Db 9255 GTACACGATTAAACGAAAGCTGACGTCGGAGA-----TTGCCGAGATTATACAC 9305
 QY 2583 AspGlyGlnIleGlnAspArgSerAlaHisMetAlaProArgThrGlnIleAlaIle 2602
 Db 9306 GACTCCGCG-----CAGTCTCTGTACAGCCACCAAGAACATATGAGGCCAAG 9356
 QY 2603 LeuCysAspGluPheAlaValIleGlyPheGln-----ValGlyIleThrAspAsnPhe 2621
 Db 9357 ATGTGACGACTGTGGAAATCCGCTTGGGAATGAGGATGCCGATATCGACGACATCG 9416
 QY 2622 PheAspLeuGlyGlyHisSerLeuMetAlaThrIleValAlaValArgIleGlyHisArg 2641
 Db 9417 TTCAACTGGTGGCGACACATCATCTTCGATCTCGTGGCCAGATTCAACACAG 9476
 QY 2642 LeuAspThrThrValSerValIleAspValPheAspHisProValLeuPheGlnLeuAla 2661
 Db 9477 GTGGCGTCGACAGATCACCGGTATATTGAACT-----CGTACCGCC 9524
 QY 2662 IleAlaLeuAspAsnLeuValGlnSerIleThrAsnGluIleValGlyIleArgGluMet 2681
 Db 9525 CGAGCCCTCATATCATCGTCTTCATGAGACATCC-----GACCGG 9566
 QY 2682 AlagluTyrSerProPheGlnLeuLeuPheThrGluAspProGluGluPheMetAlaSer 2701
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 QY 2702 GluIleIleProGlnLeuGlnIleIleIleGlnAspIleTyrProSerThrGln 2721
 Db 9618 CCCCTACTGCG-----ATTCAAGACTGGTTTGTTCAAAGCT 9656

QY 2722 MetGlnIleAlaPheLeuPheAspHisThrThrAlaArgProArgProPheValProPhe 2741
 Db 9657 CTCAGCATCCGATGATGATGATACACT-----TTC 9689
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 QY 2836 MetArgValIleMetArgIleSerHisAlaLeuTyrAspGlyLeuSerLeuGluHisVal 2855
 Db 9975 GCGCGAGTGTGTTCCCTCCCTACCATATGAGCCATTGACACCGCTGAGCTGAGATCTT 10034
 QY 2856 ValArgIleLeuHisMetLeuTyrAsnGlyArgSerLeuLeuPro----- 2871
 Db 10035 GTCCGTGACTTGAGACGCTGTAACGAAATGAAAGCTCGGAACGAGGACGACGCTTTC 10094
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RESULT 14
 US-08-222-617A-1
 ; Sequence 1, Application US/08222617A
 ; Patent No. 5882879
 ; GENERAL INFORMATION:
 ; APPLICANT: Veenstra, Annemarie E.
 ; APPLICANT: Martin, Juan F.
 ; APPLICANT: Garcia, Bruno D.
 ; APPLICANT: Gutierrez, Santiago
 ; APPLICANT: Barredo, Jose L.
 ; APPLICANT: Von Doehren, Hans
 ; APPLICANT: Palisae, Harriet


```

APPLICANT: Van Liempt, Henk
APPLICANT: Montenegro, Eduardo P.
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
NUMBER OF SEQUENCES: 27
TITLE OF INVENTION: Quantities of ACV Synthetase
CORRESPONDENCE ADDRESSES:
ADDRESS: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12364 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Penicillium chrysogenum
ORGANISM: Penicillium chrysogenum
FEATURE:
NAME/KEY: CDS
LOCATION: 264..11600
OTHER INFORMATION: /function= "enzyme"
OTHER INFORMATION: /product= "ACV Synthetase"
US-08-222-617A-1

Alignment Scores:
Pred. No.: 6 46e-130 Length: 12364
Score: 1342.50 Matches: 748
Percent Similarity: 36.31% Conservative: 525
Best Local Similarity: 21.33% Mismatches: 1244
Query Match: 8.32% Indels: 992
DB: 2 Gaps: 136

US-09-482-788-2 (1-3129) x US-08-222-617A-1 (1-12364)
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QY 278 SerAsnSerAlaIleCysArgThrAlaLeuSerIleLeuSerIleArgTyrThrHisSer 297
DB 589 ACCAGGAGCGCTGATGATGACGCTCC-----CTGTTGACGATCATGCCGCGCTCC 636
QY 298 AspGluAlaLeuPheGluAlaVal-----ThrGluGlnSerLeuProPheAspIleHis 315
DB 637 AAGAGCTGCTCCATGAAGCGCGGTGTGAGCGGTGGATCCGTCATTAA-TTCTCCGTGCAC 695
QY 316 TyrLeu-----AlaAspGlyThrTyrGlnThrValAlaProLeuArgValHis 331
DB 696 CAGATGCTGAAGGGGTTTGAAGAAATGACACACACTATCAACGCGCTCTCG-----CAC 749
QY 332 CysGlnSerLeuAlaGalaSerAsp-----ValMetAspAlaIleSerSer 347
DB 750 CGTAGCAGAAATTTTGGAAATTTCTTTCGCATCTCGGGTAGTCTCCCAACATGCTGACC 809
QY 348 TyrAspAspArgLeuGluHisLeuAlaProPheGlyLeuArgAspIle-----Arg 364

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DB 870 GGTTCGAGAAAGATGATGACTGCGATTGAC-----TCGCG 908
QY 385 GlySerHisValAsnAsnGlyIleAsnGlyPheLeuGlnGlnIleThrGlySerSerHis 404
DB 909 TCAAGTCTGTAATAATGGGTTATTGACTTCTGTCAAGCTTGTGCATGCGAGAGAT 968
QY 405 Phe---MetProCysAsnAsnArgAlaLeuLeuLeuHisCysGlnMetGlySerGly 423
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QY 424 AlaLeuLeuValAlaTyrTyrAspHisAsnVal-----IleAspSer 437
DB 999 GCAGGTATGATGGGTAGTGATGCCAACCTCTCGCTAGCTGCGTTTCTCCGACTGT 1058
QY 438 LeuGlnThrThrArgLeuLeuGlnGlnPheGlyHisLeuLeuLeuLeuLeuLeuLeuLeu 457
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QY 534 SerLeuGlyLeuArgAlaGlnGlnAlaIleIleProValTyrPheGlyLeuSerLeuTrp 553
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QY 574 AsnAspProProAlaArgThrAlaGlnValValThrGlnThrArgAlaThrValAlaLeu 593
DB 1476 ACTTATCCGATGAGCGAGTCCGCTGCTGCTGATGACACCAAGCAGCGGCATCATC 1535
QY 594 ThrSerLeuLeuHisArgGluThrValGlnLeuVal-----GlyAspCys 609
DB 1536 GCCAGTATCAACATGTGAGAGGCTCCACGAGAGTCAATCGCGATAGAAACCTATGC 1595
QY 610 ValValValAspAspGlyLeuLeuGlnSerValSerAlaSerAsp----- 624
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QY 625 -----AspPheSerSerLeuThrIleSerGlnAspLeuAlaTyrValIlePheThr 641
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QY 662 AlaLeuLeuPheGlyIleAspLeuGlyIleAsnSerAspThrArgAlaLeuGlnPheGly 681
DB 1773 ATTAACGACCTGTCTGCAAGTACGGGCTG-----GCCGGG 1808
QY 682 ThrHis-----AlaPheGlyAlaCysLeuLeuGlu----- 691

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D 5931 CAGTCTGGCTCCCTGGCTACATGTCGCCCTCTGTCATCTTCGTACAGCAAGTCC 5990
Q 2017 -----HisAspHisSerGlu 2021
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Q 2044 ----- 2044
D 6171 GACAGCTAAAGACACAAAGCTTTCCTTCATGATTCAGAGTCTTTAACCGCGCGTC 6230
Q 2044 ----- 2044
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Q 2085 ThrIleuHisAspAsnArgSerLeuGlyAsn----- 2094
D 6456 TCGCTTCTGACAGCGCGCTGCGTGAACCTTGCTGACATGAGCGGTTGAGAACTTGA 6515
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D 6516 CTGTGACAGATCACGCAACCGCATCTTATTCAGAAAGTATGATGCCGATGAAGCC 6575
Q 2102 SerGlyMetIleLeuPheAsnLeuAspSer----- 2111
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Q 2112 -----ArgLeuGlnSer----- 2115
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D 6756 GATGATGTCATTGAAAAGTCTTCGACAAAGAGCTTCGGGCTTTGACGAGCGCTCAG 6815
Q 2121 ProSerArgSerAlaAla----- 2126
D 6816 AAAACCAAAAGTGCAGGGAATTACAGCCCTCAAAAGCGATACAGAAATACGCGCTC 6875
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Qy	2400	-----	-----	2400
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Db	8319	GACTGTACCAAGCATCATGCGCTCTGTCTGTGTCACATCACTGCTTCGACTTCTCCGTC	8378	
Qy	2407	-----CysSerSerGlnGlyArgThrLeuValAsnProThrAsp---	2420	
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Db	9255	GTGACGATTAACGMAAGCTCGACGTCCGGAGA	9305
Qy	2583	AspGlyGlnGlyGlnAspArgSerAlaHisMetAlaProArgThrGlnIle	2602
Db	9306	GACTCCGG-----CAGTCTCTGTACAGCCCAACGAAACATATTCGAGGCCAAG	9356
Qy	2603	LeuCyAspGlnPheAlaIysValLeuGlyPheGln--ValGlyIleThrAspAsn	2621
Db	9357	ATGTGACAGACTGTGGGAATCCGCTTGGGAATGAGAGATGCGGTATTCGACGACACTG	9416
Qy	2622	PheAspLeuGlyGlyHisSerLeuMetAlaThrIysLeuAlaValAlaGlyIleGlyHisArg	2641
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Db	9477	GTGGGCTGCAGAACATCACCGTTCGGGAAATATTTGAACAT	9524
Qy	2662	IleAlaLeuAspAsnLeuValGlnSerIysThrAsnGlnValGlyGlyArgGluMet	2681
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Qy	2742	TyrIleAspPheProSerThrSerGlnProAspAlaAlaGlyLeuIleIysValaCysGlu	2761
Db	9690	TACGTC-----CGAACGCGAGCGTGGATGTGATTCCTTAACGCGTGTGACG	9740
Qy	2762	SerLeuValaAsnHisLeuAspIlePheArg---ThrValPheAlaGluAlaSerGlyGlu	2780
Db	9741	GACTTGCACACGATTCACGATGTTTCCGATCGGACGTCAAGCCGCGAGAAAGTGGATTTC	9800
Qy	2781	LeuIysGlnValValLeuSerCysLeuAspLeuProIleGlnValIleGlnIleThrGlnAsp	2800
Db	9801	GTGCAGTCCTTGTGCGAGACTTCTCTCTGCCAGCTTCGGGTGCTGMAACGTAAAGAT	9860
Qy	2801	---AsnIleAsnThrAlaThrAsnGlnPheLeuAsp-----GluPheAlaIys	2815
Db	9861	GTTCAGCGGTCGCGGCGCGCTCAACGAGATATTTGATGGGTGACGTGCGCTTCAACTT	9920
Qy	2816	GluProValaIArgLeuGlyHisProLeuIleArgPheThrIleIleIysGlnIleIysSer	2835
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Qy	2856	ValaIArgIysLeuHisMetLeuIysThrAsnGlyArgSerLeuLeuPro-----	2871
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Db      10095 CCGCAGTGGGCTGAAGCCATCCAAATTACAGAGCGTCCAGACTCTGAGAGAACCAT--- 10151
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      10152 ---TGGAAATAGCTCGCATGGAACAGCTTCCAGCATATCCGATTCGCTACG----- 10202
Qy      2911 AspGlyAsnAspAlaThrCysIleValAlaLeuHisIleuSerIleValIleAsnIleProSer 2930
      10203 -----TCMAACCGGTTCGCGCTGCGCTGAGCAGAACTTTGAGC---CTTGAG 10247
Qy      2931 GlnValLeuArgIleSerSerAsnIleIleThrGlnAlaThrValPheAsnAlaIleCys 2950
      10248 AAGACA----- 10253
Qy      2951 AlaLeuValLeuSerArgIleuSerAspSerIleAspVal---ValPheGlyArgIleVal 2969
      10254 GCGCTACTGATCCAAAGAGAAATCGATCGACAGATGCTCCGCTGACGATCCCTCCTG 10313
Qy      2970 SerGlyArgGlnGlyLeuProValGlyIleValGlnAspIleValGlyProCysThrAsnAla 2989
      10314 ACTTCA---GTTGATTTGGGCTCCAAACATATCGCTCCAAACCGGCCA-----AGTATG 10364
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Qy      2990 ValProValArgAlaHis 2995
      10365 GTTACGATCGAGGAGCAT 10382
Db

RESULT 15
US-09-252-991A-9182.
/ Sequence 9182, Application US/09252991A
/ Patent No. 6551295
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252.991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074.788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094.190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 9182
/ LENGTH: 7911
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9182

Alignment Scores:
Pred. No.: 1,42e-126 Length: 7911
Score: 1307.50 Matches: 569
Percent Similarity: 40.15% Conservative: 312
Best Local Similarity: 25.93% Mismatches: 831
Query Match: 8.11% Indels: 484
      4 Gaps: 89

US-09-482-788-2 (1-3129) x US-09-252-991A-9182 (1-7911)
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      124 CTGCGAGGGAGGGAATCGATTCTCGCTGTTCCCGGTCGCGCGCGTCTTCCGCC 183
Db
Qy      1110 GlnGln-----SerTyrSerGlnGlyArgLeuThrPheLeuAspGlnLeuAspVal 1126
      184 GAGCGGACCGCGCTGCTCTAGCCGACGACGATGCGTTCCTCTGACCTGAGACCA 243
Db
Qy      1127 GlySerLeuThrTyrIleuIleProTyrAlaValArgMetArgGlyProValAsnValAsp 1146
      244 CAAAGTGGCCCTCAACACTGCCAGCGGCTGCGCTGAAACGACGCGTGAATCGCCAG 303
Db
Qy      1147 AlaLeuArgArgAlaLeuAlaIleuGlnGlnArgHisGlnThrIleuArgThr----- 1164
      304 GCGCTGAGAGCGCGCTTTCGCGACCTGTGCGAGCGTATGAACCCCTGCGTACGCTGTC 363

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Qy      1165 -----Thr 1165
Db      364 CCGCGCGGCGCGACGACAGCTGGCGAGCGCCCTCGCAACCGCGCTGAGAGTTGCC 423
Qy      1166 PheGlnAspGlnAspGlyValGlyValGlnIleValHisGlyIleuSerGlnGlnMet 1185
      424 TTGAGGATTTGACGCGCGCTGCTGAGCGCGACGAGAACCGCGCTGCGCGAGAGCG 483
Qy      1186 LysValIleAspLeuCysGlySerAspLeuAspProPheGlnValLeuAsnGlnGln 1205
      484 CAG-----CGGAGTGC 495
Db
Qy      1206 ThrThrProPheAsnLeuSerSerGlnAlaGlyTyrArgAlaThrIleuLeuArgLeuGly 1225
      496 TTGACGCGCTTCACACTGTGCGAGGCGCGCTTCTGCGGAGTCCCGCTGATCCCTCGGCG 555
Qy      1226 GlnAspAspHisIleLeuThrIleValMetHisIleIleSerAspGlyTyrProSerIle 1245
      556 GAGGAGCGGATGTGCTGTGTTGACCTGATCAATCGTGTCCAGCGGCTGTGATG 615
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Qy      1246 AspValLeuArgArgAspLeuAsnGlnLeuTyrSerAlaIleuLysAspSerLysAsp 1265
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Db
Qy      1266 ProLeuSerAlaLeuThrProLeuProIleGlnTyrSerAspPheAlaLysTyrGlnLys 1285
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Qy      1363 TyrArgLeuThrAlaValGlnAspAlaValIleGlyThrProIleAlaAsnArgAspArg 1382
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      1027 GCCGAGGTGGAAGGCTGATCGCGCTGTTCGTCACACCGACGCTGCGCTGCTGATTC 1086
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      1087 GAGCGCGGACGCTGCGGTGCGACCTGTGCGCGGCTGACGACACCGCTTGGCGCC 1146
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Qy      1476 ProSerLysAlaThrThrArgPheAspMetGlnPheHisIleuPheGlnGlnThrAspSer 1495
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Qy	1496	neulysbglserValaamPha1aDapgluueuPhelysmetG1uthrValaGluasnaVal	1515
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Qy	1516	ValaPrgValPhepneGluileLeuAargnaBng1lyeugInserSerArgThProValSer	1535
Dp	1432	CGCGGCGCTTGGCAAAACCTCTCTCGCGGACTGTCTGAAAAACCCGACAGCCAGGCTGCAC	1491
Qy	1536	lLeuueProleuthrAapglYileValThrlengluYuleuAapValaLueuAaVallys	1555
Dp	1492	TGCGCTGCCAGATGCTCGATGCGCGAGAGCGCTATGACGTTCGAAAGGCTGGAAGCCACT	1551
Qy	1556	HisValaaprrYrProAargluInserSerleuAaAapValaPheGlnThrlGlnValaSerAla	1575
Dp	1552	CGCGGCGCAAGTACCGCTGCGACCGCGCGCTGTGACCGGTGTTCGAGAGACGCTGACGCC	1611
Qy	1576	TyrProAapSerleuAaValaValaAapSerSerCyAargleuThrYrThG1ueuAap	1595
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Qy	1596	ArgInserAaprlleLeuAaIag1YrTpleuAargAargAserMetProAgluThrlleu	1615
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Dp	1732	GTCGGCGGTGCGCATATGCAACGTTTCCATGCAATGTGTCGTGGCGCTCGATGCGCATCTTCAAG	1791
Qy	1636	AlaAamleuAa1aYrGleuProleuAapValaAargSerProSerAlaAargValaGlnAaplle	1655
Dp	1792	GCGGCGCGCGCTTACGTGCGCGGTGACCCGAGATATCCCGAGAGCGCGCACGCGCTTACGTG	1851
Qy	1656	LeuSerGluYleuSerGluYrProThrlleValaLueuIleGlnHisAapThrlaAProProAap	1675
Dp	1852	CTGAGAGCAAGCGCGGTGCAACCTGCTGTACAGCAGTGCACGCTGAAGCTCCGCTGGCG	1911
Qy	1676	lLeGluValaThraAapValaGluPheValaAarg1leAargAapAlaAeuaAapSerAapAla	1695
Dp	1912	CMAAGCGTGCAGCGGATGCAACCTG-----GATCGCGGCTGCG	1947
Qy	1696	AapGluPheGluValaIleGlnHisAapSerThrlYrPro-----SerAlaThr	1711
Dp	1948	CCCTGGTTCGAG-----GATTACAGTGAAGCGCAACCGGATATTATCATCTGATGCGAG	2001
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Dp	2002	AACCTCGCGCTATGTCATTAACACTCGCGCTCCACCGGCAAGCCMAAGGCGCGCGCAAC	2061
Qy	1732	GluHisAargValaIleleAargThrValThrSerGluYsile-----ProAapYrPro	1749
Dp	2062	CGGCATTCGCGCGTGA--GCAACGCGCTGTGCTGGATGCACAGAGCGCTTACCGGCTGGCG	2119
Qy	1750	SerGluThraAargMetAlaHisMetAlaThrlleAaPheAapGluYAlaSerTYrGluile	1769
Dp	2120	TGCGCGACACGCGTGTGCGAAG--ACCCGTTCAAGCTTCGACGTCGTGCTGCGAAGTTC	2178
Qy	1770	TyrSerAlaLeuLueuPheGluYArgThrlleuValaCyValaAapYrMetThrThrlleuAap	1789
Dp	2178	TTCCTGCGCGCTGATGAGCGGGGCAAGCTTGGTGTGTCGCGCGCGCGGAGCAATCGCAT	2238
Qy	1790	AlaAargAlaLeuYsAapValaPheAargGluHisValaAaAlaAaSerHisValaThr	1809
Dp	2239	CGCGCGAAGCTGTGAGACTGATCAATGCGAGGGGGGTGACACGCTGCACTTGTCGTCG	2298
Qy	1810	Seiser-----SerGlnAapValaProleuAaGluValaProAargValleuSerArg	1825
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Qy	1826	ThrlleuMetPhePhePheLueuValaValThraPserThrlaAProAapAlaAeuaAapAla	1845
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Qy	1846	Gln-----GlyleuYrGlnGluYalGlnCyAaYr	1855

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QY 2244 GluPro-----AlaPhePheThrSerLeuLysAspArgPheProGlyLeuValGlu 2260
Db 3415 AAGCGCGCGGACGCGCTGAAATGCCAAGGACCTCGAAGCGGCTTGCGAGCGCTGGTGA 3474
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QY 2281 AlaAlaValValHisValArgGlySerLeuGlyAspGluLeuValLeuProValGluLys 2300
Db 3526 GCGGAA-----CATGCGGAAGCAACGCTGGCGGCTGCTGCTGCGCGGACGCGC 3579
QY 2301 AspAspTrpIleAspPheGlnAlaAsnGlnLeu-----AsnGlnLysSerLeu 2316
Db 3580 -----GTGACCGACAAAGCGCTGAGTCCGCTTCGACGAGAGTGCAGCGAGCTCG 3630
QY 2317 -----GlyAspLeuLeuLysSer-----SerAspAlaAlaIle 2327
Db 3631 GACCTGGCTGACGCGCCACCTGTTGCGGAGCTGTTGATGATAGCGCGAGCGCGC--- 3687
QY 2328 MetAlaValSerLysIleProPheGluIleThrAlaPheGluArgGlnValAlaIleSer 2347
Db 3688 -----CAGCGTCTGTGTTGGTATC 3708
QY 2348 LeuAsnSerAsnIleAsp-----GluTrpGlnLeu-----SerThr 2359
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Db 3769 TACCAGACGAGCTCCGCTGGGAAAGCTCG---CGGCTGCTCCT 3807
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Db 3808 GGC-----AAGACCAAGCCCTTCAAGGCTGCGGC--- 3837
QY 2400 LeuAspAlaValPheHisIleCysCysSerGlnGlyArgThrLeuValAsnPheProThr 2419
Db 3838 -----GGCCGA-----GTG 3846
QY 2420 AspHisIleLeuArgGlySer-----AspLeuLeu 2429
Db 3847 AGCGAGCATCCCGTGTGATGATGATGAAGCGGACGATTGTCGCGGACGCTGCTG 3906
QY 2430 ThrAsnArgProLeu-----GlnArgLeuGlnAsnArgIle 2442
Db 3907 GAAGTGGCGCGGACGCTTCCGCTGCGTCATCCGACAGCGCTGACGACGCGTTTC 3966
QY 2443 AlaIleGluValArgIleArgLeu---ArgSerLeuLeuProSerTyrMetIleProSer 2461
Db 3967 GCCATCTCCGTCGAGCTCGCTTCGACCGGACGCTTGACCGAAGC--- 4011
QY 2462 AsnIleValIleLeuAspLysMetProLeuAsnAlaAsnGlyLysValAspArgGlyGlu 2481
Db 4012 -----CTGCGAAGCAAGGCGCGGACGCTACCGTACCAAGCTCAACGATCTTCTG 4062
QY 2482 LeuSerArgArgAlaLysValValProLysGlnIleThrAlaAlaProLeuProThrPhe 2501
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Db 4108 -----TCAAGCTG 4116

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QY 2635 AlaVal-----ArgIleGlyHisArgLeuAspThrThrValSerVal 2648
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QY 2669 GlnSerLysThrAsnGlnIleValIleGlyArgGluMetAlaGluTyrSerProPheGln 2688
Db 4480 ---AGTCTCAATGCGCGGCTGTTCGACGCTGAACGTGACATGACATGACGAGCTCAGCTCG 4536
QY 2689 LeuLeuPheThrGluAspProGluGluPheMetAlaSerGluIleLysProGlnLeu--- 2707
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QY 2707 ----- 2707
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QY 2708 -----GluLeuGlnGluIle 2713
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QY 2714 GlnAspIleTyrProSerThrGlnMetGlnLysAlaPheLeuPheAspHisThrThrAla 2733
Db 4714 GAGGACATCTATCCGCTGTCACCAACGACGAGGAGCATGCTGTTTC---CATTCGCTG--- 4767
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Db 4768 -----TACAGACAGCATGACGAGGACTTACATCAATGATGCTGTGAGTGTG 4815
QY 2754 AlaGlyLeu-----IleLysAlaCysGluSerLeuValAsnHisLeuAsp 2768
Db 4816 TCCGGCTCGATATCCCGGCTTCGCGGACGCTTGACAGTCCGCGTGGACGCGGACGCG 4875
QY 2769 IlePheArgThrValPheAlaGluAlaSerGlyGluLeuTyrGlnValValLeuSerCys 2788
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QY 2908 Thr---ValValAspGly-----AsnAspAlaThrCysLysAlaLeu 2920
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QY 2959 AspSerLysAspValValPheGlyArgIleValSerGlyArgGlnGly---LeuPro--- 2976
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QY 3036 AlaIleThrAsnPheSerCysValIleThrTyraHis-----PheGluTyraHis 3052
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Job time : 1993 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 18:24:23 ; Search time 4856 Seconds

(without alignments)
12431.365 Million cell updates/sec

Title: US-09-482-788-1

Perfect score: 11212
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Gapox 10.0 , Gapext 1.0

Searched: 3611042 seqs, 2692057975 residues

Total number of hits satisfying chosen parameters: 7222084

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	153.4	1.4	9590	US-10-282-122A-33351	Sequence 33351, A
3	145	1.3	10002	US-10-282-122A-14471	Sequence 14471, A
4	138.4	1.2	15450	US-10-282-122A-7449	Sequence 7449, Ap
5	134.8	1.2	5127	US-10-156-761-3630	Sequence 3630, Ap
6	134.8	1.2	9025608	US-10-156-761-1	Sequence 1, Appl
7	133.8	1.2	3954	US-10-282-122A-30194	Sequence 30194, A
8	129.6	1.2	2811	US-10-282-122A-33871	Sequence 33871, A
9	129	1.2	10296	US-10-282-122A-33665	Sequence 33665, A
10	127.8	1.1	9748	US-10-282-122A-31388	Sequence 31388, A
11	119.6	1.1	3789	US-10-156-761-3185	Sequence 3185, Ap
12	115.2	1.0	15738	US-10-329-079-46	Sequence 46, Appl

13	115.2	1.0	61944	US-10-329-079-34	Sequence 34, Appl
14	111.2	1.0	8138	US-10-369-493-35302	Sequence 35302, A
15	111.2	1.0	9683	US-10-369-493-38492	Sequence 38492, A
16	110.6	1.0	11007	US-10-402-842-5	Sequence 5, Appl
17	110.6	1.0	47988	US-10-402-842-1	Sequence 1, Appl
18	109.2	1.0	6522	US-10-282-122A-31533	Sequence 31533, A
19	104.8	0.9	8646	US-10-282-122A-33353	Sequence 33353, A
20	104.6	0.9	3048	US-10-156-761-3146	Sequence 3146, Ap
21	104	0.9	13029	US-09-815-242-4052	Sequence 4052, Ap
22	104	0.9	13029	US-10-282-122A-7240	Sequence 7240, Ap
23	104	0.9	77536	US-09-940-3168-1	Sequence 1, Appl
24	101.2	0.9	7788	US-10-329-079-8	Sequence 8, Appl
25	101.2	0.9	37360	US-10-329-079-6	Sequence 6, Appl
26	99.8	0.9	135638	US-10-314-657-1	Sequence 1, Appl
27	99	0.9	3726	US-10-282-122A-33927	Sequence 33927, A
28	98.8	0.9	15738	US-10-329-079-12	Sequence 12, Appl
29	97.2	0.9	2460	US-10-282-122A-30195	Sequence 30195, A
30	95.4	0.9	7347	US-09-815-242-7773	Sequence 7773, Ap
31	95.4	0.9	7347	US-10-282-122A-7467	Sequence 7467, Ap
32	95.4	0.9	7347	US-10-324-967-17	Sequence 17, Appl
33	94	0.8	11058	US-10-156-761-3629	Sequence 3629, Ap
34	91.6	0.8	4020	US-10-369-493-43172	Sequence 43172, A
35	86.8	0.8	8244	US-10-402-842-3	Sequence 3, Appl
36	84.8	0.8	590	US-10-425-115-175139	Sequence 1, Appl
37	84.6	0.8	88421	US-09-976-059-1	Sequence 1, Appl
38	83.4	0.7	12951	US-10-282-122A-31678	Sequence 31678, A
39	83	0.7	3471	US-09-974-300-2167	Sequence 2167, Ap
40	82.4	0.7	4659	US-10-369-493-42939	Sequence 42939, A
41	80.6	0.7	9399	US-10-369-493-42604	Sequence 42604, A
42	80.6	0.7	18876	US-10-329-079-42	Sequence 42, Appl
43	80.2	0.7	135638	US-10-314-657-1	Sequence 1, Appl
44	79.4	0.7	7925	US-10-282-122A-33350	Sequence 33350, A
45	76.4	0.7	7155	US-10-329-079-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-282-122A-33846
; Sequence 33846, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27

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: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/267,636
: PRIOR FILING DATE: 2001-02-09
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: Remaining prior Application data removed - See File Wrapper or PALM
: NUMBER OF SEQ ID NOS: 78614
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 33846
:
: LENGTH: 6288
:
: TYPE: DNA
:
: ORGANISM: Pseudomonas syringae
US-10-282-122A-33846

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Query Match	1.5%;	Score 172.4;	DB 16;	Length 6288;
Best Local Similarity	43.9%;	Pred. NO. 1.1e-42;		
Matches 1196;	Conservative	0;	Mismatches 1481;	Indels 45;
				Gaps 9;

Qy	3580	CTCATGAGGAGCACTGTTAGACAGTCTTATATCACAAGGCCGAACTATAGTCTTCGATCACT	3633
Db	3125	CACGAGAGATGCCATTGCTCCCGCTGTCGTTTGGCTCAGCAAAACGGCAGTGGTTTTCGCGCCACA	3188
Qy	3540	TGGAAGTTGGCAGTCTGTGATATCTGATTCATATGCTGTGAAATGCGCGGCGCTGTCA	3698
Db	3185	TGGAAGGTGCCAGCGTGTCTTACCAATACCGGCGGGCGTGGCATTCGCGCGCGCTGG	3244
Qy	3700	ATGTCGACGCGTTACGTCGGGCTCTTGACGCGCTTGAACAGCGACACGAGACTCTTAAGA	3755
Db	3245	ATGAGCCCGGCTTGGCAAGATCGTTGAAACCGGATATGGCGCGGTACAGAAATCTGCCCA	3304
Qy	3760	CGACATTTGAAAGACCGAGATGGTGC-----GGGTACAATTGTTCACGAGAGC	3811
Db	3305	CAAGCTTTGTCCAGCAGACCGGGACCACTCCGTGCTGCGATCATCCCGGAGAA	3366
Qy	3811	TTTCTGAGGAATGAGAGTCAATTGATCTCTGTGATTAGACCTTGACCGGTTTGAG----	3866
Db	3365	CAGGCTGCCCTTGCGGCAAGTACATCTCAGACGCAATGCCGATGGCTCGGTGAGTTGG	3422
Qy	3867	-----GTGTGAACCCAGAACAGACTACTCCCTTCATCTCTCATCTGAAGCTGCTGGA	3921
Db	3425	CACGACTGGTGAACGAAAGCCATTAGAGCGCTTGATCTTCAGCAGGAGCCGCTGATTC	3484
Qy	3922	GAGGAGCGCTCTTACGAACTTGTGTGAAGTACACAAATCTCACTATTGTCAATGATTCACA	3983
Db	3485	GAGGAGCGCTGTGTGCTGTGAGCCGATGGAAGACATGTCTGTGTTGACCAATGCCACA	3544
Qy	3982	TCATCTCGAATGAGTGTGATCAATTGATGCTTGCAGCGGATCTCAATGAGCTCTACAG	4041
Db	3545	TCGTATCGGATGCGTGTGCTGATGGGCATTTTGAACGCGGAGTGGGAGCGCTCTACGGGA	3600
Qy	4042	CTGCGCTCAAGAGACTCAAAAGACCGGCTGTACGACTCACTCTCTACCTATCAGTACA	4101
Db	3605	GCGGTGCGCAAGATGAGGCGAGCCCGTTGCGCGCGTGTGATTCAGTACGGCGACTACG	3666
Qy	4102	GCGACTTTGCAAAATGCGAAGAGCACTATCATATGAGCAGAGAAAGCACTCACTACT	4163
Db	3665	CGATGTGGCAACGAAGTGTGTGACCGGCGAGGTATTCACAAAGCAAAACATTCTGCG	3722
Qy	4162	GGAGAAGACCACTCAAAAGACTTCTCCAGCAAAAGATCCGACCGACTTTGCGCGCGCTG	4222
Db	3725	AGACGCGCTCTGCTCGATGCGCGGCAATGTGCTGATTTGCCGCTACCGGTGACGTCTCG	3786
Qy	4222	CACTTCTGTGAGAGACGAGGTGCGTATCATGTTACATCGACGCGAGCTCTACAGT	4281
Db	3785	CGCAACAGGACTATACGGGTGCTGCTGATGCTGTGCTGTGATGCAACGCTGAGCAATG	3844
Qy	4282	CCCTTCGAGCTTCTGCAACGACCAACACGACCTCTTTCGTGCTTCTTACGTGCGT	4341
Db	3845	AGCTCAAGACGTTGATGCGCGGCGACGGGACCACTTTTATGACACTACTGCGGGGT	3904
Qy	4342	TCCGTGCCCTCATTATGCTCTCACAGCTGTTGAAGCGCTGTCAATTGGTACCAATTTG	4401

Db	3905	GGGCAACGGATTAGTCGTTTGGCAGGGACAGATGAGTGGTAATCGATTGCGCGGTGG	3964
Oy	4402	CGAATCCGCAACCCGACTGGAACCTGGAGAGATATATCACTCGGCTGCTTTGTCAATACGACGTGA	4461
Db	3965	CGAATCCGATGAGCGCGAGAGGTTCAGAGGACCTGATCGGATTTTTTTTGGCCAAACCTTGCGGT	4024
Oy	4462	TGCGAATCAACATATGATCATCATACAGATACCTTTTGGGACTTTTGATCAACCAAGTCAGGCTGA	4521
Db	4025	TGCGGGTATGATGTGTCAAGACGACCCGACGGTCGAGGCAATTGTGTAGTCTGATGTAAGGCTT	4084
Oy	4522	CGACGACGACGACATTCGAGAACGAGGATATTCGCTTTGAGCGCGTGTGTATCAGACATAC	4581
Db	4085	GCACGCTGGCGCGCTGATGAACACAGAGATCTGCGGTTCGAGCAGTGTGGAGTTGTCTCA	4144
Oy	4582	AGCCTGGATCCAGAGATCTGTCAAGGACACTCTTCGACAACTCATTTTGGTGCATGCACT	4641
Db	4145	AGCCGGTGGCGAGCTTGTCCCATGCGCCG---TGTTCCAGGGAGATGCTGTCTGGCAC	4200
Oy	4642	CACAGAAAGACCTTGGAAAGATTCAAGTTTCCAGGGTCTCGAGTCCGTAACCTGTGCGCTAGCA	4701
Db	4201	AACATGCCGACGGCGGAACTGCGATGACGGGCTGGAGCTGACGCTGTGTGATTTCCGTA	4260
Oy	4702	AAGCGTA-CACTCGATTTGGACATGAGATTCCATCTGTTTCAAGAAACCGACAGCTTTAAA	4760
Db	4261	GTACGCAACACCAAGTACAGATGTGTCTCGACTTGGCGGAGGTAGAGGGCGGATGCTC	4320
Oy	4761	GGTAGCGTCAACTTTGCCGATGAGCTGTTCAAAATGAGACTGTTGAAAATGTGTGACA	4820
Db	4321	GGTTCGCTGGATATGTGGACCGGCGCTTGTGACAGAAATACGGGCAAAAGCTAGTGGCG	4380
Oy	4821	GTATTCCTTGGATTCTGAGAAAACGGGCTTCAAAAGTTCCGGGACACCAAGTCTCAATCTT	4880
Db	4381	TATCTGGAACGGGTCTGTGCTGCAATGTGAGAACGAGCGCCAGGTATGTGAGGCATC	4440
Oy	4881	CGTTTGACTGATGCACTTGTGACTCTTGAAGAAATTTGATGTCTCAACGTCMAACATGTC	4940
Db	4441	AAGCTCTTTGGCGGAAACCGAACCGCGGGAAGTACTTGTGAGTTCAACGCAACACACAG	4500
Oy	4941	GACTATCCCGGAGATGAGCTTGGCTGATGTCTTCCAGACCCAAAGTCTCTGCTTACCC	5000
Db	4501	GCTTTGGACACGAGATTATGTGCTTCATCAGCTTTTCCAAACAGACGAGCGACAGACACCG	4560
Oy	5001	GATAGTCGGGTGATGGAGACTCCTCGTGCAGATTAACACCGAGTTGGATCGCGAG	5060
Db	4561	CAGCGCTGGCGCTGTGATGTGCGGACGAAACGATGACTTACCGGATCTTCACAAACGC	4620
Oy	5061	TCTGATATTCCTCGCTGATGGCTTCGTGACGGGTCAATGCTCTGACGAGACGCTTGTGCA	5120
Db	4621	AGTATACAGTTGTGTCAATGTCTGTCTGTCACTGGGCAATTGTTGCGACGACCGCGTGGCG	4680
Oy	5121	GTATTTTGGCCCCAGGTCATGTGAGACAAATGTGCGCTTCTTTGTGTGTTGAGGCGAAC	5180
Db	4681	ATCTGTGTGGAACCAAGTGTGAGATATGTGTGGCTTGTGCGGAGATCTGTGAAGCTGGCG	4740
Oy	5181	TTGGCCATATCTTCTCTCGATGTACATTCGCGCTCGGCGAGAGTTACAGAAATATCTTCT	5240
Db	4741	GGTGCATATGTGCGCTGAGACCTTGGGATATCGCTGAGCGGTTGTTTACATGTGAGAG	4800
Oy	5241	GGACTTTTCTGGGCTTACCATTTGTTTATTTGACCATATACAGCGCTCCCGATATGAG	5300
Db	4801	GACAGCGCGCGGTGGCGGTCTGTGTGACGCCGAAACCCGGAGACTGTGGGTGGCGCTG	4860
Oy	5301	GTTATCTAACGTGAGATTGTTCGTATCCGGAGTCCGCTGATGTACAGCAATGACGATGCG	5360
Db	4861	GGTGGCGCTGGAGATGCGGAGTCTGGATCTTGAAAGCGCAATCGGGCGGCTGAAGCTGAG	4920
Oy	5361	TTTGAAGTCATGAGCAGACAGACAAAGCCCTCAGCAGATCTTCGCATATAGTGTCTG	5420
Db	4921	CAT-----GATCGGTGTGTGTGACAGGTACCGCCACAGCACCTGGCTTATGTATC	4971
Oy	5421	TATATCCTCAGGATCCATGCGCCGACCAAAAGGCGCTCATGATTGACACCGGTATATT	5480
Db	4972	TATATCCTCGGGTTGACCGGCGACGCCAAAGGCGCTGATGATTGTGCAATTGGCCATTTGT-	5030

Qy	5481	CGAACAGTCAACAAGTGGCTGTATATACCCAACTATCTCTCGAAACGAGGATGGCT-----C	5535
Db	5031	-GAACCGCCTTTATATGGCCGACGACACTATCGGCTAGTCCGAAACCGCTTTCTTGC	5089
Qy	5536	ACATGGGACCAATTGCGTTTTCAGCGCGCGCATCGTAGAGATCTACAGCGCCCTTTTGTTCC	5595
Db	5090	AGAGACACCGTTCGGGTTTACCGTGTGGCTGGAGTTTCTTCTTGTGCTCGCCG	5149
Qy	5596	GAAGACACTTGTTTTGGCTTGACTACATGACAAACCCTGACGCTTAGAGACTCAAGATG	5655
Db	5150	GTCGGCAATTGGTATGTCGACGTCGCGGAGGCCATCAAGAACCCGAGTATCTGGCCAGT	5209
Qy	5656	TGTTTTCCGAGACATGTCAACGCGGCAAGTCATGTCACAGCTCTTCTCAAGATGAC	5715
Db	5210	TGATCGACAGCTCGGAGATGACGATTTGCACTTTTGTACCTTCATGTTGAGAGCTTCC	5258
Qy	5716	CTCTCCGAGTCCCGAAGAGCTCTCGAAGACCTTGATGTTCTTCTTGGTGTGACAG	5775
Db	5270	TCATTCAGAGTTGGCCCGCTGGCACTGTAGCACTTGGCGCAGAGTGTGTGACGGCAGG	5329
Qy	5776	ATTGACGGGCCCCAGATGCTCTCGATGCGGACGGGACTTTATCAAGGGTCCAGTGTACA	5835
Db	5330	CGTTGCCCTATATGTTTGCMAAAGCACTTCGAGCAACGCTTTGCGCATGTGCAATTGCATA	5389
Qy	5836	ATGGTTACGGCCCCAACAGAGATGAGTCAATGAGTACAACTATATCCACTGACTGACTG	5895
Db	5390	ACCTGTATGGGCTCTACTGAAACCGCTGTGCAATGTCACCTACTTGGCAC---TGCGTCCCG	5446
Qy	5896	AGTCGTTTCATCAATGAGAGTCCCAATTGAGCAGAGCTCTGAAACACTCAAGAGCGTATGTCG	5955
Db	5447	ACCTGCATATACGGGAGATCGTGCCGATGTGGCCGGCCCGTGCACCAATACCGGCGTATCTGT	5506
Qy	5956	TGATTCCTGAGCAACAGCTTGTTGGCAATGTTGTGATGCGAGAGCTTGTTTCACCTGGCG	6015
Db	5507	TGGACCCGCAATGAGAACCGGATCCCGGTTGGCGTGCGGCGGAGATTTTACATCGCGGTA	5566
Qy	6016	ATGATCTTTCGCGGGGCTA---CAATGCAAAAGCCCTTGACGAGAACCGTTTTGTGACA	6072
Db	5567	TACAGCTCGCTCGCGGCTATTGTAATGATGCGCTGACCGCGGAGGAGATTGCGTAAAG	5626
Qy	6073	TTACTGTCAATGACCAACAGTGAAGGCGTATGCGACTGCGGATTCGATGCGGGTATACAGA	6132
Db	5627	ACCGTTTCAGTAAAGCAACCGACGCGCGCGATGTATAGGAGGGGCGGATCTGGGGCGTTGGC	5686
Qy	6133	TTGAGAGATGGCCTCATCGAGTTCTTCGACGATATGAGCAACCAGTTCAAAGATTGTTGGCA	6192
Db	5687	TGGCAGACGTAATATTCAGATATCTGGGACCGCAACGATCAGGTCAAATCTCCGTGGGT	5746
Qy	6193	ATCGTATCGATCAGCTGAGATTGAAGCGGCGCTTCTGCGGCACTCCTCCGTCGAGATG	6252
Db	5747	TCCGTATCGACTGGGCGCACTTGAAGGCGCATCTGGCTGGGTGTGCTGTGCGGAGAGG	5806
Qy	6253	CTGCTGTGTCCTTCAAGACAA	6274
Db	5807	CTGTGTGTGTGCTCCAGAGAGA	5828

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RESULT:
US-10-262-122A-33351
Sequence 33351, Application US/10262122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Habelbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyekind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trewick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
```

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1  APPLICANT: Foresyth, R.
2  APPLICANT: Xu, H.
3  TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
4  FILE REFERENCE: EUTIRA.034A
5  CURRENT APPLICATION NUMBER: US/10/282,122A
6  PRIOR FILING DATE: 2003-02-20
7  PRIOR APPLICATION NUMBER: 60/191,078
8  PRIOR FILING DATE: 2000-03-21
9  PRIOR APPLICATION NUMBER: 60/206,848
10 PRIOR FILING DATE: 2000-05-23
11 PRIOR APPLICATION NUMBER: 60/207,727
12 PRIOR FILING DATE: 2000-05-26
13 PRIOR APPLICATION NUMBER: 60/230,335
14 PRIOR FILING DATE: 2000-09-06
15 PRIOR APPLICATION NUMBER: 60/230,347
16 PRIOR FILING DATE: 2000-09-09
17 PRIOR APPLICATION NUMBER: 60/242,578
18 PRIOR FILING DATE: 2000-10-23
19 PRIOR APPLICATION NUMBER: 60/253,625
20 PRIOR FILING DATE: 2000-11-27
21 PRIOR APPLICATION NUMBER: 60/257,931
22 PRIOR FILING DATE: 2000-12-22
23 PRIOR APPLICATION NUMBER: 60/267,636
24 PRIOR FILING DATE: 2001-02-09
25 PRIOR APPLICATION NUMBER: 60/269,308
26 PRIOR FILING DATE: 2001-02-16
27 Remaining Prior Application data removed - See File Wrapper or PALM.
28 NUMBER OF SEQ ID NOS: 78614
29 SOFTWARE: PatentIn version 3.1
30 SEQ ID NO 33351
31 LENGTH: 9590
32 TYPE: DNA
33 ORGANISM: Pseudomonas syringae
34 OS-10-282-122A-33351

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Query Match	1.4%;	Score 153.4;	DB 16;	Length 9550;
Best Local Similarity	44.4%;	Pred. No. 2e-36;		
Matches 1199; Conservative	0;	Mismatches 1436;	Indels 64;	Gaps 12;

Qy	3587	GGGACCGTGTGAGAGAGCTTAATTATACAAAGGCGGACTGTGTTCCGTGATCGATGTTGGAGGT	3646
Db	3347	GGCAGCGCTGCGCGCTGTGATGTGGCGAGCAGCGGCAATGATCATCTGGCAACTGGAAAC	3406
Qy	3647	TGGCAGCTGTGTGATCTGATTCGATATAGCTGTGTAGAAATGGCGGGGCTGTCAATGTGTGA	3706
Db	3407	GCAACGGCGCGGCTTCACAACTTCCGCTGTGGCGCTGCGCTGCATGGCGGCGCTGTGATGTGCA	3466
Qy	3707	CGGCTTACGTCGGGCTCTTGCAGGCGTTTGAACGGCAACGAGACTGTGTGAAGACACTT	3766
Db	3467	GGCGTTGCGGGGCGCGCTTGAACGCTGTGATCGACGCTGACGAAACCTGCGCCACACACTT	3526
Qy	3767	TGAAGACGAGAGTGTGTCCGTTGTACAAATTTGTTACGAGAGAGCTTTCAGAGAGATGAA	3826
Db	3527	TGAACAGCAGGCGCACGAGCGCTTGACAGTGTGTCAATCCGCGTCCGCTTTGGGCTTCA	3586
Qy	3827	GGTCATTGATCTCTGTGTGTGACGCTTGAACCCGTTTGAAGTGTGAAACCAAGAACAGAC	3886
Db	3587	CGTTGATCAACTGCGCGCTGGGCGAAACGGTGCAGAAAGTATGTGATCTGGAAGTACAG--	3644
Qy	3887	TACTCCCTTCAATCTTCAATCTGAAGCTGGCTGAGAGCGACGCTCTTACGACTTTGGTGA	3944
Db	3645	-CGGCTTTGATCTGCAACATGGGCGCGCTGTTCGGGTCAAGGCTGTGAACTGAGGGA	3703
Qy	3947	AGATGACCAACTCTCACTATTTGTCAATGACATCATCATCTCAAGTGGTTGGTCAATTGA	4006
Db	3704	ACAGAGAACAGCTGCTGGTGGCTGACCCAGCACCAATGCTCTCCGATGGCTGTGTGATGCC	3753
Qy	4007	TGCTTTCGACGCGCATCTCAATCAGCTCTACTCAGCTGCGCTCAAGACTTCAAAAGACCC	4066
Db	3764	GATCATGTTGAGCAGGCTGATGAGTGTCTAACGGCCGC-----CTGCGTGGGTGCG	3814
Qy	4067	GCTGTACGACTCATCTCTTACTTATTCAGTACAGGACTTTTGCAAAATGGCGAGAGGA	4126


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RESULT 3
US-10-282-122A-14471
; Sequence 14471, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
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; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14471
; LENGTH: 10002
; TYPE: DNA
; ORGANISM: Burkholderia mallei
US-10-282-122A-14471

Query Match      1.3%; Score 145; DB 16; Length 10002;
Best Local Similarity 43.2%; Pred. No. 1.1e-33;
Matches 1186; Conservative 0; Mismatches 1515; Indels 42; Gaps 9;
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Db 5379 CGAGCAACCGGTTCAAGCGCGTGCACCGCGATGATGCGCGGCGCTTGCATCGA 5438
Qy 3830 CATTGATCTCTGTGTTAGACCTTGACCCGTTTGAGTGTGTAACCAAG-----ACA 3883
Db 5439 CGATCTGCGGCGGTGCGCCGACCGCGCGCGCGCGCGCGCGATCTTGGCCGGGACGGC 5498
Qy 3884 GACTACTCCCTTCAATCTCTCATCTGAGCTGGCTGGAGACGACTTTACGACTTGG 3943
Db 5499 GACGAGCGGTTGATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5558
Qy 3944 TGAAGATGACCAATCTCTCATTTGTCATGATCATCATATCTCAGATGTTGTTAAT 4003
Db 5559 CGACGACGTGACACCGCTATGCGTGAAGATCATCATGCTGTGCGACCGCTGTGCTGAT 5618
Qy 4004 TGAATCTTGGCGAGCGGATCTCATATGACTCTTACTGAGCTGCGGCTCAAGACTCAAGA 4063
Db 5619 CGAGGTGTTTGGCGGACGTGACGAGTGTGATCGCGCAATTGCGCGCGCGCGCGCGCG 5678
Qy 4064 CCGGCTGTGACACTGACTCTCTTACCTTACAGTACAGCGACTTTCGCAAAATGCGAGAA 4123
Db 5679 CCGGTTCCCGCGCGCTGCGCGGTGACGATACGCGCATTTACGCGGATGCGAGCAAGCGG 5738
Qy 4124 GAACCAATTATAGACGAGAGAGACCACTCACTACTGGAAGACCACTCAAAAGATC 4183
Db 5739 CGGCGGTGCGCGCTGACCGCGAGCGCGAATTACTGGCGCGCATGCGCTCGCGGCGCGCC 5798
Qy 4184 TTCCCGACGAAGATCCGACCGACTTGGCGCGCGCGCGCTTCTGTCTGGAAGCGAGG 4243
Db 5799 GAGCGTGTGAACTGCGCGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 5858
Qy 4244 TTGCGTACATGTTACATCGACGCGGAGCTCTACAGTCCCTTCGAGCTTTCGACGA 4303
Db 5859 GAGGTCGGGCTGCGCTGACCGCGCGCTGACGCGCGCGCTTGGCGCGCGCTGCGCGCG 5918
Qy 4304 ACACAACGACCTCTTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4363
Db 5919 TCAAGCGGCGACCTCTTCAATGACCGGTTTGGCGCGGAGGAGGCTGTGCTGCGCGCT 5978
Qy 4364 CACAGCTTTGAAGACGCTGTCTATTTGTCACCAATTGCGAATTCGCAACCGACTGAAT 4423
Db 5979 GTGCGCGCAACCGAGTGTGATCGGACGCGAGCGCAACCGCGCGCATGCGCGAT 6038
Qy 4424 GAGGATATCATGCGGCTCTTGTTCATTAACGAGTGTATGATCAATCAATAGATCATCA 4483
Db 6039 CGAGGCTTATGCGCTTTTTCGTCACACGATGCGGCTGCGGCTGCGGCTGCGGCGCG 6098
Qy 4484 CGATACCTTTGGACCTTTGATCAACCAAGTCAAGGCTTACGACGACGACGATTCGAGAA 4543
Db 6099 GCGGACGTTGGCGAGCTGCTCGCGCGCGGCGGAGGCGCGCGCGCGCGCGCGCGCG 6158
Qy 4544 CGAGATATTCGCTTTGAGCGCGCTTGTATGACACTACAGCTGTGATTCGAGATCTGTC 4603
Db 6159 TCGAGCATTTCCGTTGAGAGTGTGTCAGCGGCTGACCGCGCGCGAGTCTTCGCA 6218
Qy 4604 AAGCACACCTCTGCGACCACTCAATTTTTCAGTGCACCTCACAGAGGACCTTGGAAAT 4663
Db 6219 TAGCCGCGTTCACAGCATGTTCCGCTGCGAGCAGCGCTCGCGCGCGAGATCGGCT 6278
Qy 4664 CAAATTCAAGGCTCTGAGTCCGATCTGTGCTTACGAAAGCGTATCACTGATTTGACAT 4723
Db 6279 CGAAGGCGTTCGCGCGGAGCGCTCGACGACGCGCGCGCGCGCGCGCGCGCGCGCG 6338
Qy 4724 GAGATTCATCTGTTTTCAGAAACCGACAGCTTAAAGTATGAGTCACTTTGCGCATGA 4783
Db 6339 GAGCGTGTGCTGCGGAGAGCGCGGATGAGTCAACGCGGCTCTCAATATACGAGCGC 6398
Qy 4784 GCTGTTCAAAATGAGACTGTTGAAATGCTCAAGATATTTCTTTGAGATTTCTGAGAAA 4843
Db 6399 GCTGTTGAGCGCGGACGATGACGCGCTTTCGCGGCTTACTCGCGGCTTTCGCGAAG 6458
Qy 4844 CCGGCTTCAAAAGTTGCGGACACCAAGTCTCAATATCTTCTTGAAGTATGATGAC 4903
Db 6459 GATGTCGCGGATGACACGAGCGGCTGATGATTCGATTCGATTCGCGCGACGAAAG 6518
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QY 4904 TCTTGAATAATGATGTTCTCAACGTCACAAATGTCAGTATCCCGAGATTCAGACTT 4963
 DB 6519 GCGCGATCTGATGAGGCGCGGAAACGCGACCGCGCGCGATTCGCGGAAACAGCGCGCT 6578
 QY 4964 GCGTATGTTCTTCCAGACCCAACTCTCTGCTTACCCCGATATGTCGCTGTGTGACATC 5023
 DB 6579 GCAATCGGCTTTGAGGCGCGAGCGCGCGACCGCCGATGCGACCCGATGCTGCAACG 6638
 QY 5024 CTGTGCGCATTTGATGACACCGAGTTGATTCGCGCATGATATTCCTGCGGATGGCT 5083
 DB 6639 GCGGACGACGCTGACATATGCGCGCTGATGCGCGCGCGACCGCATTCGACACGCGCT 6698
 QY 5084 TCGTCGACGCTCAATGCTGTCAGAGACGCTTTCGAGTATTTGCCCCACGCTCATGTA 5143
 DB 6699 CCGGACGCGCGCGTGGCGCGCGCGATTCGCGTGCCTGATCTCAGCGCTGATCGG 6758
 QY 5144 GACATTTGTGCGCTTTCTTGTGTGTGTAAGGCGCACTTGGCCCTATCTTCTCTCATGT 5203
 DB 6759 GCTGCTGCGCGCGACGCTCGCGGTCTCAAGCTCGCGCGCGCTACGTCGCCGCTGATGT 6818
 QY 5204 ACGATGCGCTCGCGCGAGTTCAGATATCTTTGACCTTTCTGAGCTTTCTGAGCTTATGT 5263
 DB 6819 CCGCATTCGCGCGCGCGCGCAAGCGCTTTCGCGCAAGACAGCGCGCGC----- 6868
 QY 5264 TTTGATTTGCGCATGATACAGCGCTCCCGATATCGAGGTTACTAACGTCGATTTGTTG 5323
 DB 6869 --GGCTGTGCTGGCGACCGCGCGCTCGACTGCGCGCGCGCGCGCGCGCGCGCGCG 6926
 QY 5324 TATCCGGGATGCGCTGATGACAGCAATGCAATGCTTTGAGTACTCGACGACGACG 5383
 DB 6927 CGATTCGCGCGCGCTGCTGCC-----GGGCGCGCGCGCTGCGACGCGCGCGCTGCGCG 6981
 QY 5384 CACAAAGCCCTGACGCGACGATCGCATGCTGCTGATATACCTGAGATTCACACTGCGCG 5443
 DB 6982 CCGCATGCGCGCGCGCGAC-AACCGGCAATGATGATGATGATGATGATGATGATGATGAT 7040
 QY 5444 ACCAAAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5503
 DB 7041 GCGGAGGCGGTGCTGCTCAAGATGCGGATGCGCGCGCGCGCGCGCGCGCGCGGTTA 7100
 QY 5504 ACCCAATATCTTTCGAAACGAGATGCTCACATGCGGACCATTCGCTTTGACGCGCG 5563
 DB 7101 TGGACCTTTCGACGCGCTGCGACCGGTTTCGCTTTCGATTCGAAACCGCGCTTCGACG 7160
 QY 5564 ATGTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5623
 DB 7161 GACGTTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7220
 QY 5624 GACAACTTCGACGCTGAGCATCAAGATGTTTTCGAGAGCATGTCACGCGCG 5683
 DB 7221 CGATGCTGCTGATGCTGCGCGCGCTGCGCGGAAAC-TGTGCTGATGCGCGTCACTGCGC 7279
 QY 5684 AAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5743
 DB 7280 TGTTCCTTCAGACGCGCTGTTCAACCGGTGCGGTGCTGATGATGATGATGATGATGAT 7303
 QY 5744 AACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5803
 DB 7338 GCGGCTGCGCTGCTGATCTGCGCGCGAGCGCGCGCGATTCGCGGATGATGATGATGAT 7397
 QY 5804 GCAAGGCTTATATCAAGGCTGACAGTGTATCAATGTTTACGCGCGCAACAGAGATGAGT 5863
 DB 7398 GATGGAAGCGCGCGCGCGCGCGCATGCTGATGATGATGATGATGATGATGATGATGAT 7457
 QY 5864 CATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5923
 DB 7458 GTTCGCGCGCTGCGGAGCGCGCGCGCATGCTGCGCGCGCGCGCGCGCGCGCGATGCGG 7517
 QY 5924 ACGAGCTGTAACAACTCAGAGGCTATGCTGATGATGATGATGATGATGATGATGATGAT 5983
 DB 7518 GCGGCGCATGCGCAATGCTGCTGATGCTGATGATGATGATGATGATGATGATGATGATGAT 7577

QY 5984 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6043
 DB 7578 CCGCGTACCGCGGAGATTCACATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 7637
 QY 6044 A---GGCCTTGAAGAGAACCGTTTGTGACATTAATGATGATGATGATGATGATGATGAT 6100
 DB 7638 ACCGCGCTTTCGCGCGAGCGCTTCGATGCGCATTCGTTGCTGCGCGCGCGCGCGAT 7697
 QY 6101 GTATGCACTGCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6160
 DB 7698 GTACCGGAGCGCGCGCGCGCGCGAT---GGCGCGCGATGCGATGCTGATGATGATGAT 7754
 QY 6161 ACGTATGACACCGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6220
 DB 7755 CCGCGCGCTTTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7814
 QY 6221 GCGCGCTTTCGCGCGATCCTCGCTCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 6283
 DB 7815 GTGCTGCTGATGACAGCGCGCGCTCGCGCGCGCGCGCGCGCGCGCGCGCTGCTGCT 7857

RESULT 4

US-10-282-122A-7449
 ; Sequence 7449, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Onlsen, Karl
 ; APPLICANT: Zyckind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA.034A
 ; CURRENT APPLICATION NUMBER: US/10/282,122A
 ; CURRENT FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-06
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7449
 ; LENGTH: 15450
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-10-282-122A-7449
 Query Match 1.2%; Score 138.4; DB 16; Length 15450;
 Best Local Similarity 44.2%; Pred. No. 2e-31;

	Matches	805	Conservative	0	Mismatches	1001	Indels	16	Gaps	5
QY	3411	TTCTTTCGAACTCGGAGGAAATCTTATCATCTCTATCAAGATG	---	GAACATGCGCAGG	3467					
Db	7561	TTCTTTCGAACCTCGCGCGTCACTTCCCTCAACCCACCGGGGAGTCTCGCGCTCGCCAG			7620					
QY	3468	TCGCTTGATGAGACCTCAAGGTCTCTAACTCAACAGCAGCCGACGCTTGCGGGAA	TT		3527					
Db	7621	GACCTGAGACTGGACGTAACCTTGGCGACTCTGTTCAGACGGGCGGATCTTGGCAGATTC			7680					
QY	3528	TCCCGCGGTGTCAGAGGTGATCTCTG	---	TCTACA	3584					
Db	7681	GCGCCTTCCCTGAGATGCCAGGGCGGAGCGCTGCCCTGTGCTGCAAAATATGCGCGGA			7740					
QY	3585	GAGGAACTGTGGAGCACTTTATTCACAGCGCGACTATGTTCTTGAGATCTTGAC			3644					
Db	7741	GTCCCGCAGCTCCCTTGTGTCCAGTCTCAGCAAGCAATGTGGTTCTCTTGAAATCTGAG			7800					
QY	3645	GTTGGAGCTGTGATGATCTAATTCATATGCTGTGAGAAATGCGGGCCGTCAATGTC			3704					
Db	7801	CTTAAAGCGCGGCTTATCATCTCCAGGCTACGACGTGCGGTGCTCTGAAACAG			7860					
QY	3705	GACCGTTTACCTCGGGCTCTTGACAGCGCTTGAACAGCAGACAGACTTTAGAAGCA			3764					
Db	7861	CGCGCGTTGACAGCAGCGCTTGCATTTGGTGTGCTGCGCCACAGAACCTTGGCACCCCG			7920					
QY	3765	TTTGAAGCCAGATGCTGCGGTGTCMAATTGTTACAGAAAGCTTTCTGAGAGATG			3824					
Db	7921	TTTCGAGGAGTGCAGCGGTCAAGCGCGGCAGACGATCTCGGAAATGCTCCGTCGCA			7980					
QY	3825	AAGGTCATGATCTCTGTGTTCAGACCTTGAACCCGTTG	---	AGGTGTTAA	3881					
Db	7981	GTCTTGAGGATTCGCGCGGGGCGAGCAACAAAGTTGCCACAGCGGGTGGCCGAGAA			8040					
QY	3882	CAGACTACTCCCTTCAATCTCTCAATCTGAAGCTGGCTGAGAGGACGCTTTACACT			3941					
Db	8041	ATCCGCCAGCACTTGCACCTTGGCTGTGGGCGCTGTCGCGGTGCGCTCTCGGCGCTG			8100					
QY	3942	GGTGAAGTGAACAATCTCTCAATATGTCATGCAATCATCTCAGATGATGTTGCA			4001					
Db	8101	GCTGGGCGAGGACGATGTTGTGATCAACCCAGACCAATATGTTGTCGACGGTTGGTGC			8160					
QY	4002	ATTGATGCTTGGCAGCGGATCTCAATCACTCTAATCACTGCTGAGCTCAAGATCTCAAA			4061					
Db	8161	ATGCAAGGTGATGTCAGAACCTGCTCAAGGCTCATGCGGGGCGCGCGGCGGAACAA			8220					
QY	4062	GACCGGCTGACGACTCACTCTCTACTATTCACGTAACAGCACTTTGCAAAATGCGAG			4121					
Db	8221	CCGAGCGCTGCGCAATTCAGACCTGAGACGCCCACTATGCTGCTGGCATGCGGCTTGG			8280					
QY	4122	AAGGACCAATTCATAGAGCAGAGAGCAATCTCAACTCTGAGAAAGCACTCAAAAGAC			4181					
Db	8281	CTGGAACAGCGCGGAGGGCGCGCGGAGCTGGAATTACTGGCGTAGCGCTGGGGCGCGAG			8340					
QY	4182	TCTTCCCGAGCAAGATCCCGACCGACTTTGCCCCGCTGCACTTCTGTCTTGAGAGCGCA			4241					
Db	8341	CAGCCGGCTCTGGAATCTGCCCGCAGCCGGGTGCGCCCGGCCACAGGCAAGCGCGAG			8400					
QY	4242	GGTTGCGGTAATGTTACATGACATGACGCGGACGCTTACACATGCTCCCTTGACGCTTTCTGCAAC			4301					
Db	8401	CAGCGTCTGGAACATAGCGCTGCGGCTGTCATTTATCGAGAGAGCTGCTGGGCTTGCGCCGG			8460					
QY	4302	GAACACAACAGACCTCTTTGCTGCTTTCTTAGCTGAGTTCGCGACGCTCATTTATGCT			4361					
Db	8461	CGGAGGGGTGACACCCGTTTATGCTTTATTTGGCTGTTCCAGGTGCTGTGAAGGCG			8520					
QY	4362	CTCAACGCTGTTGAAGAGCTGTCAATGTTGTAACCAATTGCGAATGCGAACCGACTGAA			4421					
Db	8521	TATAGCGGGCAGTGCAGACATTCGCGTGGGGTAACTTACGCCAACCGCAACCGCGCGAG			8580					
QY	4422	CTGGAAGATATCATTCGGCTGCTTTGTTCAATACGACAGTATGCGAATCAATAGATCAT			4481					
Db	8581	GTGACGCGCTGATTCGGTCTTCTGTCAATACCAAGGTGCTGCGTTGCAAGTGCATGCT			8640					

Qy	4482	CAGATACCTTTGGGACTTTTGATTAACCAAGTCAAGGCTACGAGACAGACGATTCGAG	45411
Db	8641	GGCTGGCTTTCCGGCATCTACCTGAGCCGGGTGGCGGAGCGGCGCTGGGCGCCGACGC	87000
Qy	4542	AACGAGATATTTCCGTTTGAACGGCTGTATACGACCTACAGCCTGATCCAGATCTG	46010
Db	8701	CACCAAGATCTGGCGTTTGAAGCAATTGTGGATGCTCTTGACGCCGAACGCA-----ATC	87555
Qy	4602	TCAAGCACACCTCTCGGACAACATCATTTTTCAGTGCATCTCACGAAGAGACCTTGAAGA	46610
Db	8756	TCAGCCACACACCGCTTGTTCAGAGTGTATGATTAACACACAGAGGGGAGGAGGAGATG	88150
Qy	4662	TTCAAGTTCCAGGGGTTCGAGTCCGTAACCTGTGCTGTGCA--AAGCGTACACTGATTTG	47190
Db	8816	CCCAAGTCGATGAGTTTGACATCGAAGGTTTGGCTGGAGATGAGTCTGCCACAGTTTC	88755
Qy	4720	ACATGAGTTCATCTGTTTCAAGAAAACGACAGCCTTAAAGTAGGCTCAACTTTGCCG	47790
Db	8876	ATCTTGCCCTGATACCTGGGAAACCCCGGACGGCTTTGGGGCGGCGCTGACTACACGA	89350
Qy	4780	ATGAGCTGTTCAAAATGGAACACTGTGAAAATGTCGTACAGTATTTCTTTGAGATTCTGA	48390
Db	8936	CCGACCTGTTTCAGGCGCGGACCGCTCAGGCGCATGCGCGCATTTGCGAAGACTGCTGC	89950
Qy	4840	GAAACGGGCTTCAAAAGTTCGGGACACACAGTCTCAATCTTCTTTGACTGATGGCAATG	48990
Db	8996	GCGGCATGCTGGAAGAACCCCGACGGCCAGCGTCCACTGCTGCCATCTCGATGCCAGG	90555
Qy	4900	TGACTCTTGAAAAATTGATGTTTCTCAACGTCAAAACATGTCGACTATCCCCGAAATCGA	49590
Db	9056	AGCGTGGCCAGTTGCTCGAAGGCTGGAACGCGCACTGCCGCGGATACCCGCTGCAACGCG	91150
Qy	4960	GCTTGGCTGATGTTCTTCCAGACCCAAATCTCTGCTTACCCCGATAGTCTGGCTGTGGG	50190
Db	9116	GCGTGACACGGGTGTTTGAGAGAGGAGTTCGAGCGCACGCGACGCGCGCGCTGGCCT	91750
Qy	5020	ACTCCCTGTCGCCGATTTGACCTACACCGAGTTGATTCGCCATGATATTTCTCGCTGGAT	50790
Db	9176	TCGGCGAGGAACGCGCTGATCTACGCCCGACGTGAACCCCGGGCCAAACCGCTGGCGATG	92350
Qy	5080	GCGTTCGTTCGACGGTCAATGCTTCGACAGACGCTTGTTCGACGATATTTGCCCCACGTCAT	51390
Db	9236	CCCGATTCGAGCGCGGGGTGCGTGCAGACGCGCTGTGGGGGTGGCCATGAGAGGTTCCA	92950
Qy	5140	GTGAGACAATTGTCGCGCTTCTTTGTGTGTGTAAGGGGAACCTTGGCCATTTCTCTCG	51990
Db	9296	TCGAGAGTGTGTGGGCTCTGATGGCGATCTCAAGGCGCGGCGGCGCTCACTGTCGGGTGG	93550
Qy	5200	ATGATGATGTCGCCCTTCGGCGAG	5221
Db	9356	ACCCGAGTACCCGAGAGAGCG	9377
RESULT 5			
US-10-156-761-3630			
: Sequence 3630, Application US/10156761			
: Publication No. US20030119018A1			
: GENERAL INFORMATION:			
: APPLICANT: OMURA, SATOSHI			
: APPLICANT: IKEDA, HARUO			
: APPLICANT: ISHIKAWA, JUN			
: APPLICANT: HORIKAWA, HIROSHI			
: APPLICANT: SHIBA, TADAYOSHI			
: APPLICANT: SAKAKI, YOSHIYUKI			
: APPLICANT: HATTORI, MASAHIRA			
: TITLE OR INVENTION: NOVEL POLYNUCLEOTIDES			
: FILE REFERENCE: 249-262			
: CURRENT APPLICATION NUMBER: US/10/156,761			
: PRIOR FILING DATE: 2002-05-29			
: PRIOR APPLICATION NUMBER: JP 2001-204089			
: PRIOR APPLICATION NUMBER: JP 2001-272697			

QY	5582	CGCCCTTTTGTTCGGAAGGACACTTTGTTGGTTGACTACATGACACACCTCGAGCGTAG	5641
Db	3885	GGCCCGCGTGTACCGGGCAGCGCGTCTTCTGCTCCGACGAGCACCGACATGTCCGA	3944
QY	5642	AGCACTCAAGANTGTGTTTTTCCGAGAGCATGTCAACCGGCAAGTCATGTCACAGCTC	5701
Db	3945	GCTGGGCAAGGGCTCGCGGAGGGCCACGCCGTTTCACTGTTCTCAAGCTGACCCGGGCA	4004
QY	5702	TTCTCAAGATGTACTCTCCGAGTCCCGAGAAGGCTCTGAGAACTTTGATGTTCTT	5761
Db	4005	CCTGACATCTCGCCCTCCAGCTACACCCGGCCAGCGGGCGCGCTCGCGCGGTCT	4064
QY	5762	CTTGTGTGTACAGATTTCACGGGCCCAAGATGCTCTGATGC---GCAGGACATTATCA	5818
Db	4065	GGTGTGTGGCGGGCAGAGGGTTCACCCCGGCCACCTTGAGGGCTGCGCGGCACTCGCCCC	4124
QY	5819	AGGGGTCAAGTGTTCACATGGTTACGGGCCCAAGAGATGGAGTCATGATTAACAATCA	5878
Db	4125	GGACACCCGGCTGATTCACAGAGTACGGGCGCACGAGGCGTCCGTGGGACAGCGTGT	4184
QY	5879	TCCATTGACTCGACTGAGTGGTTTCATCATATGAGTCCCAATTGGAACGAGCTTGCACAA	5938
Db	4185	CGAATTTCCGAGCATG---CCGAGCGCGAGTACTGCGCATCGGACGCGCGTCCCA	4241
QY	5939	CTCAGAGCGTATGTCGTGATCCTGAGCAACAGCTGTGTGGCATTGTGTGATGGAGA	5998
Db	4242	CATCGGGGTGTACGTTCTCGACCCGCGCTCAACCGCGTCCCGGTGGGGTGTGCGCGGCA	4301
QY	5999	GCTTGTGTACATGCGCATGTGCTTTCGCGGGGGCTACAGTACAAAGCC-----CTTGA	6052
Db	4302	GCTGTACGTGGCGGACAGGGTGTGGCGCGGGCTACCGAAACCGCCCGACCTGACGCG	4361
QY	6053	CGAGAACCGTTTTGTGCACTTACTGTCAATGACACAGACTGAAGGCGGTATCGACATGG	6112
Db	4362	CGACCGGCTCTCGCCCGACCCGTCAGGACCGGCGCCCGGCGCGCATGTACCGACCGG	4421
QY	6113	CGATCGAGTGGCGGTACAGGATTGAGATGAGCTCATCGAGTTCTTCGAGCGTATGACAC	6172
Db	4422	CGACTGTGTCCGCAC---CTCCGGAGAGGGAAGTGCGCTTCTCGCGGGGTGACGA	4478
QY	6173	CCAGTTCAAGATTGTGGCAATGCTATGAAATCAGCTGATGGAAGCGGCCCTTTCTGCG	6232
Db	4479	CCAGGTCAAGATCCGCGGCTATCCGTCGAACCTGGCGAGATTCAGAGCGCTGTGCAGAC	4538
QY	6233	CGATCTCTCGGTCCGAGATGCTGCTGTGTCCTTCAGACGATATGAGA	6280
Db	4539	GCACCCCGCGTCGCGCAGCGCGTGTACCTGACCTGTGACCGGCGCAGAA	4586

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RESULT 6
US/10-156-761-1/c
Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OR INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 1
LENGTH: 9025608

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? TYPE: DNA
? ORGANISM: Streptomyces avermitilis
? FEATURES:
? NAME/KEY: misc_feature
? LOCATION: (4187715)
? OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

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Query Match	1.2%;	Score 134.8;	DB 15;	Length 9025608;
Best Local Similarity	43.7%;	Pred. No. 4e-28;		
Matches 1175;	Conservative	0;	Mismatches 1457;	Indels 56;
				Gaps 11;

OY	3612	AAAGCCGACATAGGTTCTCGGAATCAATGTAAGCTTGAGCAAGTCGTGTATTCGATTCCA	3671
Db	4514351	CAGCGCGGCTCTTGTTCTTGGAACCGAATGACCCCGGACGCCCGATGGGTGCGCCCG	4514292
OY	3672	TATGCTGTGAAGATGCGCGGCGCTGTCAATGTGCACCGCTTACGTCCGGGCTCTTGCACGC	3731
Db	4514221	CTCTTCTGTGGCGCTCCGGGGTTCCTGTGAAGCGCGGACCGTGGGCGGGGCGCTTGGAACGC	4514222
OY	3732	CTTGAAACGCGACACGAGACTCTTTAGAACCAATTTGAAGACAGATGGTGTCCGTGTA	3791
Db	4514231	CTCCGCCCGCGCACGAGCCGCTGCACCCGCTACCTGCACACGAGGCGCGACGCGCG	4514172
OY	3792	CAATTTGTTCACGGAAGCTTTCTGAGAAGATGAAGTCAATTGATCTCTGTGTTACAGAC	3851
Db	4514171	CAGATCATCGACGCGCGCGCGCGGACCGGTGAGCTGCGCTGCGAGACACCGCCCG	4514112
OY	3852	CTTGACCCGTTTGAAGTGTGGAACCAAGAAACAGACTCTCCCTTCAATCTCTCATCTGAA	3911
Db	4514111	GACGGGGTGGCGCGCTCTTGCGGCGACAGTTGAGGGGGCTTGCACCTTGCGCGGGC	4514052
OY	3912	GCTGGCTGGAAGCGACGCTTTACGACTTGTGTGAAGATGACCAATCTCATTTATGTC	3971
Db	4514051	CCGCTGTGGCGCGCTGTGCGCCCGGATGCGCGGAGAACATGTCTCTCTGACG	4513922
OY	3972	ATGATCATCATCTCAGATGTTGGTTCAAATTGATGTCTTGGACCGGCATCTCAATCAG	4031
Db	4513991	ATGATCATCATCACTTCGACGCGGTGTGACGGTATCTTGGAACGGAGCTGCGGAG	4513932
OY	4032	CTTCACTCAGCTGGCGCTCAAGAACTCAAAAGACCGCGTGTACAGACTCATCCTCTACT	4091
Db	4513931	CTGTGCGCGCC-----GACCGGGCGGCGCGCGCGGACCTGCGGAATGCC	4513881
OY	4092	ATCCAGTACAGCGACTTTGCAAAATGCGAGAAAGCAATTCATTAAGACAG-----GAG	4145
Db	4513880	CTCAGTACGCGGACTACAGGCTCTCGGACAGGTTGCCGCTCACGACGCGCGTGTGAG	4513821
OY	4146	AAGCACTCAACTGAGGAAGAACACTCAAGACTCTTCTCCGAGAAAGATCCGAC	4205
Db	4513820	GCGCAGCTGACCTCACTGGCGCGCGCCTCGACAGGACTCGCCGCGCTGCATCCCGCC	4513761
OY	4206	GACTTTGCGCGCCCTGCACTTGTCTGTGAGAGCGACAGTTGCGTACATGTAACATGAC	4265
Db	4513760	GACCAACCCCGCGCGCGGTGATTCGCGCGCGCGGATCGTACCGTTTCGGGTGCG	4513701
OY	4266	GCGCAGCTCAACAGTCCCTTCGAGCCTTCTGCACCAACAAACAGACCTCTTTCGTC	4325
Db	4513700	CCCGAATCCGCGCTCAAACTAGCCGAATGGGCGGACCCACCGCGCACCCCGTTATG	4513641
OY	4326	GTTCTTGTAGCTGCGTCCGTGCGGCTCATTTATGTCACAGCTGTTGAAGACGCTGC	4385
Db	4513640	ACGCTGTGACGCGGTGACGCCAGCTGTGCGCCGACACCGGCGAGTGGGAGTCCCG	4513581
OY	4386	ATTGTGACCAATTTGGGAATTCGAACCGACCTGAACTGAGAGATTAATTCGTGGTTT	4445
Db	4513580	GTCGGACCCCGGTGGCGCGCGCGCACCCGCGCGAGACCAAGATGTTGGGTTCTTC	4513521
OY	4446	GTCGAATACGAGTGTATGCGAATCAATAGATCATCAGATATCTTTGGGAACTTTGATC	4505
Db	4513520	CTCAATCTCTCTGTGTACGTGTGGGCTCACCGCGAATCTGGGCTTCAACGAGGCCCTG	4513461
OY	4506	AACCAAGTCAAGGCTACGACGACGACGACTTGGAGAACAGAGATATTTCCGTTGACGC	4565

Db 4513460 CGCCGGGTGAGGAGCGGGCCGCGCCCTCTCCACGAGGAGCTGCCCTTCGACGG 4513401
Qy 4566 GTTGTATCAGACACTACGCTTGATCCAGAGATCTGTCAAGACACCTCTCGACAACTC 4625
Db 4513400 CTGTCGAGAGAGCTTCAGCCCGAGCGC---GACCTGTCCGACACCCGCTCTACAGGTG 4513334
Qy 4626 ATTTTTCAGTGCATCAGACAGAGACCTTGAAGATTCAAGTTCCAGGGTCTCGAGTCC 4685
Db 4513343 GCGCTTCAGCTGCACAGCGAGGGGCTGACCGAGCTCTCACCATTACAGTACAGTCTGGCC 4513284
Qy 4686 GTACCTGTGCTAGCAAGCGTACACTGATTGACATGAGATTCCATCTTTCAAGAA 4745
Db 4513283 GCGTTCGCCAGAGCGCTGCGAGGTGCGAAGACCGATCTGTGCTTCAATGCGGCAACG 4513224
Qy 4746 ACCGACAG---CCTTAAGGATGAGCGTCACTTTGCCGATGAGCTGTTCAAATAGAGACT 4802
Db 4513223 CCGGACGGCTCTCCCGAGCGGGGTCTGAAATGCGCACCTGCTGTTTCGAGCGGGGACCC 4513164
Qy 4803 GTTGAATAATGTCTCAGAGATTTCTTGAAGATTCTGAAGAAACGGGCTTCAAAAGTTGCGGG 4862
Db 4513163 GCGGAGCGCATGACCGGCACTTCTCACCCTCTCCAGACAGGTGGCCGAGACCGCGAG 4513104
Qy 4863 ACACCAATCTCAATCTTCTTGAATGAGTGGCATTTGTGACTTTTGAATAATTTGAGTGT 4922
Db 4513103 ACCCGGCTCGGCGCTCTGAGAGTGTCTCGCGCGACGACGACCGCCCTCTCTGTCGAG 4513044
Qy 4923 CTCAGAGTCAAAACATGTGCAATATCCCGAGAAATCGAGCTTGGTGAATGTTTCAGAGC 4982
Db 4513043 TGGAAACACA---CGGCGGAGACACCGAGACCGTACGGTCTTCGAAAGCTTCGAGAG 4512987
Qy 4983 CAAATCTCTCTTAAACCCGATGATCTGTGTGTGTGAATCTCTGTGCGCAATTTGACTAC 5042
Db 4512986 CAGGCGCGGACGCGCCCGGACCGACCGCTGACCTTCCGACCGAGACCGGTACATAC 4512927
Qy 5043 ACCGAGTTGATCGCCAGTCTGATATTTCTGCTGATGAGTGGTCTGTCAAGCTCAATGCT 5102
Db 4512926 GGGGAACTGAGACCGCGGCGCAACCGGCTGCGGAGACCTGCGCACCCGCTGTGCGGC 4512867
Qy 5103 GCAGAGACGCTTGTGCGAGTATTTGCCACGCGTCAATGTGAGCAATTTGCTGCTTCTT 5162
Db 4512866 GCGGAGTCAAGCGCTGCGGCTCTGCTGACCGGGGTCCGAACTGTCTACCGCGCTCTC 4512807
Qy 5163 GGTGTGTGAAGGGAATTGGCTTATCTTCTGATGATGATGATGATGATGATGATGATGAT 5222
Db 4512806 GCGGTGTGAAGGCGGCGCGGCTTATGTGCGGTGACCGGTCTTACCGGCGGAGCGC 4512747
Qy 5223 GTTCAAGATATCTTCTGCACTTCTGCGGCTTACATGTTTGTGATTTGGCATGATACA 5282
Db 4512746 ATCGCGGCGA-----TGTGCGACACGCGCGGCGTACGACGCGGCTGAC 4512703
Qy 5283 GCGGCTCCCGATATCGAGGTTTACTAAGTCAATGTTGCTGATCCGGGATGCGCTGAAT 5342
Db 4512702 CACTTCGCGTACGCGGCGCGCTTCACTCTCCGCGACCGCGCTGCTCTCTGAGAC 4512643
Qy 5343 GACAGCAATGAGTGCCTTTGAAGTATCGAGACGACAGACAAAGCCCTCAGCGACG 5402
Db 4512642 GGAACGCGAGACATGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4512583
Qy 5403 A-GTCTGCGATAGTGTCTGATATCTGAGATTCATCTGCGCGACCAAAAGGCGTCAATGAT 5461
Db 4512582 ACGGCTGCGTACACATCTTTCACCTCGGCTGACCGGCGACACCAAGGCGCGTCAAGT 4512523
Qy 5462 TGAGCAACGCTGTCTATTTGAACAGTCAACAGTGGGCTGTATACCAATCTCTTCCGGA 5521
Db 4512522 CACCCACAGAGGTTCCGCAACACGTCGCTGGCGCGCGCGGCACTCGCGGCGAGGA 4512463
Qy 5522 AACGAGATGCTCAGATGCGGACCATGCGCTTTGAAGCGCGCATCTGACGATCTACAG 5581
Db 4512462 CTACGCGGGGCGCGCTGTTCTCTCGCGCGCGCTTGAACCTGTCGTCGCGCAACGCTGTG 4512403
Qy 5582 CGGCTTTTGTGGAAGACACTTGTGTGCTGATCAATGCAACCTCGACGCTAG 5641

Db 4512402 GCGCGCGCTGTGATACCGGCGAGCGGCTGTTCTCTGCTCCGCGAGACACCGCATGTCCGA 4512343
Qy 5642 AGCATCAAGATATGTGTTTTCGAGAGCATGTCAAACGCGCAAGTCAATGTACAGCTTC 5701
Db 4512342 GCTGGGAGAGCGGCTCGCGAGGCGCCAGCGCTTACAGTTGTCAAGTGAACCCCGGCGCA 4512283
Qy 5702 TTCTCAAGATATCTCTCTCGAGTCCCGAAGAGCTCTCGAAGAACTTGAATGTTCTTCT 5761
Db 4512282 CTTGCAATCTCGGCTTCAAGTCAACCGCGCGCGCGCGCGCGCTGCGCGGCTGT 4512223
Qy 5762 CTTGTGTGACAGATTCGACG 5818
Db 4512222 GTGTGTGCGGCGGAGCGCTTCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4512163
Qy 5819 AGGAGTCAAGTGTTCATATGAGTTCAGCGCCCAACAGAGATGAGTCAATGATCAATCTA 5878
Db 4512162 GGAACCGCGCTGATCAACAGATACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4512103
Qy 5879 TCCCATTTGACTGACATGATGCTTCAATGAGATTCATGAGTCCCAATGAGTCAAGTCTGA 5938
Db 4512102 CGAATTTCCGAGCATG---CGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 4512046
Qy 5939 CTCAGAGCGTATGTGTGATCTGAGATCTGAGCAACAGCTTGTGCGATTTGATGAGGAGA 5998
Db 4512045 CATGCGGATGTAGTCTCTGACCTCGGCGCTTCAGCGCGCGCGCGCGCGCGCGCGCG 4511986
Qy 5999 GCTTGTGTCTACTGCGAGATGCTTTCGCGGCGGCTCAAGTCAAAAGCC-----CTTGA 6052
Db 4511985 GCTGTACGTGCGGCGCGCGGCTGTGCGGCGCGCTACGCGAACCGCGCGCGCGCGCGCG 4511926
Qy 6053 CGAGAACGTTTGTGTGCAATTAATCTCAATGACAGACAGATGAGAGCGTATGCACTGG 6112
Db 4511925 CGACCGCTTCTCCG 4511866
Qy 6113 CGATGAGTGCAGTACAGATGAGTGGCTCATGAGTTCATGAGTTCCTGCGAGTATGAGAC 6172
Db 4511865 GCACTGTGTCCGCGC---CTCCGAGCGGAAAGTGTGCTCTCTGCGCGGCTGACGA 4511809
Qy 6173 CCAATCAAGATTCGTCGCAATGTATGCAATGAGTCAAGTGAAGAGCGGCTTCTGCG 6232
Db 4511808 CCAAGTCAAGATTCGCGGCTATGCGGTGCAATCTGCGGAGATCAAGCGCGTGTACAGC 4511749
Qy 6233 CGACTCTCTGCTCGAGATCTGTCTGTCTTCAAGCAATGAGGA 6280
Db 4511748 GCAACCGCGCGCTCGGAGCGCGGTGTCAACCGCGCGCGCGCGCGCGCGCG 4511701

RESULT 7
US-10-282-122A-30194
; Sequence 30194, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727

;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 30194
;; LENGTH: 3954
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
US-10-282-122A-30194

Query Match 1.2%; Score 133.8; DB 16; Length 3954;
Best Local Similarity 46.8%; Pred. No. 2,2e-30;
Matches 528; Conservative 0; Mismatches 552; Indels 9; Gaps 3;

QY 3472 TTGGTATGACCTTCAAGGTCTTAACATCTAACAGACCCGACGCTTGGCGGAATTTCCG 3531
DB 593 TCGGTATCGAAGTCAGCCTGAAGAGCTTTTCGAGCAGCGGTCCTGACAGGATTCGTG 652

QY 3532 CGGTCCGTCAGAGGTGATCTCTGTCTTCACTCTCATCCCAATCACTCATGAGGAC 3551
DB 653 AGAGCCCTGGGCGAAGAACCCGCGAGGTTCCGCGATCAGCCCGTTACCCGACGAGC 712

QY 3592 CTGTGAGCAGTCTTATTCAAGAGCCGACATAGTTCCTGATCAGTTGAGCGTTGGCA 3651
DB 713 CGGTCCGTTGTCTTATGACAGAGCGCAGTGTCTCTCTGCAATTGGAAACCGAGA 772

QY 3652 GTCTGTGATCTGATTCATATGCTGTGAGAAATGCGCGGCGCTGTCAATGTGACGCGT 3711
DB 773 GCGCGGCTATCATATCCGCGCGCTGCGCTTGGCGGCGGCGCTGATGTCTGCGCG 832

QY 3712 TACGTGGGCTCTTGACGCGCTTGAAGAGACACGAGCTCTTGAACGACATTTGAAG 3771
DB 833 TACAGCGCATTTGAGAGCGCTCGCACAGGCTCAAGTGTGCGTACCCGCTTCCGCC 892

QY 3772 ACCAGATGATGTGCGGTGTAACAATTGTTACAGAGAACTTTTGAAGATGAAGTCA 3831
DB 893 AGGAGGCTCGCGTACCGTTCAAGGTGTGAGCGCCGATGGGCACTTCCCGCGC 952

QY 3832 TTGATCTGTGTGTTGACCTTGACCCGTTTGAAGTGTGAACCAAGAAAGA---CTA 3888
DB 953 ATAACTGGGAATGTGATGAGCGCTGCTCAGAGGGGAGTGAAGCGGAGATGCGCA 1012

QY 3889 CTGCTTCAATCTCTCATCTGAAGCTGCTGAGAGGAGCGCTTTCAGACTTGTGTAG 3948
DB 1013 GGGCCTTTCGACCTAAGAGCGATGCGTGTGCGGATCAGTCTTGAAGTGTGCTCGA 1072

QY 3949 ATGACCATCTCTCATATTGTGATGATGATCATCATCTGAGATGTTGGTCAATTGATG 4008
DB 1073 ATGACCATGTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1132

QY 4009 TCTTGGACGCGATCTCAATCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 4068
DB 1133 TGATGTGCGAAGAGCTGTGCTCAAGCTTATGCGCTCAAGCAGAGGCGCGAAGCGGCC 1192

QY 4069 TGTGACGACTCATCTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 4128
DB 1193 TGCGGCGGCT---GCCATACAGTATCGGATGTGCGCTGTGCGACGCGGAATGTG 1249

QY 4129 AATTGATAGAGCAGAGAGCACTCAACTGAGAGAGCACTCAAGACTCTTCCC 4188

DB 1250 AGGCGGAGAGAGAGAGCGCCAGTGGCGTATGATCGGCTGTGGGTGGCAACAGC 1309
QY 4189 CAGCAA---AGATCCGACCGACTTGGCCCTTGCATCTGTCTGAGAGACGAGTT 4245
DB 1310 CGGTGTGAGAGCTGCGGTGTGATGCTCCGCTCTGGAGAGAGCTTTCCGCGCGC 1369
QY 4246 GCGTACATGTTACATCGACGAGGAGCTTACAGTCCCTTTCAGCTTCTGCAACAGAC 4305
DB 1370 GCGTGAAGTTCAACTGCGGCGGAGCGGAGCGGCTGGAAGCGCTTCCCAAGGC 1429
QY 4306 ACAACAGACCTTTCGTGTTCTTCTAGCTGCTTCCGTGCGCTCATATCTCTCA 4365
DB 1430 AGGTGAGATACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1489
QY 4366 CAGCTTGAAGAGCGCTGTATGCTATGATCAACCAATTTGGATTCGCAACCGACTG 4425
DB 1490 GCGTCACTGCGATATCCGTGCGGCGTGGCGGCTGCGCAATCCCAACCGGTCGAA 1549
QY 4426 AGGATATCATCGGCTGCTTGTCAATACGAGTGTATGCGAATCAATGATCATCAG 4485
DB 1550 AGGACTGATCGGCTTCTTCTTCAACACCGAGTGTCTCAAGCGGACATGATGAGCA 1609
QY 4486 ATACCTTGGGACTTGTATGATCAACCAAGCTAAGCTAAGAGACAGACATTGAGAAC 4545
DB 1610 TGGGGTTCGACCACTTGTCTGACACAGGTTGCCAGCGCTGCTGAGAGCGCAGCG 1669
QY 4546 AGGATATCCGTTTGAAGCGGCTGTATCAGACTACAGCTGATTCAG 4594
DB 1670 AGGACTTGCCTTTCAGAGCACTGTGAGACCTTTCAGACCGAGCGCAG 1718

RESULT 8
US-10-282-122A-33871
; Sequence 33871, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Twawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OR INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33871
; LENGTH: 2811
; TYPE: DNA
; ORGANISM: Pseudomonas syringae
US-10-282-122A-33871

Query Match      1.2%; Score 129.6; DB 16; Length 2811;
Best Local Similarity 44.5%; Pred. No. 3.8e-29;
Matches 851; Conservative 0; Mismatches 1024; Indels 37; Gaps 7;

QY 4359 CGTCTCAGACCTGTTGAAGCGCTGTGATGTAACCAATTGGGAATCGCAACCGACT 4418
DB 100 CGGTTACGGGGAGATGAGTGTGATGGGCACACCGGTGGCAATCGCCGAGC 159
QY 4419 GAATGAGATATATATCGGCTGCTTTGTCAATACGAGTGTATGCGAATTCACATGAT 4478
DB 160 GAATGAGATATATATCGGCTGCTTTGTCAATACGAGTGTATGCGAATTCACATGAT 219
QY 4479 CATACGATATCTTTGGGACTTTGATCAACCAAGTCAAGGCTACAGACAGCATTC 4538
DB 220 GGAAGCTGAGCGCGCGCGCTTCTGAGAGAGTCAAGCGGCTCATGCTGGCGGCAT 279
QY 4539 GAGAACGAGATATTCGCTTTGAGCGCGGTGTATCAGCACTACAGCTGATCCAGAT 4598
DB 280 GCGCATAGAGACCGCGCTTGCAGACAGTGTGTGAGGCGTGTGAGC---ACCGCGAGC 336
QY 4599 CTGTCAAGCAACCTCTCGCAACACTATTTTGCAGTGCACCTACAGAAAGACCTTGA 4658
DB 337 CTGGCCCATATGCCGATCTTCAGGTATGCTGGCGCTGAACCAACCCCGCGCGCGC 396
QY 4659 AGATTCAAGTTCAGGGTCTCGAGTCCGTAACCTGTGC---CTAGCAAGCGTACACTGA 4715
DB 397 GAATCAGCTGCGCGAGCTGAGCGTGAAGCGCGTGCMAAGCCGCGACAGACAGCCAG 456
QY 4716 TTGTACATGAGTTCATCTGTTTCAAGAAACCGACAGCTTAAAGTACGTCACCTT 4775
DB 457 TTGCACCTGTGCTTTCATCTGTGAGGCGAGGAGGAGGAGTGTGCTGCTCTGGAATAC 516
QY 4776 GCGCATAGCTGTCAAAATGAGACATGTTGAATAATGTCAGAGATATCTTTGAAT 4835
DB 517 GCGAGCATCTGTTCAGCGGTGCGACATGATGATGAGGAGGAGATTTGCAAGTCTT 576
QY 4836 CTGAGAAACGGGCTTCAAGTTCGCGGACACCACTCTCAATCTCTTGTGATGATGCG 4895
DB 577 CTGAGAAAGATGATGAGGAGATGACCAACAGCGGTTCGAAATCTACCGCTGTCTGC 636
QY 4896 ATTGTGACTTTGAAAAATGAGATGTTCTCAACGTCAAACATGTGACATATCCCGAGAA 4955
DB 637 GCGCAACGTCGGCGAGTGTGAGACATGTCMAACATACGCGGAGGCGCTACCCCGAGAC 696
QY 4956 TCGAGCTGTGCTGATGCTTCCCAAGACCAAGTCTCTGCTTACCCCGATAGTGGCTGTG 5015
DB 697 AAGCTGCTTCACTCACTGTTGAGAGAGCGGTGCAACAATTCGGAATGCCCTGGCGGTG 756
QY 5016 GTGACCTCTCTGTCGCGATGACCTACACCGATGATGCGCAGTGTGATATCTGCT 5075
DB 757 GTGATGAAACCGGAAACCTGACCTTATGCGCAACTGATATGCGGAGGAAATCGACTGCA 816
QY 5076 GGAATGCTTGTGCTGAGCTCAATGCTTCGACAGACAGCTTGTGAGATATTTGCCCAAG 5135
DB 817 CATATATGATTCGGCTGTGAGAGAGCGGTGCAACAATTCGGAATGCCCTGGCGGTG 876
QY 5136 TCATGTAGACAAATGTGCGCTTCTTGTGTGTGTTGAAGGGAACCTTGGCTATCTTCT 5195
DB 877 AGTCTGAAATATGATGAGGCTTGTCTGAGAAATTTTGAAGGCGGAGTGTGCTATGTCGCG 936
QY 5196 CTCGATATGAGATGCGCTCTGCGGAGAGATTCAGAGATATCTTGTGACCTTCTGGGCT 5255
DB 937 CTGAGACCTGATATTCGCGCAGAGCGGTGCGCTATATCTGGAAGACAGTGCCTGCTG 996
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QY 5256 ACCATTGTTTGAATGGCCATGATACAGCGCTCCCGATATCGAGGTACTAAGCTCGAG 5315
DB 997 GGGTTGCTGTGGAGG-----GGAAACCGGATGTTGTTGGCGAG 1038
QY 5316 TTTGTTGATATCCGGGATGCGGATGAGATGACAGCAATGACAGATGAGCTTTGAAGTATCGAG 5375
DB 1039 TTGGCGGTGCGGATGCTTGTATCTGCAAGAAAGGAGCATGGGAGGTGTAAGCTGATCATAT 1098
QY 5376 CACGACAGCAAAAGCCCTCAGCAGAGTCTGCAATCGTGTGATATCTGAGATCC 5435
DB 1099 CCGGTGTGCGGACCATCAAGCGCGAGACCTGGCTATGTGATATCTCAGGTTCC 1158
QY 5436 ACTGCGGACCAAAAGCGCTCATGATTTGAGACCGGTCTATTTTGAACATGACAACT 5495
DB 1159 ACTGTAAACCCAAAGGTGTGGCAACAGCATTAAGCGGCTGT---AAACGGTGTGTGT 1216
QY 5496 GCGGTATACCAACTATCCCTTGGAAGAGGATGG---CTCATGCGGACCATTTG 5550
DB 1217 GGGGCGAGATGAAATACCAAGCTCGGGCGGAGCATGTGTCTTGCAGAAAGATCTCATTCG 1276
QY 5551 CGTTTACGCGCGCATGATGAGATCTACAGCGCCCTTTTGTTCGAAAGGACATTTGTT 5610
DB 1277 GCTTCGATGATCGTCTGGGAGATCTTCTCTCTGCTTGCAGAGACAGACTGCTCA 1336
QY 5611 GCGTTGACTATGACAAACCTCAGAGCTTACAGACTCAAGAGATGTGTTTCCGAGAGC 5670
DB 1337 TGCGCGCGCCCGGAGGCGCATCAAGACCTTCACTCACTGATGAGAGTATGAGCGCGAA 1396
QY 5671 ATGTCAAGCGGCAAGTATGTCAACAGCTCTTCTCAAGATATGATCTCTCGAGTCCGA 5730
DB 1397 GCATTAGCATGTGCACTTGTCTTCTTCCATGCTGAGGCTTTGTCAATACAGCGCAG 1456
QY 5731 GAAGCTCTCGAAGACCTTGAATGTTCTTCTTGTGTGTGACAGATTCAGCGGCCAG 5790
DB 1457 CAGGCGGCTGTTCGACGCTCAAGCGATATTTGCAAGTGAAGAAACACTCCGATATCTT 1516
QY 5791 ATGCTCTGATGCGGAGGACCTTATTCAGGGTCCAGTGTTCATATGTTAGGCCCA 5850
DB 1517 TGCATTTGCAAAACCGGCGCATTTCCGAAAGCGATGTGCAATATCTTTATGAGCCCA 1576
QY 5851 CAGAGATGAGATGATGATGATCAATCATATCCATGATGCTGAGTGTGATCATGATG 5910
DB 1577 CCG---AAGCAGCATTTGACGTACATGATGATGATGATGATGATGATGATGATG 1633
QY 5911 GAGTCCCAATTTGACGAGCTCTGACAACTCAGAGCGTATGTGTGATCTGAGCAAC 5970
DB 1634 TCGTTCGATGCGCGCGTCCGATGACGAAATACAGGATTTATCTGTTGATATGACAGGCC 1693
QY 5971 AGCTTGTGCAATTTGTGTGATGAGAGAGTGTGTGCTGCTGCGATGTCTTCCCGGG 6030
DB 1694 AGCCAGTGCCTATCGGATCAGCGCGGAGATTTATATCGGCGGAGATGAGGAGTGCCTGGC 1753
QY 6031 GCTA---CAGTGAACAAAGCCCTTGAAGAGACGTTTGTGACATTAATCTGATATGAC 6087
DB 1754 GTTATTTGATTCAGACCGGAATTTGACGCGGAGGCTTTCCTGAGAGATCCCTTACATGAC 1813
QY 6088 AGACATGAAAGGCGTATTCGACATGCGGATGAGTGCAGTACAGAGTTGAGATGAGCTCA 6147
DB 1814 GCGCGGCGGCGGAGATGATACAGAGCGGTGATCTGAGGCGCTGAGCGGAGCGCAATTA 1873
QY 6148 TCGAGTCTTTCGAGCGATGATGACACCACTTCAAGATTTGCTGCGCAATCTGATGAAATCAG 6207
DB 1874 TCGAGTATCTGAGGCGGATGAGAGATCAGGTCAAGCTCCGAGGCTACCGTATGAACTGG 1933
QY 6208 CTGAGATTAAGGCGGCTTCTGCGGAGTCTCTCGGCTCGAGATGCTGTGT 6259
DB 1934 GCGAGATGAGTGCAGCTTTCGCGCTTGTCTCGGAGTCAAGGAGCGAGTGT 1985
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RESULT 9
US-10-282-122A-33665
; Sequence 33665, Application US/10282122A
; Publication No. US20040029129A1
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/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3365
/ LENGTH: 10296
/ TYPE: DNA
/ ORGANISM: Pseudomonas syringae
/ US-10-282-122A-3365

Query Match      1.2%; Score 129; DB 16; Length 10296;
Best Local Similarity 46.3%; Pred. No. 1.6e-28;
Matches 506; Conservative 0; Mismatches 575; Indels 12; Gaps 2;
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QY 3954 CACATCTCACTATTGTGATGATCATCATCTCAGATGGTGGTCAATTGATGTCTTG 4013
D 442 CATGTCTGCTGCTGACACCTGATCATATCTTGCAATAGGCTGTGATGATG 501
QY 4014 CGACGATTTCAATCAGCTTCACTCAGCTGCTCAAGACCTCAAAAGACCCGCTGCA 4073
D 502 CTGGACCAACTCAGTGGCTCTCAACAGCGAGCTGAACGGCCGTGACCTTCA 561
QY 4074 GCATCACTCTCTCACTATTCAGTACAGGACTTTTGCAAAATGGCAAGACCAATTC 4133
D 562 GCGCTTGAATATCACTATGCGACTAGCCGTGCGCAAGGAATGGCTGCAAGAG 621
QY 4134 ATAGACGAGGAGAACTCACTCACTAGGAAAGAACTCAAAAGACTCTTCCCAACA 4193
D 622 GTGCTGACACCAAGCTGATATATGGGAATCTCAGTCAAGATGGCCAAAGCTTCT 681
QY 4194 AAGATCCGACCGACTTTGCCCCGCTGCACTTCTGTGGAAGCAGAGTTGCTACAT 4253
D 682 GAATGCCGACCGACCGGCCCCGCTGCAAGACTGACTATATGGGGTAAACGGGTTAC 741
QY 4254 GTTACCATCGACGCGGAGCTTACCAATCCCTTGAGCTTTGCAACGAACACACAG 4313
D 742 TTACACTTCCCGCCGAATCGAGCCCAACTCCAGAACTCAACGCAACCATATGTG 801
QY 4314 ACCCTTTGCGTCTTCTTATAGTGGTCCGTCGCGCTCATTTATGCTTCACAGCTGTT 4373
D 802 AGCTGTTCACAGACCTGATATATGCTTCAATACGCTGCTGCTGCTGACATACAG 861
QY 4374 GAAGACCTGTCAATGTGTACACCAATTCGAATCGAACCGACCTGAACTGAGATATC 4433
D 862 CCGATATCTGTATCGGGTATCCGGTGCCAAATGCGGCTGTGCGAAATTCAGCCGCTG 921
QY 4434 ATGCGCTCTTTGTCAATATGCAATGAGTATGCAATCAATATGATCATACGATACCTTT 4493
D 922 ATGCGCTCTTTCGCAACACCTCGTCTGCGAGTGAATGAGCAGCAACGACCTTT 981
QY 4494 GGGACTTGTATCAACCAAGTCAAGGCTAGACGACGACGACGATTCGAGAAAGAGATATT 4553
D 982 GCGCTTATCTGCAACAGACCCCAATCGACTGCTGACTGCACTTGAATCAGAAATC 1041
QY 4554 CCGTTTGGCGCGTTTATATGACGACTACAGCTGATTCAGAGATCTGTCAAGACACT 4613
D 1042 CCGTTGAAAGACTGCTGAGAGGGTTACGCCCTG---CAAGGAGCTGAACCACTCCCG 1098
QY 4614 CTGCGCAACTCATTTTGTGAGTGCATCAAGAGAACTTGAAGATTCAGTTCAG 4673
D 1099 CTCTTTCAGTCTGTTTCTTTCTTCAACAGAGACCTGCGCGAGAGACTGACCTCAGT 1158
QY 4674 GGTCTCGAGTCCG 4686
D 1159 GGGACAAAGTCCG 1171

RESULT 10
US-10-282-122A-3365
/ Sequence 31388, Application US/10282122A
/ Publication No. US20040029129A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Liangsu
/ APPLICANT: Zamudio, Carlos
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Karl
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
```

1 CURRENT APPLICATION NUMBER: US/10/282,122A
2 CURRENT FILING DATE: 2003-02-20
3 PRIOR APPLICATION NUMBER: 60/191,078
4 PRIOR FILING DATE: 2000-03-21
5 PRIOR APPLICATION NUMBER: 60/206,848
6 PRIOR FILING DATE: 2000-05-23
7 PRIOR APPLICATION NUMBER: 60/207,727
8 PRIOR FILING DATE: 2000-05-26
9 PRIOR APPLICATION NUMBER: 60/230,335
10 PRIOR FILING DATE: 2000-09-06
11 PRIOR APPLICATION NUMBER: 60/230,347
12 PRIOR FILING DATE: 2000-09-09
13 PRIOR APPLICATION NUMBER: 60/242,578
14 PRIOR FILING DATE: 2000-10-23
15 PRIOR APPLICATION NUMBER: 60/253,625
16 PRIOR FILING DATE: 2000-11-27
17 PRIOR APPLICATION NUMBER: 60/257,931
18 PRIOR FILING DATE: 2000-12-22
19 PRIOR APPLICATION NUMBER: 60/267,636
20 PRIOR FILING DATE: 2001-02-09
21 PRIOR APPLICATION NUMBER: 60/269,308
22 PRIOR FILING DATE: 2001-02-16
23 Remaining Prior Application data removed - See File Wrapper or PALM.
24 NUMBER OF SEQ ID NOS: 78614
25 SOFTWARE: PatentIn version 3.1
26 SEQ ID NO 31388
27 LENGTH: 9748
28 TYPE: DNA
29 ORGANISM: Pseudomonas putida
30 US-10-282-122A-31388

Query Match 1.1%; Score 127.8; DB 16; Length 9748;

Best Local Similarity 42.9%; Pred. No. 3.8e-28;

Matches 1166; Conservative 0; Mismatches 1512; Indels 41; Gaps 9;

3566 CATCCCAAGTCAATCTATGAGGAGCTTTGAGCACTTTATTCACAGGCGCACTATG 3625
3566 CATCGCTGTGTGTCACGGGAGAGCCCTGCGCTGTGTATGCCAGCAACCTCATG 6744
3626 GTTCCTGATCATGTGACCTTGCGTGTGTATCTGATTCATATGCTGTGAAT 3685
6745 GGTACTGTGCACTGAGCGCGCACAGCGCGCTTCAACATCGCGTGGCTTGCATT 6804
3686 GCGCGGCTGTCAATGTGACGCGTTCACGCTTCTTGACGCGCTTGAACGCGCA 3745
6805 GCGCGGCGCTGTGATGTGGGCGCTGACAGAGCGCTTCAAGCGCTTGGTGGCA 6864
3746 CGAGACTCTTAAGACGACATTTGAAGACAGAGTGTGTGCTTCAATTTTCA 3805
6865 CGAAGCTGTGCGCACCTTTCGTCAGTTCAGCGGAGCGCGCAAGTGAATTCAGC 6924
3806 GAAGCTTTGAGAGATGAAGTCAATTCCTGTGTGTTCAGACCTTGACCGCTTGA 3865
6925 CCGCGAGCGGAGGTGATGCTTGCAGCGGAGGTGATCTGTTCGATTTGACGCG 6984
3866 GGTGTGAACCAAGACAGACTACTCCCTTCAATCTCTCATCTGAAGCTGTGAGAGC 3925
6985 CAGGTGAGAGATGTGCGCGTGAACCTTTCAGCTGTGTAAGCGCGCACTGATCGCGT 7044
3926 GAGCTCTTAAGACTGTGTGAAGTGAACACATCTTCACTATTGTCAATGATCATCAT 3985
7045 TGACCTTTTGTGCTGAGCGCGCGAGCGCATGTGCTGTGTGAACCTGACACATCAT 7104
3986 CTAGATGTGTGCTCATTTGATGTCTTGCGAGCGGATCTCAATAGCTCATCAAGTGC 4045
7105 CACCGATGTGTGCTGATGTGGGTGTGTGTCAAGAGTGTGCGCGCTGACAGGGCTA 7164
4046 GCTCAAGACTCAAAAGACCGCTGTGAGCACTCACTCTTCACTTCAAGTACAGCA 4105
7165 TCGTCAATGGGAGCGCGCTGCACTGCGCGCTGTGGGTGCAATACCGCACTACGCGGC 7224
4106 CTTTGCAAAATGGCAGAGGACCAATTCATGAGCAGAGAGCACTCACTACGAAA 4165

7225 TTGGCAGCGCAATGCTGAGGCGAGCGAGCAAGCGCGGCACTGAGCTTACGGAAGC 7284
4166 GAAGCAACTCAAAAGACTTTCCCGAGCAAAAGATCCGAGCACTTTGGCCCGCTGACT 4225
7285 AAGTTGGGCGGTGAACAGCGGTGTGTGAATTTGCCAGCCGATACCGCGCGCGGCA 7344
4226 TGTGTGAGAGCGAGGTTGCGTACATGTTACATGACGAGGCTTACAGTCCCT 4285
7345 GCCAAGCGCGGTGCGGCGCATGTAAGCTGCGCTGAGCGCGCGCTGTGTGAGGCACT 7404
4286 TCGAGCTTTGCAAGAAACAAACAGACCTTTTGTGTGTCTTCTGAGTGTGCG 4345
7405 CAGCGGAGCGCGAGCGCGCGCGCTCACCTGTTCATGTCTGTGTGCGAGCTTCCA 7464
4346 TGCGCTCATTTATGTTCTCAAGCTGTGAGAGCGGTGATTTGTAACCAATTCGAA 4405
7465 GACCTGTCTTCACTGTTACTGACTCAGCGGACATCCGCTGGCGGTGCGGTCGCA 7524
4406 TCGCAACCGACTGAACCTGAGAGATATCATGCGCTGTGTGTCAATACGAGTGTGCG 4465
7525 TCGCAGCGCGGCGAAACGAAAGGCGTGTGCGCTTCTGTCAATACCGAGGTGCAAA 7584
4466 AATCAATATGATCATCATCATATCTTTGAGACTTTGATTCAGCAAGTCAAGCTACAG 4525
7585 GCGCGAGTTTCACCTGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7644
4526 GACAGCAGCATTTGAGAACGAGATATTCGCTTTGAGCGCGGTGTGTATCAGCACTACAGCC 4585
7645 GCTGATATGCCAGGCCCATATGAGACCTGCGCTTGAACAGTTGTGTGCGCGCTTGAAC 7704
4586 TGAATCCAGATCTGTCAAGCAACACCTCTGCAACAATCTATTTTGAAGTCACTCACA 4645
7705 GGCAGCGATCTCAACCAAAACCGCTGTTC---CAGGTATTTTCAACCAACAGCGCGA 7761
4646 GAAGACCTTGAAGATTCAGTTTCAAGTTCAGGCTGTGAGTGTGCTGTGCTTGAAGCAAGC 4705
7762 GGCAGAGCGCGCGCGCGAGAGTGTGCGGCTGTGAGTGTGAGCGGTGTGCTGTGAGGT 7821
4706 GTA---CACTGATTTGACATGAGATTCATCTGTTTCAAGAAACGACAGCTTAAAG 4762
7822 GCACAGACCCCATTTGACCTGTGCGTGTGATACCGCGAGCAAGCTGAGCGGACAGCGC 7881
4763 TAGGCTCACTTTGCGGATGCTGTTCAAATGAGACTGTGAAATATCTGTCAAGT 4822
7882 AGCTTTTACCTTGCACACCACTGTACGACCGCGAGCACTGAGCAATATGCGCGCA 7941
4823 ATTCTTGAATCTGAGAAACGCGCTTCAAAATTTGCGGACACAGTCTCAATACCTTC 4882
7942 CTGCGCAATCTCTCCAGGCGCATGCTGCGAGCGCAACAGGTGTGCGCACTGCG 8001
4883 TTTGACTGATGAGATTTGTGACTCTTTGAAATTTGATGTTCTCAAGTCAAAATGTGCA 4942
8002 GATGTGTGATGATCTGAGAGAGAGTGTGATGCTGTGATGATGAGAGCGCGCAAGTGGC 8061
4943 CTATCCCGAGAAATGAGCTTGTGTGATGTTCTTCAAGCCCAAGTCTTCTTACCCCGA 5002
8062 CTACCGGAGAGCGCGCTGTGTGATCAATTTGTGAGATCAAGCGCGAGGTATCCGCA 8121
5003 TAGTGTGTGTGTGAGCTCTCTGTGCGCATTTGACCTTACAGAGTGTGATGCGCAGTC 5062
8122 GCGCGCGGTATATTTTGTGCGATGCACTTTAGTATACCAAGATGAGTATGAGGTGC 8181
5063 TGAATATCTGCTGATGAGCTTGTGATGCAAGTCAATGCTGTGAGAGAGCTTGTGCACT 5122
8182 CAACCGCTGTGCAAAATGCTGTGAGAGAGTGTGCGCGGAGTGTGATTTGGCGT 8241
5123 ATTTGCCCGAGGTCAATGTGAGCAATTTGTGCGTCTTTGTGTGTGAGCGCAATTT 5182
8242 GCGGATGAAAGAGCTGTGATGAGCTGTGATGAGCTGTGATGAGCTGTGATGAGCTGTG 8301
5183 GCGCTATCTCTCTGCA--TGTACATGCGCTGTGCGGAGATTTCAAGATATATCTTCT 5240
8302 CGCTATGTATCGCTGAGCCGAGATTAACCGAGCAGCGCTGTGCTTACATGATTCAGAGA 8361

QY 5241 GGACTTTCTGGGCTTACCATTTGTTGATTGGCCATGATACAGCGCTCCCGATATCGAG 5300
 DB 8362 CAGCGGCGATCGGCTCTGCTCGACCGCAGCAAGCATTTGCGCGAGCTGCGGATGCCG-- 8419
 QY 5301 GTTACTAAGCTGAGTTTGTCTGATCCGGGATGCGCTGATATGACAAATGACAGATGCG 5360
 DB 8420 -----GCAAGCGGTACCTATCTCTGCTGACCAAGACCGCGAGTGGCTGGCC 8467
 QY 5361 TTGAAGTCAATCGAGCAGCAGACCAAAAGCCCTCAGCCAGGTCTCGATACGTGCTG 5420
 DB 8468 GAGTATGCGACACCGCCCTGAGGTGAGAGTTCGCTCCCACTGGCCTTATGATC 8527
 QY 5421 TATACCTCAAGATCACTGCGCAGCAAAAGCGTCAATGATGACACCGTCAATTAT 5480
 DB 8528 TACACCTCGGTTCCACAGGGCGGCGCAAGGGCGGCGGCAACCCACGAGGGGCTGCT- 8586
 QY 5481 CGAAGCTCAAGATGCTGTATACCACTATCTTGGAAAC-----GAGATGCTC 5535
 DB 8587 -CAACGCGCTGAGTGAATGCAAGGCGCTATGCGCTGATGCGCAGCGACACGCTGCTGC 8645
 QY 5536 ACATGCGACCATTTGGTTGAGCGGCGATCGTACGAGATCTACAGCGCCCTTTTGTTCG 5595
 DB 8646 AGAAAACCCCTTACGTTGAGTGTGAGTGTGAGGATTTCTTGGCCCTGATGACCG 8705
 QY 5596 GAAGCACTTTGTTGCTGTTGACTATCAATGACAAACCTTCAGCGGTAGAGACTCAAGATG 5655
 DB 8706 GCGCGGCGCTGCGCGCTGCGCTTCGCGCGGCGATACCGCGACCGCGCGCTGTGCCAGA 8765
 QY 5656 TGTTTTCCGAGCATGTCACCGGCAAGTCATGTACACAGCTCTTTCGAAGATGAC 5715
 DB 8766 CCATCATTCGACCAACAGTGAAGCACTTCGACTTCGCTCGATGCTCAGGCTTCA 8825
 QY 5716 CTCTCGAGTCCGGAAGAGCTCTCGAATCTTGATGTTCTTCTTGTGTGTGACAG 5775
 DB 8826 TGGCCAGCGCGAGTGCAGCAGTGCAGCGAGCTTCCGCGCGTGTGTGACAGTGGCGAG 8885
 QY 5776 ATTGCAAGCGCCGAGATGCTCTGATGCGAGGACTTTATCAAGGGGTCAAGTGTACA 5835
 DB 8886 CGCTGCGCGCGCTGATGCGCCCAACAGTCCGCGAGCGCTGCTCATGCGCGGTGTACA 8945
 QY 5836 ATGTTACGCGCCCAAGAGATGAGTCAATGATCAATCTATCCATTGACTGACTG 5895
 DB 8946 ACTGTACGCGCCGACCGAGGCGCCATCGACGTGACCTGAGACTGCGGCGACAGC 9005
 QY 5896 AGTCTTCATCATGAGTGTCCCATTTGAGAGAGTCTGAACCACTGAGAGCGTATGCTG 5955
 DB 9006 AGGGCTTCA-----GGTGCAGATCGGCCAACCGATCGAACCTGCGACCCACATTC 9059
 QY 5956 TGGATCTGAGCAACAGCTTGTGAGCATTTGATGAGGAGCTTGTGTCACTGGCG 6015
 DB 9060 TCGAACCCGACTGCTGCTGCGCGCTGCGCGCGCTCAATGAGGAGCTTACTGCGCGCA 9119
 QY 6016 ATGCTTTCGCGCGGCT--ACAGTGAACAAAGCCCTTGAAGAACCGTTTGTGTGACA 6072
 DB 9120 TTGCGCTGCGCGGCGGTACACAGGTGCGCGGAGTGAAGCGGCTTGTGTGCGG 9179
 QY 6073 TTAATGTCATGACCAAGAGTGAAGCGGTATGCGCATGCGATCGAGTGGGTGACAGA 6132
 DB 9180 ATTCGTTCAAGAGCAGGCGGTGTGTGATCCGCACTGCGCACTTGGCGCGCTATG-- 9237
 QY 6133 TTGAGATGCGCTCATGAGTTCCTTGGAGGTATGACACCGATTCAAGATTGCTGGA 6192
 DB 9238 -CCCGAGCGGTGTGATGATTAAGCGCGGCGGTATGACACAGGTAAAAATTCGCGGCC 9286
 QY 6193 ATGATTCGATAGTGAAGTGAAGCGGCGCTTCTGCGCGACTCTCTCGTCCGAGATG 6252
 DB 9297 TGGTATTCGAGCTGGGTGAATGAGACAGACGACTGCGCGACGCGCCAAAGTGGCGAGG 6256
 QY 6253 CTGCTGTCTCTTACGA 6271
 DB 9357 CAGTGTGCTGCGCCACAGA 9375

RESULT 11
 US-10-156-761-3185
 ; Sequence 3185, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRO
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; PRIOR FILING DATE: 2001-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 3185
 ; LENGTH: 3789
 ; TYPE: DNA
 ; ORGANISM: Streptomyces avermitilis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(3789)
 US-10-156-761-3185

Query Match 1.1%; Score 119.6; DB 15; Length 3789;
 Best Local Similarity 45.7%; Pred. No. 8,2e-26;
 Matches 619; Conservative 0; Mismatches 714; Indels 21; Gaps 5;

QY 4915 TGAATGTTCTAAGTCAAGTCAATGTCAGTATTCCTCCGAGATGAGTGGCTGATGCT 4974
 DB 620 TGGTGAATCTCAACCGGACGACGCTCCCTACCCGCGGAGACACCGCGTGAAGAGCTGT 679
 QY 4975 TCGAAGCCCAAGTCTCTGTTACCCCGATAGTGTGCTGTGTGAGTCTCTGCGCGAT 5034
 DB 680 TCGCCGAGCGGCGCGGACCGCAACCGGACACCGGCGGTGTGCAAGGAGACACCTGCC 739
 QY 5035 TGAATCAACGAGTGGATGCGCAGTGTATTTCTGCTGATGAGTGTGCTGTCAGCGT 5094
 DB 740 TGAATGCGCGCAACTGACACAGGTGAGAGTGTCTGCGCGCGCGCGCGAGG 799
 QY 5095 CAATGCTTCGAGAGAGCGTTGTGCAATTTGCCCCACGCTGATGAGACAAATGCTG 5154
 DB 800 GGTGCGCGCGGCGGAGAACCGGTGCGCTGCTCTGCGGCGCGAGCCACCTGCTGCTG 859
 QY 5155 CGTCTTTGTTGTTGTTGAGAGCGCAACTGCGCTATCTTCTCTGATGTACATCGCCCT 5214
 DB 860 CCGCGCTGCGGCTCTCAAGGCGCGGCGCTTACCTGCGCGGTGACCCCGACTACCCCG 919
 QY 5215 CGCGAGAGTTCAAGATATATCTTCTGAACTTTCTGAGCTTACCATTTGTTGATTTGCC 5274
 DB 920 CCGACCGGTTGGCTATCTCTGCGGAGACGCGGTGCGCGCGGTGCTACCGTACGCG 979
 QY 5275 ATGATACAGCGCTCCGATATG-----AGTTACTAAAGTGAAGTGTGTTGTA 5325
 DB 980 ACTGCGCGGCGCAACTCAAGCGGTGCAACGCGGTGCGAGATGACCTACCGTCTGCG 1039
 QY 5326 TCGCGAGTGTGCTGATGACAGCAATGAGTGTGTAAGTGTGATGACAGACAGACGA 5385
 DB 1040 CCGTTCAGCACTTGGAGTGTGCGACGACCCCGCGACGCGCGCGCGCGCGCGCGCC 1099
 QY 5386 CAAGCGCTCAGCGACAGAGTCTGCAATAGTGTGATATCTTGAAGTTCAGTGGCGGAC 5445
 DB 1100 GCGCGGAGACGCGCGGTGAGCGGCGCTTACTGATGTACCTTCGATGACACCGGAGC 1159
 QY 5446 CAAGCGCTCATGATGAGCAACGTTCAATTAATTCGACAGTACAAAGTGTGATATAC 5505

Db	1160	CCAAAGGCGTGTGTCGCCGATCAGGAGCATCAGCGTCTGTAGCGGAGATCGGCTATG	1219
Qy	5506	CCAACTATCTCTTGGGAAACGAGATGGCTACATGGGACCATTCGTTTGAACGGCGAT	5565
Db	1220	TACGCTTGAGACCCGACGACCAAGATGGCGAGGTCCGACAGCCGGTTTTCACCGCTTCG	1279
Qy	5566	CGTACGAGATCTTACAGCGCCCTTTTGTTCGGAAGACACTTGTGTTCGTTGACTACATGA	5625
Db	1280	TGTGGAGAGTGTGGGGCCCGCTGCTCGGCGGGCGGACCTCTGTGATCCTTGAACCGCAGA	1339
Qy	5626	CAACCTTCGACGCTAGACACTCAAGATGTGTTTTCCGAGACATCTCAACGCGGCA	5685
Db	1340	CCCTGCTCGACACCGAGAACTCGGCGGGCCCTGCGCAACAGCATCACACCGC-C	1398
Qy	5686	GTCAATGTACCAAGCTTTTCTCAAGATBTACTCTCCGAGTCCGAGAAAGGCTTCAGAA	5745
Db	1399	CTGTTACCTTCGCGGTGTGTTACCGCGCTGCGCAGCAGAGAC-GTAGCCTGTGTTCCGTC	1456
Qy	5746	CGTTGATGTTCTTCTCTTGGTGGTGCACATTCGACGGCCCGCAGATCTCTCATGCGC	5805
Db	1457	CGCTCGGCACTCTGCTGTGGGGCGGACGTGCTCTCCGCCCGGACGCCCGGAGGTGC	1516
Qy	5806	AGGACTTTATCAGGGGTCACAGTGTTCACATGGTTACCGGCCCAACAGAGATGAGTCA	5865
Db	1517	TGGCGGCAACCCCGGCTGCGGCTGGTCAATGCTACGGGCGACGAGAACCCGCTGA	1576
Qy	5866	TGAGTACATCTATCCATTGACTCGACGTAGTGTTCATCAATGAGATCCCATTTGGAC	5925
Db	1577	TCTCAACCTGCAGATGCTGCGC-----CAACCTGTCGGGCGCCGGGTGCGATCGGCC	1630
Qy	5926	GAGCTCTGAACAACCTCAGAGCGTATGTCTGATCTCTGAGCAACAGCTTGTGGCATTTG	5985
Db	1631	GCCCGGTGCCCAACGCGACCGCGTACTCTCAACAGAGACGACTGCGGTGCCACCG	1690
Qy	5986	GTGTATGGAGAGCTTGTGTTCATGCGATGTCTTTCGCGGGGCTCAAGTACAAAG	6045
Db	1691	GCGTCCCGGCGAACTCAATGTGGGCGGCGACGGCTGCGCGTACCAACGAGCGCC	1750
Qy	6046	CCCTTGAACGAAACCGTTTGTGTGACATTTACTGTCAATGACCAACACTGAAGCGTATC	6105
Db	1751	CCGACCTTACGGAACGTGCTTGTATCCGATCCGTTCCGACCCCGGCGAAGGCTGTACC	1810
Qy	6106	GCACTGGCATCGAGTGGGTATCAGATTTGAGAGTGGCTCATCGAGTTCTTCGACGTA	6165
Db	1811	GCACGGGGGACCGGGTTCGGCT---GCTGCCGAGCGGCGCGGTGACTTCTTCGCGGGA	1867
Qy	6166	TGACACCCAGTTCAAGATTCGTGGCAATGTATCGATACGCTGAGATTGAAGCGGCC	6225
Db	1868	CCGACCAACAGGTCAAGTGGCGGCTTCCGGGTGAGACCGGCGAGATCGACACACCC	1927
Qy	6226	TTCTGGCGCACTCTCCGTCGAGATGCTGCTG 6259	
Db	1928	TGTCGCGCTGCCGCGGTGCGGAGCGCCGCTGT 1961	


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RESULT 13
US-10-329-079-34
: Sequence 34, Application US/10329079
: Publication No. US20030198981A1
: GENERAL INFORMATION:
: APPLICANT: FARNET, Chris
: APPLICANT: ZAZOPOULOS, Emmanuel
: APPLICANT: STAFFA, Alfredo
: TITLE OF INVENTION: GENES AND PROTEINS INVOLVED IN THE BIOSYNTHESIS OF LIPOPEPTIDES
: FILE REFERENCE: 3002-11US
: CURRENT APPLICATION NUMBER: US/10/329,079
: CURRENT FILING DATE: 2002-12-24
: NUMBER OF SEQ ID NOS: 66
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 34
: LENGTH: 61944
: TYPE: DNA
: ORGANISM: Streptomyces refuensis
US-10-329-079-34

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Query Match	1.0%	Score 115.2	DB 15	Length 61944	
Best Local Similarity	45.8%	Pred. 11.9e-23			
Matches	451	Conservative	0	Mismatches 518	Indels 15
				Gaps	1
Oy	3619	GACATGATGTTCTTGATCACTTGAGACCTTGAGACTGTGTGATATCGATTCCATATGCTG	3678		
Db	30368	GACTGTGGTTCCTCCACCAAGATGAGCGCCCGACGCCACATCAACATCCACGCGCG	30422		
Oy	3679	TGAGAAATGCGGGGACCTGTCAATGTGACCGCTTACGTCGGGCTTTGACGCGCTTGAAAC	3738		
Db	30428	TGCGGAATGACCGGGGCGCTGGACCTCCCGCGCTGCGGAGGCGCTGCGCGACGTGTGC	30487		
Oy	3739	AGGACACGAGACTCTTAAACGCACTTTGMAAGCAGATGAGTGTGCGGTGTAACAATTG	3798		
Db	30488	GGCGCCACGAGACCTCCGACAGCTTTTCCCGACGCCGCGACAGCGCGCCGACGACG	30544		
Oy	3799	TTCAACGAAACCTTCTGAGAGATGAAAGTCAATGATCTGTGTGTTGACACTTGACC	3858		
Db	30548	TCTGTCCCGCGCGGCGGAGCGCGCGGTGAGGTGACCGTCAACCGGGAACACCGAGCGGAAAC	30607		
Oy	3859	CGTTTGAGGTGTGAACCAAGACACACTCTCCCTTCAATCTCTCATCTGAAGCTGGCT	3918		
Db	30608	TGCCGGCGTCTGTGGCCAGAGAGCGCGCACGCTTTCGACTGTGGCCCGGGAAGTCCCC	30667		
Oy	3919	GGAAGACGAGCTCTTACACTTGGTGAAATGACCACTCTCATATTTGATGATGATC	3978		
Db	30668	TGAGGGGCGGCTCTCGCGCTCCGCGCAAGGAGACAGTGTGTGCTGTGATTCACC	30722		
Oy	3979	ACATCATCTCAGATGTTGTGTCATATGATGTCTTTCGACGCGATCTTCAATCAGCTTACT	4038		
Db	30728	ACATGTGCGAGGAGCGGTGTGTGTGGCGGCGCGCTCGAGCGGACCTTACACGCGCTTACG	30787		
Oy	4039	CAGCTGGCTCAGAGACTCAAAAGACCGGCTGTACACTCACTCCTTACTATTCAGT	4098		
Db	30788	CGCGCCGACGAGGCGCGCGCGCGCGAGTGGAGAACTCCCGTTCAGTACGCCGACT	30847		
Oy	4099	ACAGCGACTTTGCAAAATGCGAAGAGACCAATTCATAGAGCAGAGAGCAACTCAACT	4158		
Db	30848	ACACCTCTTGCGACGGGAGGTGCTGGACTTCGAGATCCGAGAGACCCCGAGAGCTGTCTAGCC	30907		
Oy	4159	ACTGGAAGAACCACTCAAGAATCTTTCGCCAG-----CAAAAGTCCGCA	4203		
Db	30908	GCCAGACGGGTATCTGAGAGAGGCGTCCGCGGTCTGCCGAGCGCATGACCTGCGCT	30966		
Oy	4204	CGGACTTTGCCCGGCTTGCACTTCTGTGTGAGACGCGAGTTGGGTACATGTTACATG	4263		
Db	30968	TGACCGCGCCCGCGCCGATCGCGGACACCGCGGCGCACACCGTGCATCACCTTCG	31027		
Oy	4264	ACGGGAGCTTACAGTCCCTTGAGACCTTCTGACCTTCTGACCAACCAACACGACTCTTTGG	4323		
Db	31028	CGCGCGGACCAAGAGGATGCGCGGCTGTGGCGCGCGCCACAGGCGCAGACGTTCA	31087		

QY	4324	TCGTTCTTTACGCGCGCTTCCGCGCGCATATTATGCTCAACAGCTGTGGAAGCGCTG	4383
Db	31088	TGCTGTGTGCAGCGCGCGCTGCGCGCTGTGTGTCCGGCTCGGGCGGGGCAACGAAATCC	31144
QY	4384	TCATTGTGTACCAACATTGGCAATTCGAAACCGACTGAATTGAGATATCATTCGCTGCT	4443
Db	31148	CCCTGGGCAACATCGTGTGGCCGGACGCAACCAACAGCGCGCTGTGAGGGGACTCATATCGGCTTGT	31207
QY	4444	TTTTCATTTACGAGGTATATGCGATCAACATAGATCATCAATCATCTTTGGGACTTTGA	4503
Db	31208	TCGTCTAACACCTTGTGTGTCTGTGGCAACGACACTCTCGGGAAACCCGACTTTGCAGCAACTGG	31267
QY	4504	TCAAACCAAGTCAGACTACGACGACGACAGACGATTCGAGAACGAGATATTTCCGTTTGACC	4563
Db	31268	TCGAGAGGGGCGCGGAGACCGGCGCTTGACCGCTTACGCCCAACGAGACGTCGCGTTTCGAGC	31327
QY	4564	GCGTTGTATACGACACTACAGCCTTG	4587
Db	31328	GCGTGTGTGAGGCACTGCGCCCGG	31351

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RESULT 14
US-10-369-493-35302
; Sequence 35302, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 35302
; LENGTH: 8138
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-35302

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Query Match	1.0%	Score 111.2	DB 15	Length 8138
Best Local Similarity	46.2%	Pred. No. 7,66-23		
Matches	Conservative	0	Mismatches 513	Indels 12
			Gaps	2
Qy	3607	ATTCAACAAGCCGACATAAGTCTCTGATCATGTTGAGCGTTGGCAGAGCTGTGTATCTGA		3666
Db	640	ATGCCACGAAGCATATCGTTGTCGACGAGATGACGCCGCGACAGCGCATATTGCA		699
Qy	3667	TTCCATATGCTGTGAGAAATGCCGGGCGCTGTCAATGTGACGCGTTACGTGGGCTCTTG		3726
Db	700	TACCCGTGGCCATCAGGCTGGAAAGCCCGCTCGACCCGACAGGCTTAGATCTGCTTCG		759
Qy	3727	CAGGCGTTGACACAGCAGACGAGACTCTTAAAGACACTTTGAAGACAGGATGCTGCG		3786
Db	760	ATATCGTGTGACAGGCGCCATBAAGACCTGCCGACAGTTTTCGAGTTTCAGGACGCGAC		819
Qy	3787	GTCATCAATTTGTTACAGCAGAAAGCTTTCTGAGAGATGAAGTATTGATCTCTGTGTT		3846
Db	820	CGTTTCAGGTATGTTTCGCAAAACAAGCGAGACTTCAGTTTTCATGAACCGGGCGATG		879
Qy	3847	CAGACCTTGACCCGTTTGAAGTGTGTTGAACCAAGAACAGACTACTCTCCTTCATCTTCAT		3906
Db	880	ACGAAGCCGACGCGAGATGTCGCCATCGGCGCTTCGCGCAGAAACCGTTTCATCTTCGC		939
Qy	3907	CTGAAGCTGGGTGAGAGCGACGCTCTTACGACTTTGGGAAGATGACACATCTCTCACTA		3966
Db	940	AGGTCGCGCTTTTCGCGCTCGGCGCTGTCTTCGTCGACCTGAGAGATATCTCTGCTCA		999

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 5, 2004, 10:54:02 ; Search time 780 Seconds

(Without alignments)
10217.135 Million cell updates/sec

Title: US-09-482-788-1

Sequence: 1 aattagatccactagtagc.....ttttgtacagacataatt 11212

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/prodata/1/ina/5A COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
5: /cgn2_6/prodata/1/ina/PC/US COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1306.8	11.7	46899	1 US-08-471-119A-1	Sequence 1, Appl
2	408.2	3.6	1713	1 US-08-471-119A-4	Sequence 4, Appl
3	136.6	1.2	7527	4 US-09-252-991A-71	Sequence 71, Appl
4	136.4	1.2	6573	4 US-09-252-991A-9183	Sequence 9183, Ap
5	104	0.9	77536	4 US-09-410-551B-1	Sequence 1, Appl
6	104	0.9	77536	4 US-09-410-551B-1	Sequence 1, Appl
7	103.8	0.9	10023	4 US-09-252-991A-8997	Sequence 6997, Ap
8	97.8	0.9	3315	4 US-09-252-991A-8892	Sequence 8892, Ap
9	97.8	0.9	7911	4 US-09-252-991A-9182	Sequence 9182, Ap
10	95.4	0.9	7374	4 US-09-252-991A-9100	Sequence 9100, Ap
11	94	0.8	4242	4 US-09-252-991A-7056	Sequence 7056, Ap
12	82.8	0.7	4236	4 US-09-252-991A-7057	Sequence 7057, Ap
13	80.2	0.7	792	4 US-09-252-991A-9098	Sequence 9098, Ap
14	79.4	0.7	2219	3 US-08-510-646B-17	Sequence 17, Appl
15	74.8	0.7	1172	3 US-08-861-774E-17	Sequence 17, Appl
16	67	0.6	532	4 US-09-252-991A-8884	Sequence 8884, Ap
17	67	0.6	532	4 US-09-252-991A-8886	Sequence 8886, Ap
18	67	0.6	1239	4 US-09-252-991A-8991	Sequence 8991, Ap
19	65.2	0.6	1260	3 US-09-252-991A-8992	Sequence 8992, Ap
20	65.2	0.6	1260	3 US-09-252-991A-8992	Sequence 8992, Ap
21	62.8	0.6	178	1 US-08-471-119A-3	Sequence 3, Appl
22	62.8	0.6	993	4 US-09-252-991A-9093	Sequence 9093, Ap
23	61.6	0.5	648	4 US-09-252-991A-9095	Sequence 9095, Ap
24	61.6	0.5	759	4 US-09-252-991A-8775	Sequence 8775, Ap
25	61.4	0.5	1222	3 US-08-861-774E-83	Sequence 83, Appl
26	61	0.5	1368	4 US-09-252-991A-64	Sequence 64, Appl
27	61	0.5	4403765	3 US-09-103-840A-2	Sequence 2, Appl

C	28	61	0.5	4411529	3	US-09-103-840A-1	Sequence 1, Appl
	29	60.4	0.5	474	2	US-08-403-852D-14	Sequence 14, Appl
	30	60.4	0.5	474	3	US-08-510-646B-14	Sequence 14, Appl
	31	60.4	0.5	474	3	US-09-231-818-14	Sequence 14, Appl
	32	60.4	0.5	474	4	US-09-635-359B-14	Sequence 14, Appl
	33	60.2	0.5	810	4	US-09-252-991A-8770	Sequence 8770, Ap
	34	60.2	0.5	951	4	US-09-252-991A-8774	Sequence 8774, Ap
	35	60.2	0.5	1857	4	US-09-252-991A-8888	Sequence 8888, Ap
	36	60.2	0.5	2025	4	US-09-252-991A-8891	Sequence 8891, Ap
	37	59.6	0.5	1171	3	US-08-861-774E-81	Sequence 81, Appl
	38	58.6	0.5	378	4	US-09-252-991A-8993	Sequence 8993, Ap
	39	57.6	0.5	741	4	US-09-252-991A-7023	Sequence 7023, Ap
	40	57.2	0.5	741	4	US-09-252-991A-27	Sequence 27, Appl
	41	57.2	0.5	1204	3	US-08-861-774E-87	Sequence 87, Appl
	42	56.8	0.5	1122	4	US-09-252-991A-1175	Sequence 1175, Ap
	43	56.8	0.5	2484	4	US-09-252-991A-1388	Sequence 1388, Ap
	44	56.8	0.5	6858	4	US-09-252-991A-1219	Sequence 1219, Ap
	45	56.6	0.5	681	4	US-09-252-991A-8887	Sequence 8887, Ap

ALIGNMENTS

RESULT 1
US-08-471-119A-1
; Sequence 1, Application US/08471119A
; Patent No. 5827706
; GENERAL INFORMATION:
; APPLICANT: Letener, Ernst
; APPLICANT: Schneider, Elisabeth
; APPLICANT: Schoergerdorfer, Kurt
; APPLICANT: Weber, Gerhard
; TITLE OF INVENTION: Cyclosporin Synthetase
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5827706artis Corporation
; STREET: 59 Route 10
; CITY: East Hanover
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07936
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,119A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kassenoft, Welynn
; REGISTRATION NUMBER: 26,389
; REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 503 8474
; TELEFAX: 201 503 8807
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 46899 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Toxoplasma gondii
; STRAIN: ATCC 34921
; US-08-471-119A-1
Query Match 11.7%; Score 1306.8; DB 1; Length 46899;
Best Local Similarity 58.4%; Pred. No. 0;

Matches 2680; Conservative 0; Mismatches 1822; Indels 90; Gaps 19;

QY 3489 GTCTCTAATCTACACGACCCGACGCTTGGCGGAATTTCCGCGTGTCTAAGGTGAT 3548
Db 25224 GTCAAGGACGCTTTGACGAGCAATCTGCTGACCTCGCTGATCATCTCCGCGGAGT 25283
QY 3549 CCTGTGCTTACACTCTCATCTCCCAAGTCACTATAGAGGACCTGTGGACAGTCTTAT 3608
Db 25284 TCCCATCGCACGATCGGATTCCTGCGCATCTCATACAGGCGCCCTGTGCAACATCTTC 25343
QY 3609 TCAAGAGCGGACATAGGTTCTGATCAGTTGACGCTGGCACTGTGTATCTGAT 3668
Db 25344 GCTCAGGCGCGCTGTGTCTTGGAACTGAACCTAGTGGACAGTGTACTTATG 25403
QY 3669 CCAATAGCTGTGAATAGCGCGGCTGTCAATGTGACGCGTTCAGTGGGCTCTTGA 3728
Db 25404 CCTGTGCGATCGGAGTGGCGGCGCTCCAGCAAAAGGCGTGGTGGCACTAAC 25463
QY 3729 GCGCTTGAACAGGACGACGACTCTTGAACGACATTTGAAACGACAGATGTGCT 3788
Db 25464 GCGTTGTGACCGGACGAGGCGTTCGCGACGCTTTCGAGACACGATGGGTTGT 25523
QY 3789 GTCAATTTGTTACGAGAGCTTCTGAGAGATGAAAGTCATGTATCT-----CTGT 3842
Db 25524 GTTCAGGCTCATCAACCAAGTCAAGCCAAAGCCTGGGATCATGACTATCAGACGT 25583
QY 3843 GGTTCAGACCTTGACCCGTTTGAAGTGTGAACCAAGACAGACTATCCCTTCAATCTC 3902
Db 25584 GTAGATGATCTGCTTATCTCGCGGCTCAAGAGGAAAGCAACAGCCTTGACCTG 25643
QY 3903 TCACTGAAGCTGGCTGGAAGGACGCTCTTACGACTTGTGTAATGACACATCTTC 3962
Db 25644 ACCTCTGAAACGAGGTGGAAGTGTCACTTACGCTAGGTGACGATGATTCATCTT 25703
QY 3963 ACTATTGTACGACATCATCATCTGATGTTGTGCTCAATGTATCTTGGCGAGAT 4022
Db 25704 TCTATCTTATGACCACTATCTTGTATGCTGACCTGTATGTGCTACGAAAGAA 25763
QY 4023 CTCATTCAGCTCTACTAGCTGCGCTCAAGGACTCAAAAGACCCGCTGTGACACT 4082
Db 25764 CTGGGCGAGTTCTATTCAGGCTGGATCAGGG-----GTCAAGAGCTTATGCGAGCGCAAG 25820
QY 4083 CCTTACTTATCCAGTACAGGACTTTGCAAAATGCGA-----AGACCAATTGATA 4136
Db 25821 TCCCTCCCTATTCAMTACCGGACTTGTGTTGGAGAGGACGAAACCAATCAG 25880
QY 4137 GAGCAGAGAGCACTCACTGAGAAAGCACTCAAAAGCTTTCCCGACAAAG 4196
Db 25881 GAGCAAGCAAGGACTCAAGTATTTGTCACAGAGCTTCGAGATAGCAACCCCTGCGAG 25940
QY 4197 ATCCGACCGACTTGGCCGCTCTGCACTTCTGTCTGAGACGAGGTTGCTATGTT 4256
Db 25941 TTCTTAAGGAGCTCCCTCGGCGCTTATCTGTCTGTGAGTGAAGCGCGTTCTATG 26000
QY 4257 ACCATGACGCGGAGCTTACAGTCCCTTGAAGCTTTTGGAAAGAACACACACGACC 4316
Db 26001 GTGATGATGAGCAGGCTGTATCAGCTCTTACTGATTTCTGCGGAGACCAAGTACA 26060
QY 4317 TCTTGTGCTGTTCTTCAAGTGGCTTCCGCGCGCTATTAATGCTCAACAGCTTGA 4376
Db 26061 TCGTTTCAAGTCTGCTGCGAGCTTCCGACCTGCGACATACCGCTTACCGGAGCACTC 26120
QY 4377 GAGCGTGTCAATGATGACCAATTCGAATGCAACGCACTGAACTGAGATATATC 4436
Db 26121 GAGCGACGCTTGGCAACCAATGCTTACCGGAAACCGGCGCAAGTTGGAAGTCTATC 26180
QY 4437 GCGCTGTTTGTCAATGACGAGTGTATGCAATCAATATGATCAATCAATCTTTGGG 4496
Db 26181 GGTTCCTTGGTTAAACGACAGTGTATGAGATGCGCAATCAAGTGAATGAAACCTTTGAG 26240
QY 4497 ACTTATGAAACGAGTCAAGGCTAGACGACAGACACATTCGAAACGAGATATCCG 4556
Db 26241 TCACTAGTCAAGGCTTCCGCTTGAATGACGACAAAGCCTTTGGAAACAAAGATGCGG 26300

QY 4557 TTTGAGCGCTGTGTATCAGCACTACAGCCTGTATCCAGAGATCTGTACAGACCTCTC 4616
Db 26301 TTTGAGCAGATGTGTATCAACCTTTCTTCCGAGTCAAGATATAGTCAAGAAACCGCTT 26360
QY 4617 GCACAATCACTTTTGTGAGTGCATCAGAAAGACCTTGGAAATTCAGTTCAGAGGT 4676
Db 26361 GTGAGGTCAATGTTTGTGCGCAATCAGAAAGACCTCGGAAGATTCAGCTGGAAGGT 26420
QY 4677 CTCGAGTCCGTACCTGTGCTTACAAAGCTTACACTGATTTGACATGAGAGTTCATCTG 4736
Db 26421 ATGACGACCAAGCTCTGGAAGCGCGCTGTGACAGACTGACCTTGAAGTTCACTTC 26480
QY 4737 TTTCAAGAAACGACAGCCTTAAAGGTAGCGTCACTTTGCGATGAGCTTTCAAAATG 4796
Db 26481 TTTCAAGAGGTTGAAAGCTGACGCGAGCCTCTGTGATCTCAAGGACCTTTGAGGTG 26540
QY 4797 GAGACTTTAAAATGTCCTCAGAGTATCTTTGAGATTTGAGAAACGCGGCTTCAAAAGT 4856
Db 26541 GAGACGATGTGGAATCGTGTATGTTCTGGAATCTTGGCGCGGCTTGAAGCAA 26600
QY 4857 TCGGAGACACAGTCTCAATCTTCTTGACTGATGACATGTGACTTTGAAAAATTTG 4916
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QY 4917 GATGTTCTCAAGCTCAACATGTGACTATCCCGAAGATCGAGCTTGGCTGATGTTCT 4976
Db 26661 GGTCTCTTACAGTGGGAAACAGGCTTACCTCGGAACTGAGTGCATATGCTGTTTC 26720
QY 4977 CAGACCAATCTCTGTTTACCCCGATGCTGTGTGTGTGGAATCTGTGCCATTTG 5036
Db 26721 AGACAGAGGTTCCCGGACCGAGGCCATGCTGTGTGGAATCTCTCAACATTTG 26780
QY 5037 ACCTACACGAGTTGATCGCAGTCTGATATTTCTGCTGATGAGTGGCTTCTGACGCTCA 5096
Db 26781 ACCTATGCGACCTCATGAGGCAATGAAACAACTGCGCCACGCTGTGCGACGCAAT 26840
QY 5097 ATGCTGACAGACGCTTGTGCAATTTTGGCCACGCTCATGTGAGCAATTTGCGG 5156
Db 26841 ATGCGCCCAAGACCTTGTGAGCTGATTCGCGCCACGCTCATGCTCAACATCTGTGCA 26900
QY 5157 TTTCTTGTGTGTGAAGGGAACCTTGGCTATCTTCTCTGATGAGATGGCCCTCG 5216
Db 26901 TTTCTGCTGTGTGAAGGCTATCTGCTTACCTGCTTGTGATGCAATGCGCTGCT 26960
QY 5217 GCGAGATTCAGATATCTTCTGACCTTCTGAGCTTCAATGTTTGTATGAGCCAT 5276
Db 26961 GCTCTATGAGGCTATCTCTGACAGTACAGGCCACAAAGCTGTCTGTGCAAGCT 27020
QY 5277 GATPAGCGCTCCGATATCAGGTTACTPAGCTGAGTTTGTGTATCCGGAGTGG 5336
Db 27021 CATGGGCCGAGCTTGGCTGACGATGGCTGATGAACTGCTGAGTGCAGACGAGCA 27080
QY 5337 CTGAATGACGAATGAGATGCTTTGAAGTATGAGAGACGACAGCAAAAGCCCTCA 5396
Db 27081 CTTGATTCAGTTTATCCGCTGACATGAGCAGATCCATGCTGCGG-----CTTACT 27134
QY 5397 GCCACGAGTCTGCAATCGCTGTATACCTCAGATTCAGTGGCGACCAAAAGGCTC 5456
Db 27135 GCCACAGTCTTGTCTGAGTGTATGTTTACGTCAGGCTCTATCTGGAAACCAAGGCTC 27194
QY 5457 ATGATGAGACCGGTGCTATTTGAAACAGTC---ACAAGTGGCTGTATACCACTAT 5513
Db 27195 ATGATGACACCGCAGCATCTTCACTTGTCAAGAAACGAGATGTTGTTGCACTTG 27254
QY 5514 CTTTGGAAACGAGATGCTCATGAGGCAACATTTGCTTTAAGCGCGCATGTATAGAG 5573
Db 27255 CTTACGCAATTCGAGATGGGAATGTATCAAACTTGTCTTCAACATTCGCTGCAAGAA 27314
QY 5574 ATCTACAGCGCTTTTGTTCGAGAGACCTTGTTCGTTGACTATGATCAACACCTC 5633
Db 27315 ATCTACAGCGCTCTTAAACGATGAGCTGTGTCTGCTTGAATCTTGAAGCTATTTG 27374

Db 29523 AGAAG--GCAATGTCAGCGCGCTTGCCTGTAATGACACCGAGATAGTTCTTTC 29579
Qy 7803 GAAGAGCCACTGAGTGTGGCATGAGTTGACATTCACCTTCTTCAATCTC 7862
Db 29580 GAGGAATACCAATATCTTGAAGAACTGAAGTTGGCATTCAGCAACTCTTCGATG 29639
Qy 7863 GGTGACACTCTCTCTTGGCCAGAGCTCATTTCTGTATGACCAAGCTCAGGTC 7922
Db 29640 GGGCGGCAATTCATCATGCTGCTACGAAAGCTCGACGCCGACTAGCCGCGCATGATACC 29699
Qy 7923 CGATACCTGTCAGAGATGCTTGAACATCCTGATTTGGATCTAGCATCTGTATC 7982
Db 29700 CGGGTTCAGGTCAAGAGGTTGATTAACCGTCTGCTGACTGCTGCTTGCATC 29759
Qy 7983 CGTCAAGGCTGGTTGCAACAACCCGTTTC 8014
Db 29760 GAACAGGCTCGACACCTCATCTGCTTATTC 29791

RESULT 2
US-08-471-119A-4
Sequence 4, Application US/08471119A
Patent No. 5827706
GENERAL INFORMATION:
APPLICANT: Lettner, Ernst
APPLICANT: Schneider, Elisabeth
APPLICANT: Schoerendorfer, Kurt
APPLICANT: Weber, Gerhard
TITLE OF INVENTION: Cyclosporin Synthetase
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5827706artis Corporation
STREET: 59 Route 10
CITY: East Hanover
STATE: New Jersey
COUNTRY: USA
ZIP: 07936
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.119A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kaesenoef, Melvyn
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 100-8029/CONT/CONT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 503 8474
TELEFAX: 201 503 8807
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1713 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Necosmospora vasinfecta
US-08-471-119A-4

Query Match 3.6%; Score 408.2; DB 1; Length 1713;
Best Local Similarity 57.3%; Pred. No. 4e-115;
Matches 950; Conservative 0; Mismatches 638; Indels 69; Gaps 9;

Qy 6403 ACATGGCCGAATGATCCCGTCAGACGATGTGTAGCGACTTCAAGGGTTGACATCAATGT 6462
Db 1 ACATGGGGGATTTGATCGGATGCTCTCGACAGACTTCTTATCTTGACATCAATGT 60

Qy 6463 ATGATGAACTCAATTCGACTTGGATGATGACGAGTGGCTTGTGAGACTAACCCGA 6522
Db 61 ACAGAGGCTCATTTGATTTCCCGGGAAGATGACGAAATGGCTCAGGACATATGACT 120
Qy 6523 CACTTCATGACATTCGCTCTCTAGGCAATCTCTTGAATTTGGAACAGTATGGGCAATGA 6582
Db 121 CACTTCATGACCAACAGCCACCCGGAAGATGCTCGAGATCGGAACCTGTATCGGTATGG 180
Qy 6583 TCCCTTCAACTTGAACA-----GCAGGTTGAGAGTTAGTTGTTGCTTGAACCAATCCA 6636
Db 181 TGGTTTCAATCTTCGGCAAGTTGAGGAACTACAGACTATGCCGCTTGAACCCCTGCG 240
Qy 6637 GATCAGACGCTGATTTGTCACAAACGTAACCGAGTCTATACATGCTTGTGGAAG 6696
Db 241 GCTCCGTCATGCTGCTGGGTTTACAAAGCAATCAAACTTTCCCAAGCTGGCAGAAAGCG 300
Qy 6697 CCAAGTTCAAGTTTGAACAGCTACAGATTTGGTCAAGTGTGATGACTTACCCCTGACG 6756
Db 301 CCGAGTCCAGTTGGAACCGCGAGAGTGTCACTCATCAATGACCTGCTGCGATC 360
Qy 6757 TCGTGTCTCAACTGAGTCAATCAGTATTTCCGCTTCCGAGTACCTTGCAGAAATCG 6816
Db 361 TCGTTGATCAACTCGGTGCGCCATATCTTCCAACTGAGAAATATCTGCTGAGCTGA 420
Qy 6817 CAGACACTTGAATTCATCTGCTTAACGTGACGCGGATTTCTTGGCGATGCCATGCG 6876
Db 421 CGGCAACTGATTTGACATGCTCGCGGCTCAAGGATATTTCTTGGCGCATGAGAACT 480
Qy 6877 AGGCCCAACGAGCACTTCTGCTGCGAGGCTATCCACACTGGGGAAGAAATGCA 6936
Db 481 ATGCAACCAATTAAGAACTTGTGTGCGACAGACAGTCCATTAAGGTTCAATGAT 540
Qy 6937 CGAAGACGATGTTCGACAGAAATGCGAATTTGAGACATGAGAGAGATGGCTTG 6996
Db 541 CTAAAGCCATGTTTCAGACACAGTGGCCCAAGCTTGAAGATGACGAGAAAGATGGCTTG 600
Qy 6997 TTGAACCTGCTTCTTCACTCTGCTTGAAGACAGGTTTCCAGGCTGTGTTGAAATGTTG 7056
Db 601 TTGACCTGCTTCTTCACTCTGCTTGAAGACAGGTTTCCAGGCTGTGTTGAAATGTTG 660
Qy 7057 AGATCTGCAAGAAACATGGAAGCTGTGAATGAGCTCAGTGGCTATGATATGCGCTG 7116
Db 661 AGATCTGCAAGAAAGAGATGGCGCGACCAACCAACTCAGCTTTCGATATGCTGCTG 720
Qy 7117 TTGTCACGTTCCGGG-----TTCACTTGAAGATGAGCTTGTGCTTCCGCTTG 7164
Db 721 TTATTCATGTGGAGGCGACAGATGCCAATGGGAGATGAGATTAAGCAATGGCTG 780
Qy 7165 AGAAGAT-----GACTGATGACTTTCAAGCAATTCATTTGAACCAAGAT 7212
Db 781 TCAAGATATGATTCGAAAGGCTGGGTGACTTCCGCGGACAGAGATGAGACCTGACG 840
Qy 7213 CACTGGGTACCTTTCAGATCTTCA-----GATGTGCTATCATGCGACAGAA 7266
Db 841 CTCTCTTGGACGCTCTTCAGAACCGCCACAGTGCATGACTGTGTTCCGTGATGACA 900
Qy 7267 TTCCTTTCGAATTCAGGCTTGTGAAGACAGGTGCTGCTCTCTCAATAGCAACATCG 7326
Db 901 TCCCATACAGCAAGACATATGAGGCGCATCTGTCTGATCACTTGAAGATGACGAG 960
Qy 7327 ATG-----AGTGCAGTATCAACCAATTCGCTCAGCGCGAGG 7365
Db 961 ACAGCACTTCAGATGACAGCAAGCAAGCGCTGATATGCGCACTCAATCAAGGCGAAG 1020
Qy 7366 GCGACTCATCATCTGCTTCCGACATCTTTCGATGCTGTGGGAAACCGGCTTCCGTG 7425
Db 1021 AATGCCCTGCTCTCTCAGTGGCGACCTGATTAAGATTTGATGAGGATGAGGCTTCCAG 1080
Qy 7426 TCGAGTCACTTTCAGACGACAGTGGTCTCAGAAATGATGATGACGCTGTTTCCATC 7485
Db 1081 TTGAGACAGCTGGGCTCGACACACTTCCAGCGCGGAGCTGATGCTGTTTCCACC 1140

Qy 7486 -----ATTGTTGCTCCCAAGGCGCTACTGTGCAACTTTTCTTACGCAACCATCACC 7536
Db 1141 GATTGCAAAAACCAAGACACTCGGGTCATGTCAATGTTCAAGTTCCCAACTGAAACAAGG 1200
Qy 7537 TTGAGGGGTCTGATC-TCTTCACCAATGACCCCTTGACGCACTGCAAAACGTCGATC 7555
Db 1201 GGGCGGCTTCGAGCACTTCACCAATGCGCCGTACACCTGTGTCAGAGCGCGGCTG 1260
Qy 7596 GCCATGCAATCCGCGAGGAGCTTCGGTCTTACTTCATGTCATGATCCCATGCAAC 7655
Db 1261 GAGGCAAAAGTCCGCGAGCGGCTGCAATCGCTGCTTCATGTCATGATTCCTCTCGG 1320
Qy 7656 ATCGTTGCTGCAAGATGCTCTCAAGCCCAATGATTAAGTTGACCGGAGAACTC 7715
Db 1321 ATCATGTGCTCATGATGATGCTCTCAAGCCCAAGGAGTGAATCGAACAAGCTC 1380
Qy 7716 TCTGCAAGGCAAAAGTTGTAACGA-AGCAGCAGACAGCGCGCTTACCGACATTTCC 7774
Db 1381 GCTGCAAGCGCCGGGTCACTCCCAACATTTGCCCAAGCAGTTTGAATTGTGCGCGC 1440
Qy 7775 CATCAGTGAAGTGAATC-ATTCTTGGCAAGAAGCACAAGAGTGTGGCATGAAAG 7833
Db 1441 ACGGACGGAATGAGGTGCGTCTCTGCAAGAAATTTACGATCTACTAGCGCTCAAGG 1500
Qy 7834 TTGACATTAACGATCACTTCTTCAATCTCGGTGACACTCTCTTGGCCAGAACTCA 7893
Db 1501 TCGGCAATTAAGCACTTCTTCAAGTTGGCGGCCATTCGCTGCTGGCAGCAAACTGA 1560
Qy 7894 TTTCTGTATGCAACCAAGCTCAAGGTCCGATCACTGTCAAGATGTCTTTGACATC 7953
Db 1561 GCCACACGTAAAGTCGACAGCTGACCGCGGTGCACTGTAAGACATCTTTGACAGC 1620
Qy 7954 CTGTATTTGGGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 7990
Db 1621 CAGTACTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCT 1657

RESULT 3

US-09-252-991A-71
; Sequence 71, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 71
; LENGTH: 7527
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-71

Query Match 1.2%; Score 136.6; DB 4; Length 7527;
Best Local Similarity 44.1%; Pred. No. 2,1e-30;
Matches 716; Conservative 0; Mismatches 899; Indels 10; Gaps 3;

Qy 3602 GTCTTATTCACAAAGCCGACTAGTGTCTCTGATCAGTTGACGTTGCGACTGTGTGTA 3661
Db 5118 GTGCAATGCTCAGCAAGCATGTGTCTCTGAAACTGAGCCTGAAAGCGGCGCTTA 5177
Qy 3662 TCTGATTCATATGCTGTGAATGCGCGGCTGTCAATGTCAACCGTTACGTCGGGC 3721
Db 5178 TCAATCTCCAGGCTACTGACGTGCGTGGCTCTGACCAAGCGGCTTGCAGCAGGC 5237
Qy 3722 TCTTGACGCGCTTGACAGGACGAGACTCTTGAACGACATTTGAAGCCAGATGG 3781

Db 5238 CTTCGATTTGCTGTGCTGCGCCACGAGACCTTGCACACCGCTTGAGAGAGTGCAGCG 5297
Qy 3782 TGTGCTGTATCAAAATGTGTACAGAAAGCTTTCTGAGAGATGAAGTCATGATCTCTG 3841
Db 5298 TCAAGCGCGCCAGCAAGTCTGTGGCAACATGCTTGGCATTTCTCTGAGAGATTTGCGC 5357
Qy 3842 TGTGTCAGACTTACCCGTTTG--AGTGTGAACCAAGAACACTACTCCCTTCAA 3898
Db 5358 CGGGGAGAGGAAGCAAGTTTGGCGCAGCGGGTGGCCGAGAAATCCGCGCATTCGA 5417
Qy 3899 TCTCTCATCTGAACTGCTGAGAGCAGCGCTTTACGACTTGTGTGAAGTGAACCAT 3958
Db 5418 CTGTGCTGAGGCGCTGTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5477
Qy 3959 CTTCACTATGTATGATGATGATCATCTGATGATGATGATGATGATGATGATGATGATGAT 4018
Db 5478 GTTGTGATCAACCCAGACCAATATGTCGAGGTTTGGTCGATGAGTGAATGATGATGAT 5537
Qy 4019 CGATCTCAATCAGCTTACTACTGCTGCTCAAGACTCAAAAGACCCGCTGTGAGACT 4078
Db 5538 GGAATCTGCTCAAGGCTTATGCTGCGGCGCGCGCGCGGCAACCAAGCGTGGCGCAT 5597
Qy 4079 CACTCTTACTATTCAGATCAGCGACTTTGCAAAATGCGAAGAACCAATTCATGA 4138
Db 5598 GACGCTGAGTACGCGCATATGCTGCTGAGCATCGCGCTGCTGCTGCTGCTGCTGCTGCT 5657
Qy 4139 GCAAGAAAGCACTCAACTATGTAAGAAAGCAACTCAAGACTCTTCCAGCAAAAT 4198
Db 5658 CGCGCGGAGCTGATTAAGCTGAGCGCTGAGCGCTGAGCGCGAGAGCGCGCTGTAAT 5717
Qy 4199 CCGACGCACTTTGCGCGCGCTGCACTTGTCTGAGAGCAGCAGTGTGCTGATCACTTAC 4258
Db 5718 GCGCGCGGACCGGCTGCG 5777
Qy 4259 CATGACGCGGAGCTTACCAAGTCTTCAAGCTTCTGCAACCAACCAACCAAGCTTC 4318
Db 5778 GCTGCGGCTGCAATTAAGAGAGCTGCTGCTGCGCGCGCGGAGGCTGTCAACCC 5837
Qy 4319 TTTGCTGCTTCTTACTGCTGCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4378
Db 5838 GTTCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5897
Qy 4379 CGCTGATTTGATCACCAATGCGAATGCGAATGCGAATGCGAATGCGAATGCGAATGCGA 4438
Db 5898 TATTCGCTGCGGCTTACTTATGCGCAACCGCAACCGCGCGCGCGCGCGCGCGCGCT 5957
Qy 4439 CTGCTTGTCAATACGAGGTATGCGAATCAACATGATCATGACGATACCTTTGGAC 4498
Db 5958 CTTCCTGCTCAATACCGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6017
Qy 4499 TTTGATCAACCAAGTCAAGCTTACGACAGCAGCATTTGAGAACGAGATATTCGCT 4558
Db 6018 TTTACTGGGCGCGCTGCGAGGCGGCTGCGGCGCGAGCGCGACAGCAATTCGCGCT 6077
Qy 4559 TGAAGCGGTTGATACAGACTACAGCTGATCCAGATCTGCAAGATCTGCAACCTCTGC 4618
Db 6078 CGAGCAATTTGCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6132
Qy 4619 ACAACTCAATTTTGCAGTGCATTCACAGAAAGACTTGAAGATTCAGTTCAGGGCT 4678
Db 6133 TTTCAAGTATGATTAACACAGAGGCGGAGCGGAGATGCGCAAGTGTGATGTTG 6192
Qy 4679 CGAGTCCGTACTGTGCTTACGAAAGGTA--CACTGATTTGATGATGATGATGATGAT 4736
Db 6193 CACATCAGAGTTTGTGCTGAGAGGCTGCGCAGCAAGTTCAGCTTGGCCCTGATACC 6252
Qy 4737 TTTCAAGAAACCGACAGCTTAAAGGTAGCGTCACTTTGCGGATGAGTGTCAAAATG 4796
Db 6253 TGGAAACCCCGAGCGGCTTTGGGCGCGCTGACCTTACGACGACGACCTTGTGAGCG 6312
Qy 4797 GAGACTGTTGAAATGTGTCAGATATCTTTGAGATTTGAGAAACGCGCTTCAAGT 4856
Db 6313 CGAGCGTGCAGCGCATGCGCGGCTTGGCAAACTGCTGCGCGCATGCTTGGAGAAC 6372

Db 4386 GCGGGCGGAGCAAGCTTCCGGAAGTCCGGGACTGAGCATGAAAGCAGCGCTGGGA 4445
 Qy 4703 AGGCTACA---CTGATTTGACATGAGATTCATCTGTTTCAAGAAACGACACCTTAA 4759
 Db 4446 AAGCCATACGGCGCAGTTGACCTGGTGTGATGATCTGATCCGAGTCCGACATCTG 4505
 Qy 4760 AGGTACCGTCACTTGGCCGATAGCTGTTCAAAATGAGATCTTGAATATGCTCAG 4819
 Db 4506 GGGGGGCGTGTATATGCGACGATCTATTCGATGCTGACCGCAGAGCGCTGGTACG 4565
 Qy 4820 AGTATCTTTGAGATTTGAGAAACGGGCTTCAAAGTTCCGCGACACAGTCTCAACT 4879
 Db 4566 GCATTTGGCAGAACCTGCTGATGATCTTCGGGATGCTGAGCTCCGCTGGGAGAGCT 4625
 Qy 4880 TCCCTTGACATGAGCATGATGATCTCTTGAATAATGAGATGTTCTCAACCTCAACATG 4939
 Db 4626 GGCATGCTGCGGAGAGAGCGGAGATCATCGGCACTCTGAAACCGCAGCGATTC 4685
 Qy 4940 CGACTATCCCGAGAAATCGAGCTTGGCTGATGCTTCAGAACCCAGTCTCTGCTTACC 4999
 Db 4686 GGGCTATCCGGCAACCGCTGATGACACGAGATGCGGCGGCGGTATGAGCGC 4745
 Qy 5000 CGATAGCTGCTGCTGCTGATGATCTCTGCGCATGATGACCTTACCGAGTTGATGCCA 5059
 Db 4746 GGTATGCGGTGCGGTGATCTTCAGCAGAGAAAACTCACTACCGCGAGCTGATAGCCG 4805
 Qy 5060 GTCTGATTTCTGCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5119
 Db 4806 GGCACACCGCTGCGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATG 4865
 Qy 5120 AGTATTTGCCCCAGGATCATGATGATGATGATGATGATGATGATGATGATGATGATG 5179
 Db 4866 GATCGCATGACGACGACGACGACGACGATGATGATGATGATGATGATGATGATGATG 4925
 Qy 5180 CTTCGCTTATCTTCT 5239
 Db 4926 CGCGCTTATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4985
 Qy 5240 TGGATCTTCTGCGGCTTACCATGTTGTTGATGATGATGATGATGATGATGATGATGAT 5299
 Db 4986 GGCACATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5045
 Qy 5300 GGTATCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5359
 Db 5046 CGAGGGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5105
 Qy 5360 CTTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5419
 Db 5106 TGATTCAGAGGTGCGCTGACGCGCCAA-----CCTGCTATGATGAT 5150
 Qy 5420 GTTATCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5479
 Db 5151 CTACACCTTCCGCTTCCACCGGATGATGATGATGATGATGATGATGATGATGATGATG 5210
 Qy 5480 T---CGAAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5536
 Db 5211 CGCCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5270
 Qy 5537 CATGCGACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5596
 Db 5271 CTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5330
 Qy 5597 AAGGACACTTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5656
 Db 5331 CGGCGGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5390
 Qy 5657 GTTTTCCGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5716
 Db 5391 GCATGCGC---ACGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5449
 Qy 5717 TCTCCGAGTCCGAGAGGCTCTGAGAAC---TTGATGATGATGATGATGATGATGATGAT 5772
 Db 5450 AGCATGCGGAGCGGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5509

Qy 5773 CAGATTCAGCGGCCGAGATGCTCTGATGCTGAGGAGACTTATCAAGGGGTCCAGTGT 5832
 Db 5510 CGGTGCGGAGGCGACACTTATGACTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5566
 Qy 5833 ACAATGTTACGGGCCCAAGAGATGAGTATGATGATGATGATGATGATGATGATGATG 5892
 Db 5567 TCACCGGATACGGCCGACCGGAGACCGGTGATGCGCGGCTGCTGTGAGAAAGCAGGCG 5626
 Qy 5893 CTGAGTCTTATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5949
 Db 5627 GCGATGCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 5686
 Qy 5950 ATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6009
 Db 5687 ACATCTTCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 5746
 Qy 6010 CTGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6066
 Db 5747 GCGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 5806
 Qy 6067 TGCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6126
 Db 5807 TGCAGGACCTTCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 5863
 Qy 6127 ACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6186
 Db 5864 GTGGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5923
 Qy 6187 GTGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6246
 Db 5924 GAGCTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5983
 Qy 6247 GAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6279
 Db 5984 GCGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6016

RESULT 5

US-09-410-551B-1
 ; Sequence 1, Application US/09410551B

; Patent No. 6503737

; GENERAL INFORMATION:

; APPLICANT: KOSAN BIOSCIENCES, Inc.

; APPLICANT: REEVES, CHRISTOPHER

; APPLICANT: CHU, DANIEL

; APPLICANT: KHOSLA, CHAITAN

; APPLICANT: SANTI, DANIEL

; APPLICANT: WU, KAI

; TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA

; FILE REFERENCE: 30062-20026.00

; CURRENT APPLICATION NUMBER: US/09/410, 551B

; PRIOR FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: US 60/139,650

; PRIOR FILING DATE: 1999-06-17

; PRIOR APPLICATION NUMBER: US 60/123,810

; PRIOR FILING DATE: 1999-03-11

; PRIOR APPLICATION NUMBER: US 60/102,748

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PasteSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 77536

; TYPE: DNA

; ORGANISM: Streptomyces hygroscopicus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (52275)...(71465)

US-09-410-551B-1

Query Match 0.9%; Score 104; DB 4; Length 77536;
 Best Local Similarity 47.1%; Pred. No. 1,8e-19;

Matches 465; Conservative 0; Mismatches 505; Indels 18; Gaps 4;

QY 3589 GACCTGTGAGCATCTTATTCAAGAGCCGACATAGTCTTGATCAGTTGACCTTG 3648
 Db 47870 GCCCGTCTTGTGCTTCTTGACAGGGGCGATCTGTTCTCCAGCAATTGGACCCGG 47929
 QY 3649 GCAGCTGTGGTATCTGATTCATATGCTGTGAGATGCGGCGCTGTCAATGTGACG 3708
 Db 47930 AGAGCAACGCTTAATCTCCCGCTGTGACAGCCCTGCGCGGTCTATTGAGACCGCGG 47989
 QY 3709 CGTTAGTGCGGCTCTTGAGCCCTTGAACAGAGACGAGACTCTTAGAACACATTTG 3768
 Db 47990 CCTGAGCGCTGTGCGCTGCTGTGCTGCGGCGCACGAGCGTTGCGACGGTGTTCG 48049
 QY 3769 AAGACGAGATGATGTGCTGTGTAACAATTGTTCACGAAAGCTTTCTGAGAGATGAAAG 3828
 Db 48050 ACACCGCGAGCGGAGCCCTTCAAGGGGTCTTCCCGCC---CGAACAACCTCTGCG 48106
 QY 3829 TCATTGATCTGTGTGTTAGACCTTGACCCGTTTGAAGTGTGAACCAAGAACAGACTA 3888
 Db 48107 GCCACGCGCGGCGGAGGAGGAGGAGCGCCCGCGCTGTCCGCGACGAGATCGCGG 48166
 QY 3889 CTCCTTCAATCTCTATCTGAAAGCTGTGAGAGGACGCTTTCAGACTGTGTAAG 3948
 Db 48167 CGCGGTTCGACTGTGCGACCGGCGGCTTGAATCAGGCGCTGTGATCCGCTCGGTGACG 48226
 QY 3949 ATGACCATCTCTCACTATTGTGATGATGATCATCATCTAGATGTTGTTCAATTGATG 4008
 Db 48227 ACACCAACGTTCTGCGGTACCTGTGACCATGTGCGCGGCGAGCGGTGCTGTGCGGC 48286
 QY 4009 TCTTGGACGCGATCTCAATCACTCACTCACTGCTGCTCAAGACTCAAAAGACCGC 4068
 Db 48287 TCTTCCCAATGAACTGACAGCCCACTACAGGCGCTGCGCA-----CACTGCGCGC 48340
 QY 4069 TGTGACAGCTCACTCTCTACTCACTCACTCACTCACTGCTTGAAGAAATGCGAAGAAC 4128
 Db 48341 CTGCGCAACTGCGCGCTGTGCGGTGAGTACGCGGCTTGTGCGGAGCGGCGG 48400
 QY 4129 AATTCA-----TAGACGAGAGAGAGCACTCAACTCTGAGAGAGCACTC---AAG 4179
 Db 48401 AACTCACCGGCGCGGAGTGAAGAGCGGTGTGCGCTACTGCGGAGACAACTCCGGGGCG 48460
 QY 4180 ACTTCTCCGAGCAAGATCTCCGACGACTTGTGCGCGCTGTGCTGTCTGTGAGACG 4239
 Db 48461 CCCGCGGCGGCTGCGCTCCCGACGACGCTGCCCGCGCGGTGCGGACGCGGACG 48520
 QY 4240 CAGGTGCGTACATGTTACATGACGAGCGGAGCTCTACAGTCCCTTCAAGCTTCTGCA 4239
 Db 48521 CGGCGCATGCGCGAGTGGCGGCGCGCGGCTGTGCGCACCGCGGTCTCACTGCGCGC 48580
 QY 4300 ACGAACACAAACGACTCTTTCGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4359
 Db 48581 GCGATCTCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 48640
 QY 4360 GTCTCAAGCTGTGTAAGAGCTGTCTGTTGATACCAATTTGCAATTCGAAACGACCTG 4419
 Db 48641 GCGAGGCGGAGCGCGGAGCGTGTGCGGACGCGCGGTGCGAACCAGACGCGGCGG 48700
 QY 4420 AACTGAGGATATCATGTGCTGCTTGTCAATAGCAGTGTATGCGAATCAACATATATC 4479
 Db 48701 CGTACGAGGCTGTATGGAATGGAATGTTGTCAACAGCTGTGCGCGGCGGCACTCTCGG 48760
 QY 4480 ATCAGCATCTTCTTGGAGACTTGTATCAACCAAGTCAAGGCTCAAGACAGCAGCATTTG 4539
 Db 48761 GCGATCTGCTGCTTCCGGAATCTCTCAACGCTGTGCGGCGGCGGACGACGACGCTTTCG 48820
 QY 4540 AGAAGAGATATTCGTTGAGCGCGT 4567
 Db 48821 CCGACGCGGACCTGCGGTGAGAAAGT 48848

Sequence 1, Application US/09940316B
 Patent No. 6759536
 GENERAL INFORMATION:
 APPLICANT: KOSAN BIOSCIENCES, Inc.
 APPLICANT: REEVES, CHRISTOPHER
 APPLICANT: CHU, DANIEL
 APPLICANT: KHOSLA, CHAITAN
 APPLICANT: SANTI, DANIEL
 APPLICANT: WU, KAI
 TITLE OF INVENTION: POLYKETIDES ENCODING THE FBA GENE OF THE PK-520 POLYKETIDE SYNTH
 TITLE OF INVENTION: GENE CLUSTER
 FILE REFERENCE: 30062-20026.11
 CURRENT APPLICATION NUMBER: US/09/940,316B
 CURRENT FILING DATE: 2001-08-27
 PRIOR APPLICATION NUMBER: 09/410,551
 PRIOR FILING DATE: 1999-10-01
 PRIOR APPLICATION NUMBER: US 60/139,650
 PRIOR FILING DATE: 1999-06-17
 PRIOR APPLICATION NUMBER: US 60/123,810
 PRIOR FILING DATE: 1999-03-11
 PRIOR APPLICATION NUMBER: US 60/102,748
 PRIOR FILING DATE: 1998-10-02
 NUMBER OF SEQ. ID NOS: 72
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 77536
 TYPE: DNA
 ORGANISM: Streptomyces hygroscopicus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (52275) ... (71465)
 US-09-940-316B-1

Query Match 0.9%; Score 104; DB 4; Length 77536;
 Best Local Similarity 47.1%; Pred. No. 1,8e-19;
 Matches 465; Conservative 0; Mismatches 505; Indels 18; Gaps 4;

QY 3589 GACCTGTGAGCATCTTATTCAAGAGCCGACATAGTCTTGATCAGTTGACCTTG 3648
 Db 47870 GCCCGTCTTGTGCTTCTTGACAGGGGCGATCTGTTCTCCAGCAATTGGACCCGG 47929
 QY 3649 GCAGCTGTGGTATCTGATTCATATGCTGTGAGATGCGGCGCTGTCAATGTGACG 3708
 Db 47930 AGAGCAACGCTTAATCTCCCGCTGTGACAGCCCTGCGCGGTCTATTGAGACCGCG 47989
 QY 3709 CGTTAGTGCGGCTCTTGAGCCCTTGAACAGAGACGACTCTTAGAACACATTTG 3768
 Db 47990 CCTGAGCGCTGTGCGCTGCTGTGCTGCGGCGCACGAGCGTTGCGACGGTGTTCG 48049
 QY 3769 AAGACGAGATGATGTGCTGTGTAACAATTGTTCACGAAAGCTTTCTGAGAGATGAAAG 3828
 Db 48050 ACACCGCGAGCGGAGCCCTTCAAGGGGTCTTCCCGCC---CGAACAACCTCTGCG 48106
 QY 3829 TCATTGATCTGTGTGTTAGACCTTGACCCGTTTGAAGTGTGAACCAAGAACAGACTA 3888
 Db 48107 GCCACGCGCGGCGGAGGAGGAGGAGGAGCGCCCGCGCTGTCCGCGACGAGATCGCGG 48166
 QY 3889 CTCCTTCAATCTCTATCTGAAAGCTGTGAGAGCGCTTTCAGACTGTGTAAG 3948
 Db 48167 CGCGGTTCGACTGTGCGACCGGCGGCTTGAATCAGGCGCTGTGATCCGCTCGGTGACG 48226
 QY 3949 ATGACCATCTCTCACTATTGTGATGATGATGATCATCATCTAGATGTTGTTCAATTGATG 4008
 Db 48227 ACACCAACGTTCTGCGGTACCTGTGACCATGTGCGCGGCGAGCGGTGCTGTGCGGC 48286
 QY 4009 TCTTGGACGCGATCTCAATCACTCACTCACTGCTGCTCAAGACTCAAAAGACCGC 4068
 Db 48287 TCTTCCCAATGAACTGACAGCCCACTACAGGCGCTGCGCA-----CACTGCGCGC 48340
 QY 4069 TGTGACAGCTCACTCTCTACTATCACTCACTCACTCACTGCTTGAAGAAATGCGAAGAAC 4128
 Db 48341 CTGCGCAACTGCGCGCTGTGCGGTGAGTACGCGGCTTGTGCGGAGCGGCGG 48400

QY 4129 AATTCA-----TAGACAGAGAGAACACTCACTACGTGAGAGAACATC---AAG 4179
DB 48401 AACTCAACCGGCGCGGAGCTGAGACAGCGGCTGTGGCGGAGACAACTCCGGGCG 48460
QY 4180 ACTCTTCCCAAGAGAGATCCGACCGACTTTGGCCGCTTGCACCTTGTCTGAGACG 4239
DB 48461 CCCCCGGCGGCTGCGCCCTCCCAACGACGCTCCCGCGCGGTGCGGACGCGGACG 48520
QY 4240 CAGGTTGCGTACATGTTACATGACGAGCGACTCAAGTCCCTTGAAGCTTTCGA 4299
DB 48521 CGGCGATGCGCGAGTGGCGCGCGCGCGCGCTGGCCACCGCGCTTCACTCCGCG 48580
QY 4300 ACGAACAACAACAGACTCTTTCGCTGCTTCTTACGTGCGTCCGCTCATATTATC 4359
DB 48581 GCGACTCGGCTGGGTGCTGTTATGACCTGCTGGGGGCTTCAAGCGGTCTCTGCC 48640
QY 4360 GTTCTACAGCTGTTGAAGAGCGCTGTCAATTGGTACCAATTGGGAATGCAACGACCTG 4419
DB 48641 GCGAGGCGGCGACGCGGAGCGTGTGCGCACCGCGTGGCGAACCTTACGCGGCGG 48700
QY 4420 AACTGAGGATATCATGCGCTTGTGCAATACGAGTATGCGAATCAACATAGATC 4479
DB 48701 CCGTACGAGGCGCTGATGAGATGTTGTTCAACAGCTGCGGCTGGCGGACCTTCG 48760
QY 4480 ATCAGCATACCTTGGGACTTTGATCAACCAAGTCAAGCTACGACGACGACTTCG 4539
DB 48761 GCGATCGCTGCTTCCGGAACTCCTGACCGGCTGGCGGACGACGACGAGCGCTTCG 48820
QY 4540 AGAAGAGATATTCGCTTGGCGGCT 4567
DB 48821 CCCACGCGGACCTGCGCTTGAAGACGT 48848

RESULT 7

US-09-252-991A-6997
; Sequence 6997, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6997
; LENGTH: 10023
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6997

Query Match 0.94; Score 103.8; DB 4; Length 10023;
Best Local Similarity 44.8%; Pred. No. 3.9e-20;
Matches 460; Conservative 0; Mismatches 552; Indels 15; Gaps 1;

QY 3585 GAGGAGCTGTGAGAGCTTATTCAAGGCGGACTATGTTCTGTGATCAGTTGAC 3644
DB 4777 GAGCAGCGGCTGCGGCTGTCTACTGCAAGAGGATGTTCTCTGGCAACTGGAG 4836
QY 3645 GTTGGCAGTGTGTGATCTGATTCATATGCTGTGAAATGCGCGGCGCTGTCAATGC 3704
DB 4837 CCGGACAGCGCGGCTTACCAAGTGTGCGGCGCTGCAAGCGGCGCGCTGAGCGTG 4896
QY 3705 GAGCGTACGCTGTGAGGCTTGAAGAGGACGACGACGACTTTTGAAGACGA 3764
DB 4897 GCGCGCTTGAAGCGCGGCTTGAAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 4956
QY 3765 TTGAAGACGAGATGCTGTGCTGATCAAAATTGTTACGAGAGGCTTTCTGAGAGATG 3824

DB 4957 TTCCCGACGCTGACGCGCTGCGGTACAGCGGCTGACGAGCGGCGCTGACATG 5016
QY 3825 AAGGTATGATCTGTGTGTTGACCTTACCCGTTTGAAGTTGAACA----- 3877
DB 5017 GACTGGAGAGATTTCTCCGCTGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5076
QY 3878 -----AGAGAGACTACTCCCTTCATCTGTCAATCTGAAGCTGGCTGAGAGCGAG 3929
DB 5077 GCGGACGAGGAGGAGCGCGGCGCTTGAACCTTGAAGAGGCGGCGGCTGAGCGGCTG 5136
QY 3930 CTCTTACGATTTGTGTGAAGTACACATCTCTACTATTGTATGATCAATCATCTCA 3989
DB 5137 ATGGTGAAGTGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5196
QY 3990 GATGTTGTGCAATGATGTTGTTGCGAGCGGATCTCAATAGCTTCACTGAGCTGCG 4049
DB 5197 GAGGCTGGGCGATGAGCATTTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5256
QY 4050 AAGGACTCAAAAGACCGGCTGTGACACTCTCTTACTTATCCAGTACAGGACTTT 4109
DB 5257 GAGGACCGGAGATGCGCGCTGAGAGCGGTTCCGCTCAGTACCTGACCTACAGGTG 5316
QY 4110 GCAAAATGCGAGAGACCAATTCAATGAGCGAGAGAGCACTCACTACTGAGAGAG 4169
DB 5317 CAGCGGAGTGGCTGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 5376
QY 4170 CAATCAAAATCTTCTCCGAGAAAGATCCGACGCACTTTCGCGCGCTGACTTCTG 4229
DB 5377 CTGGGCAACGAGATCGGCTGCTGCACTGCGGCGGCGGCGGCGGCGGCGGCGGCG 5436
QY 4230 TCTGAGACCGAGGTTGCTGATGTTACATGACGCGGCGGCTTACAGCTCTTCA 4289
DB 5437 AGCCACGAGGCGACCTTACCGCTTCACTGAGCCCGGAGCTGCGGCGGCGGCGG 5496
QY 4290 GCTTCTGCAAGAACCAACAGACTCTTTCGCTGTTTCACTGCTGCTTCCGCTCC 4349
DB 5497 CGCTTCAACCGCGCGCGGCTGACCATGTTATGACATGACCGGCACTTTCGCGG 5556
QY 4350 GCTCATATGCTCTCAAGCTGTGAAAGAGCGTGTCACTTGGTACCAATTGGGAATCG 4409
DB 5557 TTGCTTACCGCTACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 5616
QY 4410 AACGCACTGAACTGAGGATATCATGCGCTGCTTGTCAATACGAGTATGCGAATC 4469
DB 5617 ATCCGCGGAGAGGAGGAGGCTGATGCGGCTTCTCAATACGAGTGTGCGCTGC 5676
QY 4470 AACATGATCATGATCACTTGTGAGCTTTGATCAACCAAGTCAAGCTACGACGA 4529
DB 5677 CGGCTGACGAGATGAGCGGCTGCGGAGCTGTTGAGCAGGTGCGGCGGCGGCTG 5736
QY 4530 GAGCATTCGAGAACAGATATTCGTTGAGCGGCTTATACAGACTACAGCGTGA 4589
DB 5737 GATGCGCATGCGACGAGGAGCTGCGGCTTGAACCACTGTGGAAGCTTGAACCTCG 5796
QY 4590 TCCAGAG 4596
DB 5797 CGGAGCG 5803

RESULT 8

US-09-252-991A-8892/c
; Sequence 8892, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 8892
 ; LENGTH: 3315
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-8892

Query Match 0.9%; Score 97.8; DB 4; Length 3315;
 Best Local Similarity 42.7%; Pred. No. 1,2e-18;
 Matches 703; Conservative 0; Mismatches 917; Indels 25; Gaps 3;

QY 3600 CAGTCTTATTACAAAGCCGCACTATGCTTCTGATGAGTTGACGTTGCACTTGTG 3659
 DB 3207 CTGCTTACGCCCCGACGCGCATGTGTTCTCTGACACCTGAGCCACAGATGGCGCC 3148
 QY 3660 TATCTGATTCATATGCTGTGAGAAATGCGGGGCTGCTCAATGTGACGGCTTACGTCG 3719
 DB 3147 TACAACTGCGCCAGCGGGGTGGCTGACCGGATGCGCCAGGGGCTGGAGCGC 3088
 QY 3720 GCTCTTGCAGCGCTTGAACAGCAGACGAGACTCTTGAACGACATTTGAAGACAGAT 3779
 DB 3087 GCCTTGCACGCTGCTGTGACGCTGATGAAACCTGCTGACGATGTTCCGCGGGCGCC 3028
 QY 3780 GGTGTGCTGTACAAATTTGTTCAAGAGAGCTTTCTGAGAGATGAAGTCAATGATCTC 3839
 DB 3027 GACGACGCTGCGGCGAGCGCCCTGCAACGCCCTGAGAGTTCCTTCAAGATTTGC 2968
 QY 3840 TGTGCTT-----CAGACTTGAACCCGTTTGAAGTGTGAAACCAAGACAG 3884
 DB 2967 AGCGGCTGCTGAGCGCCGACAGAGAAAGCCGCTGCGCGAGGAGCGCAGCGGATCG 2908
 QY 3885 ACTACTCCCTTCAATCTCTCATCTGAAGCTGGCTGAGAGCGACTTTACGACTTGT 3944
 DB 2907 TTGAGCGCTTCACTGCTGTGAGAGGGCCCTGTGCGGGCTGATCCGCTGGGC 2848
 QY 3945 GAAGATGACCACTCTCACTATTTGTCATGATCATCATCTGATGTTGTTCAAT 4004
 DB 2847 GAGGAGGCGATGTGCTGTGATGACCTGATCATATGCTGTCCAGCGGCTGGTCATG 2788
 QY 4005 GATGCTTTGGAGCGGCTTCAATCAGCTCTCACTGCTGGCTCAAGAGACTCAAAAGC 4064
 DB 2787 AAGGTGCTGATCGAAGAAATTCAGTCTTTTACAGTCTCTATGCGATGGGCGAAGCCC 2728
 QY 4065 CCGCTGTGACACTCACTCTCTCACTATCCAGTACAGACGACTTTGCAAAATGGCAGAA 4124
 DB 2727 GGCTGTGCGGCTTGGCGGATCGATGACGCGATTAACGCCCTGTGGCAGCGAGTGGCTG 2668
 QY 4125 GACCAATTCATAGACAGAGAGCAACTCACTACTGAAAGAGCAACTCAAAAGCTT 4184
 DB 2667 GAGGCGGATGAGAGAGCGCCAGTGAATGAGCGCGGCAAGCTCGGCGAGCGGAT 2608
 QY 4185 TCCCCAGCAAAATCCCGACCGACTTTGCCCCGCTCCTCACTTGTGTGAGAGCGAGT 4244
 DB 2607 CCGGCTCTGAGTGGCGACCGACACCCGCGGTGGGCTTCCAGCTACCGTGGAGC 2548
 QY 4245 TGGCTACATGTTACATCGACGAGGAGCTCTACAGTCCCTCGAGCTTCTGCAAGAA 4304
 DB 2547 CATTACAGATTCAGATCGAGCGGCGCTGCGCAGGCGCTCGCGGACCGCCGAGCGC 2488
 QY 4305 CACAAACGACCTCTTCTGCTGTTCTTCTAGCTGCTGCTGCGGCTCATTAATGCTTC 4364
 DB 2487 CAGGCGGTGACCGCTTCACTGTGCTCGGCGGCTTCAATATCTCTGCAACGCTAT 2428
 QY 4365 ACAGCTTTGAAGCGCTGTCTATGTACACCAATTGCGAATGCCAACCGACCTGAATG 4424
 DB 2427 AGCGGCGAGACCGACTGCGGGTGGGCTCCCATGCGCAACCGCAACCGGCGAGAGTG 2368
 QY 4425 GAGGATATCATCGGCTGCTTGTCAATACAGATGATGATCAATCAATGATCATCAC 4484
 DB 2367 GAAGGCTGATCGGCTGCTTGTCAACACCGAGGTGCTGCGCTGGATTTGAGCGCGC 2308
 QY 4485 GATACCTTTGGAGCTTTGATCAACCAAGTCAAGGCTACGACGACGACGATTTGAGAAC 4544

DB 2307 ACCTGCTGCGACCCCTGCTGCGCGGCTCAAGACACCTGTGTCGCGCCAGCGCAT 2248
 QY 4545 GAGGATATTCGTTTGGCGGCTTGTATGACGACTACAGGCTGATTCAGATCTGTCA 4604
 DB 2247 CAGGATCTGCGTTTCAAGCGCTGTGTGAGGCTTTCAAGGTCAAGGCGACCTGAGCCAC 2188
 QY 4605 AGCACAACCTCTC-----GCACAACCTCATTTTTCAGAGTCACTCAAGAGAGACTT 4656
 DB 2187 AGCCCGCTGTTCAGAGTATGATCAACCAACAGCCGCTGTGCTCCGATCGAGCGCTG 2128
 QY 4657 GAAGATTCAGTTTCCAGGCTGTGAGTCCGTACTGTGCTTACCAAGCTTACATCTGAT 4716
 DB 2127 GACAGCGTGGCCGCGCTGAGCTTTCGCGACCTGACTGACTG--GAAGACCGTACCACTAGT 2070
 QY 4717 TTGACATGAGGTTCCATCTGTTTCAAGAAACGACAGCTTAAAGTAGAGTCACTTTG 4776
 DB 2069 TCGACTGAGCTGTGATACCTACGAAAGGCGGTGCTGTACGCGGCTGACTACG 2010
 QY 4777 CCGATGAGCTGTTCAAATGAGACTGTTGAATGTCGTCAAGATATCTTTGAGATT 4836
 DB 2009 CGAACGACTGTTTCAAGGCGCGGACCGTCAAGGCGCATGGCGGCAATGGCAGAACTG 1950
 QY 4837 TGAGAAACGGGCTTCAAGTTCCGCGACACCACTTCAATCTTCTTGAATGATGCA 4896
 DB 1949 TGGCGGCTATGCTGAAGAAACCCGAGCGCAGCTGCACTGCTGCGGATGCTGATGCG 1890
 QY 4897 TTGTGACTTCTTGAATTAATGATGTTCTCAAGCTCAAAACATGTCGACTATCCCGAGAT 4956
 DB 1889 AGGAGCGCTATCAGTGTCTGAAAGCTGGAAGCCCACTGCGGCTGATCCGCTGCAAC 1830
 QY 4957 CGAGCTTGGCTGATGCTTTCAGAACCCCAAGCTCTGCTTACCCCGATGTTGCTGTG 5016
 DB 1829 GCGGCGTGCACCGGTTGTTGAGAGACAGGTGAGCGCACACCGAGCGCCGCGCTGG 1770
 QY 5017 TGAATCTCTGTGCGCATTTACCTACACCGAGTTGATGCGCACTGATATCTGCTG 5076
 DB 1769 CTTTGGCGGAGAGCGCTGAGCTACGCGCAGCTGAACCGCGCCACCGGCTGGCGC 1710
 QY 5077 GATGCTTGTGACGCTCAATGCTGTCAGAGAGCGTGTGCGAGTATTTGCCCAAGCT 5136
 DB 1709 ATGCGCTGATCGAGCGGCGGTGTGTCGAGACCGCTGTGTGGCTGCGCATGMACTT 1650
 QY 5137 CATGTGACAAATTTGCGCGCTTCTTGTGTGTTGAAGGCGAACTTGGCTTATCTTCTC 5196
 DB 1649 CCAATGAGATGTGTGTCGCTGATGCGCATCTCAAGGCGGCGGCTTACGTGCGG 1590
 QY 5197 TCGATGTACATGCGCTCTGCGGAG 5221
 DB 1589 TGAACCGGAGTATCCGAGAGAGCG 1565

RESULT 9

US-09-252-991A-9182
 ; Sequence 9182, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR APPLICATION NUMBER: 1999-02-18
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 9182
 ; LENGTH: 7911
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-9182

Query Match 0.9%; Score 97.8; DB 4; Length 7911;
Best Local Similarity 42.7%; Pred. No. 2.4e-18;
Matches 703; Conservative 0; Mismatches 917; Indels 25; Gaps 3;

QY 3600 CAGCTTTATTCACAAAGCCGACTATGTTCTTGATCAGTTGAGCGTTGCACTGTG 3659
DB 196 CTGTCTACAGCCAGCAGCGATGTGGTTCTCTGACCTCGAGCCACAGAGTGGCC 255
QY 3660 TATCTGATTCATATGTGTGAGAAATGCGGGCTGTCAATGTCCAGCGTTACGTG 3719
DB 256 TACAACTGCGCCAGCGGTGCGCTGAAGAGCGCTGATCGCCAGGGCTGAGACGC 315
QY 3720 GCTCTGACAGCGCTTGAACAGCAGACGACTTTGAAAGCAATTTGAAACCAAGAT 3779
DB 316 GCTCTGCGCCAGCTGTGTGACGCTCATGAAACCTGTGTAAGGTTCCTCCGCGGCC 375
QY 3780 GGTGTGCTGTACAAATTTTCAAGAAAGCTTTGAGAGATGAAGTCAATGATCTC 3839
DB 376 GACGACAGCTGGGCGAGCGCCCTTGCAAGCCCGTGAAGGTTCCTGAGGATTCG 435
QY 3840 TGTGTT-----CAGACTTGACCCGTTTGAAGTGTGAAACCAAGACAG 3884
DB 436 AGCGGCTGCTGAGCGCCGAGCAAGCCGCTGCGAGAGGAGCGCAGCGGAGTGC 495
QY 3885 ACTACTCCCTTCAATCTCATCTGAGAGTGGCTGAGAGAGACGCTTACGACTTGT 3944
DB 496 TTGACGCTGTTCACCTGTGCGAGAGGCGCTGTGCGGGTCCGCTGATTCGCTGGC 555
QY 3945 GAAGATGACCAACCTCTCACTATTTGATGATCATCATCATCTCAATGTTGTTCAAT 4004
DB 556 GAGAGGCGCATGTGCTGCTGTTGACCTGTGATCATGTGTCGAGCGCTGGTCAATG 615
QY 4005 GATGCTTGGAGCGCATCTCAATCACTCACTCACTCACTCACTCACTCACTCACT 4064
DB 616 AAGGTGTGATTCAGAAATTCAGTCTGTTTCTACAGTCCCTATGCGATGCGCGAGCCC 675
QY 4065 CCGCTGACAGCACTCTCTCACTCACTCACTCACTCACTCACTCACTCACTCACT 4124
DB 676 GCGCTGCGGCTTGTGCTGATCACTGATCACTGATCACTGATCACTGATCACTG 735
QY 4125 GACCAATTCATAGAGCAGAGAAAGCACTCACTACTGAGAAAGCACTCAAGACTCT 4184
DB 736 GAGGCGGATGAGCAGAGCGCCAGCTGGAATCTGGGCGGCAAGCTGGGAGCGCAT 795
QY 4185 TCCCAAGCAAGATCCGAGCGACTTTGCCGCCCTGCACTTGTCTGAGAGCAGGT 4244
DB 796 CCGGTCTGAGATGCGCAGCCGACCAACCCGCTGCGCGGTTCCAGCTACCGTGCAGC 855
QY 4245 TGGGTACATTTACATCGAGCGAGGAGCTTACAGATCCCTTGAGGCTTCTGCAAGAA 4304
DB 856 CGTTACAGTTACAGATCGAGCGCGCCCTGAGCGAGCCCTGCGGCGACGCCGAGCGC 915
QY 4305 CACAACAGCACTTTTGTGTCTTCTTCTAGTGTGCTTCCGTGCGCTCAATTCGTCTC 4364
DB 916 CAGGGGTGACCTGTTTCTGCTTCTGCTGCGGCTTCAATTCCTCTGCAACGCTAT 975
QY 4365 ACAAGCTGTTGAAGAGCTGTCTATTTGTAACCAATTCGAAATGCAACCGAATG 4424
DB 976 AGCGGGGAGACGACCTGCGGGTGGCGTCCCATTCGCAACCGCAACCGCGAGAGTG 1035
QY 4425 GAGGATATCATCGGCTGCTTGTTCATATGCAAGTATGGAATCAACATATGATCATC 4484
DB 1036 GAAAGGCTGATCGGCTGTCTGTCACCAAGGTGTGCGCTGATTTGAGAGCGCGC 1095
QY 4485 GATACCTTTGGAGCTTTGATCAACCAAGTCAAGGCTGAGCAGCAGAGATTCAGAAC 4544
DB 1096 AGCTCGGTGCGACCTGCTGCGCGGCTGAGAGACACCGTGTCTGCGCGCCGACAT 1155
QY 4545 GAGGATATTCGTTTGAAGCGGTTGATCAGCACTACAGCTGATCCAGAGATCTGTCA 4604
DB 1156 CAGGATCTGCGTTGCAAGCGCTGTGTGAGGCGTTCAAGGTGCAAGCGCAGCTGAGCCAC 1215

QY 4605 AGCACACTTCTC-----GCACAACTCATTTTTCAGTGCACATCAGAGAGCCTTG 4656
DB 1216 AGCCCGCTGTTCAGGAGATGTACCAACACAGCCGCTGTGTGCGCATGAGCGCTG 1275
QY 4657 GAAGATTCAGATTTCAGGGTCTGAGTCCGTACTGTGCTTACCAAGCTACATCTGAT 4716
DB 1276 GACAGGTGCGCGGCTGAGCTTGTGCGCACTGACCTGACAGT- GAAGACCGTACACCAAGT 1333
QY 4717 TTGACATGAGATTCATCTGTGTTCAAGAAACGACAGCCTTAAAGTAGGCTCACTTG 4776
DB 1334 TCGACCTGAGCTGTGATCTTACGAGAGGCGGTGCTGTACGCCGCTGACTTACG 1393
QY 4777 CCGATGAGCTGTTCAAATGAGACTGTGAAATGTGTCAGAGATTTCTTTGAGATTC 4836
DB 1394 CGACGACCTGTTTGAAGCGCGGACCGTGAAGGACATGCGCGGCAATGSCAGAACCTGC 1453
QY 4837 TGAAGAACGGGCTTCAAGTTCCGCGACACCAAGTCTCAATCTTCTTTGACTGATGCA 4896
DB 1454 TGGCGGCAATGTGAGAAACCCCGACGCGCAGCTGCACTGCTGCGATCTGATGCGC 1513
QY 4897 TTGTGACTTGAAGAAATTTGATGTTCTCAAGCTCAACATGTGCACTATCCCGAGAT 4956
DB 1514 AGAGGCTATTCAGTTGCTGAGAAAGCTGAAACGCACTGCGCGAGTACCCGCTGCAC 1573
QY 4957 CGAGTTGCTGATGTCTTTCAGACCAAGTCTCTGCTTACCCCGATGCTGTGCTGTG 5016
DB 1574 GCGCGGTGACCGGTTGTTTGAAGAGAGTTCAGAGCGCAACCGAGCGCGCGCGCTGG 1633
QY 5017 TGAATCTTCTGTCGCAATTTGACCTTACACGAGTTGATGCGCACTGATATTTCTGCTG 5076
DB 1634 CTTTGGCGAGAGCGCTGATGATGCTGACCGCAGCTGAAACCCCGGCGCAACCGGCTGCGC 1693
QY 5077 GATGCTTGTGCAAGCTGCAATGCTGCAAGAGAGCTGTGTCAGATTTTGTCCCAAGGT 5136
DB 1694 ATCCCTGATGAGCGCGGGGTGCTGTGAGACCGCTGTGGGCGTGGCCATGGAAGTT 1753
QY 5137 CATGTGAGCAATTTGTGCGCTTCTTTGTGTTGAAAGGCACTTGCCCTATCTTCTC 5196
DB 1754 CCAATGAGATGTGTGTGCGCTGATGCGCATCTTCAAGGCGGCGGCTTACGTGCGG 1813
QY 5197 TCGATGTACGATCGCCCTCGCGAG 5221
DB 1814 TGAACCGAGATTCGCGAGAGCG 1838

RESULT 10
US-09-252-991A-9100
; Sequence 9100, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9100
; LENGTH: 7374
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9100

Query Match 0.9%; Score 95.4; DB 4; Length 7374;
Best Local Similarity 44.2%; Pred. No. 1.2e-17;
Matches 445; Conservative 0; Mismatches 556; Indels 6; Gaps 1;

QY 3581 TCATGAGGAGCTGTGAGCAGTCTTATTCAGAGCGCACTATGTTCTGTGATCAGTT 3640


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1 FILE REFERENCE: 107196.136
2 CURRENT APPLICATION NUMBER: US/09/252.991A
3 CURRENT FILING DATE: 1999-02-18
4 PRIOR APPLICATION NUMBER: US 60/074.788
5 PRIOR FILING DATE: 1998-02-18
6 PRIOR APPLICATION NUMBER: US 60/094.190
7 PRIOR FILING DATE: 1998-07-27
8 NUMBER OF SEQ ID NOS: 33142
9 SEQ ID NO 7057
10 LENGTH: 4236
11 TYPE: DNA
12 ORGANISM: Pseudomonas aeruginosa
13 US-09-252-991A-7057

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	Query Match	0.7%;	Score 82.8;	DB 4	Length 4236;
	Best Local Similarity	45.0%;	Pred. No. 6,4e-14;		
	Matches 309;	Conservative 0;	Mismatches 377;	Indels 0;	Gaps 0;
QY	3891	CCCTTCAATCTCTCATCTGAAGTGGCTGAGAGGACGCTCTTAACGACTTGGTGAAGAT	39506		
Db	2433	CCGTTTCGACCTGAAAAAGGGGCCCTCTGCGGGGCTCAGCCCTGATGGCGCTTGACGAAACAG	23744		
QY	3951	GACCAACATCCCTCACTATTGTATGATACATCATCTCAGATGGTGGTCAATTGATGTC	4010		
Db	2373	GAGACACAGCTCTGGGTACCCCTGATACATCTGCGCGATGGTTGGTGTGCTGAACCTG	2314		
QY	4011	TTGGCAGCGCATCTCAATCAAGCTCTACTCACTGGGCTCAAGAGACTCAAAAGACCCGCTG	40707		
Db	2313	CTGCTTCGACGAATTTCTGGCGGCTCTAGCCGGAAGCTGGCGGCGACCGGCGAAGCTG	2254		
QY	4071	TCAGCACTCACTCTCTTACCTTATCCAGTACAGCGACTTTGGAAAAATGGCAGAGGACCA	4130		
Db	2253	GCGCGCTGGAATCTGACACTACGCGAGTTTGGCTGCTGCGCAACGCGAGTGGCTGGAACGG	2194		
QY	4131	TTTCATAGACGAGGAGGAAGCACTCAACTACTGGAAGAAAGCAATTCAAAGACTTTTCCCA	4190		
Db	2193	GGCAGGAGCGCCGCCCAACTGGGCTTACTGGGGGAAACGCTGGGCGACACGCGCCGCTG	2134		
QY	4191	GCAAGATATCCCGACCGACTTTGGCCGCGCTGTCATCTCTGTGGAGAAGAGGTTGGCTG	4250		
Db	2133	CTGGAATCTGGCCACACGACATCTCGGACAGGCGGCGCCAGGCGGTGGCCCGCGGCTAC	2074		
QY	4251	CATGTTACATCGACGGGAGCTCTTACAGTCCCTTCGAGCCTTCTGCAAGCAACACAC	4310		
Db	2073	AGCCTGGGGGTGCAAGAACCCCTGGCGGGCTATTCGCGAGGCGCGCTGGAACATGAG	2014		
QY	4311	ACGACCTTTTGTGCTTCTTATAGCTGCGTTCCGTGCGCTCATTTATGTTCTCAAGCT	43707		
Db	2013	GCGAGTGTCTTCATGTGGCTCTGCGCGCTTTCAGAGGCGTGTGCATTCGCAACAGCGGG	1954		
QY	4371	GTTGAGACGCTGTCAATTGTATCAACCAATTCGGAATGCGAACCGACTGAACTGGAGAT	4430		
Db	1953	CAGGCGGAGATCCGCATTCGGGTGCGGCCACCGCCAGCGCTTGGAACCCAGGGG	1894		
QY	4431	ATCATCGGCTGCTTTGTTCATATACGCAAGTATGCGAATCAATAGATCATACAGTATCC	4490		
Db	1893	CTGGTTCGGCTTCTTCATACACACCTGGTCTCTGGCGGCAAGCCCGGCGCGCGCAAGC	1834		
QY	4491	TTTGGACCTTTGATTCACCAAGTCAAGGCTTACGACAGCAGGATTCGAAACGAGAT	4550		
Db	1833	TTCCGCCCATTTGCTCGGCGAGGCTTCGACGAGCGCAACCTCGCGCCACAGGCAACCAAGAC	1774		
QY	4551	ATTCCGTTTGAAGCGCGTTTATCAAGC	4576		
Db	1773	CTGCCGTTTCACAGAGTGTCCGCGC	1748		

RESULT 13
US-09-252-9091A-9098
; Sequence 9098, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

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1  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
2  TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
3  FILE REFERENCE: 107196.136
4  CURRENT APPLICATION NUMBER: US/09/252,991A
5  CURRENT FILING DATE: 1999-02-18
6  PRIOR APPLICATION NUMBER: US 60/074,788
7  PRIOR FILING DATE: 1998-02-18
8  PRIOR APPLICATION NUMBER: US 60/094,190
9  PRIOR FILING DATE: 1998-07-27
10 NUMBER OF SEQ ID NOS: 33142
11 SEQ ID NO 9098
12 LENGTH: 792
13 TYPE: DNA
14 ORGANISM: Pseudomonas aeruginosa
15 US-09-252-991A-9098

```

	Query Match	0.7%; Score 80.2; DB 4; Length 792;
	Best Local Similarity	47.4%; Pred. No. 1,1e-13;
	Matches	306; Conservative 0; Mismatches 333; Indels 6; Gaps 2;
OY	3953	CCACATCTCACTATTGTGTCATGCATCATCATCATCTCAGATGGTGTTCATTAATGATGTCTTT 4012
Dd	1	CCAATGTGTGTCTATCGTCGACGACCATAATGTCTCTCCGACGGTGTGTCTGATGACGTTGAT 60
OY	4013	GCGAGCGGATTCATGAGCTCTACTAGCTGGCGCTCAAGGAATCAAAAGAAGCCCGCTGTC 4072
Dd	61	GGTGGAAGAGTGGTCCAGCTCTACGCCGCTTAAGCAGAGGGGGCGAAGCGGCTTGCC 120
OY	4073	AGACACTACTCTTACCTTATCCAGTAACAGCACTTTGCAAAATGGCAGAAAGCAATT 4132
Dd	121	GGCCCTG---CCGATACAGTATCCGACATATCCGCTCTGGCAGCGCAATGGATGGAGGC 177
OY	4133	CATGAGCAGAGAGAAGAACATCACTACTGTGAAGAAACAACTCAAABACTTCCCAG- 4191
Dd	178	CGGAGAGAGGAGGCGCACATTTGGCGCTACTGGATTCGCGCTGTGGTGGCCGAACGCCGAT 237
OY	4192	--CAAGATCCCGACCGACTTTGCCGCCCTCTGCACCTTCTGTCTGGAGACGACAGTTTCGT 4249
Dd	238	GCTGAGAGTCCGTTTCAATGTGTCCCGTCTCGGAGACAGAGCTTTGCGCGCGCGGAGCT 297
OY	4250	ACANGTTAACATCGACGGCGGAGCTCTACAGTCCCTTCGAGCCTTCTGCAACGAACAA 4309
Dd	298	GGAGTTTGAACCTTCGCCCCCGACGGCGGACGGCTAAAGCGCTTCCCAACGGCAGGG 357
OY	4310	CACAGACCTCTTTCGTCTCTTCTTAGCTGGGTTCCGTGCGCTCATTTATGCTTCACAGC 4369
Dd	358	TGCGAGTACCTTCAATGTTGTGCTGCGTGGGTGCTTCCAGGCGTGCTGATATGCTTACAAGCG 417
OY	4370	TGTTGAAGAGCGCTGTCAATTGGTATACCAATTGCGAATCGCAACCGACCTTGAACTGGAGGA 4429
Dd	418	TCAACCGGATATTCGTTGTCGCGCGCGCGCTGCGCAATATCGCAACCGGGTTCAAAACCGGCG 477
OY	4430	TATCATGGGCGCTTTGTCAATATAGCAGTGTATCGAATCAACATATAGTATCATCGATAC 4489
Dd	478	ACTATATGGGTTCTTCTGTCAACCCAGGTGCTTAAGCCGACATCATATGGCGAGATGGG 537
OY	4490	CTTTGGGACTTTGATCAACCAAGTCAAGGCTACGACGACGACGACATTTCAAGAACGAGGA 4549
Dd	538	GTTTCGACCGGATGCTGACACAGGTTCCCAAGCGCTCCCTGGAGGCGCAGGCGCACGAGA 597
OY	4550	TATTCGCTTTGAGCGGCTGTATATAGACATCAAGCCGTGATTCAG 4594
Dd	598	CTTCCCGTGGAGCACTGGTGGAGAGCTTTCGACCGGAGCGCAG 642

RESULT 14
 US-08-510-646B-17
 ; Sequence 17, Application US/08510646B
 ; Patent No. 6077699
 ; GENERAL INFORMATION:
 ; APPLICANT: Blanc, Veronique
 ; APPLICANT: Blanche, Francis
 ; APPLICANT: Crouzet, Joel

APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibault, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved in The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fimegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
APPLICATION DATA:
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2219 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: S. virginiae
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2219
OTHER INFORMATION: /product = "virginiamycin s synthase gene"
US-08-510-646B-17
Query Match 0.7%; Score 79.4; DB 3; Length 2219;
Best Local Similarity 43.3%; Pred. No. 4.3e-13;
Matches 764; Conservative 0; Mismatches 961; Indels 38; Gaps 7;
QY 3470 CGTTGGATGGAAGCTCAAGGCTCTAATCATCTACAGACCGGCGTGGGGAAATTC 3529
Db 14 CTTGGGCGCGAAGATCGCGGCTCTGACCTGTTGAGGCAACCGTCGAGGCGCTTGC 73
QY 3530 CGCGGTCGTCAAGGGATGATCTCTGTCTCACTCTCATCCCAAGTCAACTATGAGG 3589
Db 74 CGAAACCTCTGGAAGAGCGCCGCGAGGTCCGCCGCCCTGTGGCGGCCGACCGCCCCGA 133
QY 3590 ACCTGTTGACAGTCTTATTTCACAAAGCCGACGTATGTTCTGTGATCAGTTGACGTTGG 3649

Db 134 ACAAGTCCGCTGTCCTTCCGCCAGCGCGCGCTGTGTTCTTCAGCCGCTGGAAGACC 193
QY 3650 CAGTCTGTGATCTGATTCATATGCTGTGAGAAATGCGCGGCGCTGTCAATGTCAAGC 3709
Db 194 CAACTCAGCTTACAAATCCGCTCGCCCTCGCCCTGCGGGGAGCTGAGCCGAGCGG 253
QY 3710 GTTACGTGGGCTCTTTCAGCGGCTTGAACAGGACAGAGACTCTTGAAGACATTTGA 3769
Db 254 GTGCAACAGGCGCTCAACGACCTGACGAGCCGCCAGAAAGCTCGCAGCTTACCC 313
QY 3770 AGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3829
Db 314 GAGCGCGAGCGCGCGGCTTACGACGCTCTTCGACCCGACAGGCGGAGCGCGGCT 373
QY 3830 CATTGATCTCTGTGTTAGACCTTGAACCGCTTGAAGTGTGAACCAAGAACAGACTAC 3889
Db 374 GTCTGTCTCCCGCGAGCGAGCGGAGCGGAGCTGCGGAGATGTCTGGCGAGCGCGCGCA 433
QY 3890 TCCCTTCATCTCTCATCTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3949
Db 434 CGAGTTCAGTCACTCCGACCGGCGGCTGCGGCTCTCTCTTTCACCTTCGACGGA 493
QY 3950 TGAACATCTCAGTATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4009
Db 494 CGAGCAGTCT 553
QY 4010 CTTCGACGCGATCTCAATCAGCTCTTACCTGAGCTGAGCTCAAGAGTCAAGACCGGCT 4069
Db 554 ACTCAGCCGAGACTACCGCGGCTTACACCGCGCGCGGAGAGGCGCGCGCGCGAGCTG 613
QY 4070 GTACAGACTCATCTCTTACCTTACAGTACAGC-----GACTTTCGAAATG 4117
Db 614 GGAAGCCCTCCGATCAGTACGCGAGTACAGCTCTGTGACAGAGAGATGCTCGAGCTC 673
QY 4118 GCAGAGAGCAATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4177
Db 674 GCGGAG 733
QY 4178 AGACTCTTCC---CGAGCAAGATCCGACCGAGCTTTCGCGCGCTGCACTTCTGTGG 4234
Db 734 CGCGCGCGCGAGCACTGGAATGCGCCAGCAGCAAGACCGCGCGCGCGCGCGCGCA 793
QY 4235 AGACGAGGTGGTGAATGATTTACATCGACGCGAGCTTACAGTCCCTTGAAGCTT 4294
Db 794 CCAAGCGCGAGCGCTCCCTTCCAGCTGAGCGCGAGCTGACAGAGCGGCTCAGCGCT 853
QY 4295 CTGCAAGCAACAG 4354
Db 854 GGCAGAGCTCTGAG 913
QY 4355 TTATGCTCTCAGAGCTGTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4414
Db 914 CACCAAG 973
QY 4415 ACCTGAAGTGAAGATATATGCGCTGCTTGTCAATGCAAGTGTATGGAATCAACAT 4474
Db 974 CGAGGCGCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1033
QY 4475 AGATCATCAGATACCTTTGGGACTTGTGATCAACCAAGTCAAGAGCTTACAGAGAGAG 4534
Db 1034 CTCGCGGAGATCGACCTTCCGCACTCGTGGACGAGAGAGAGAGAGAGAGAGAGAG 1093
QY 4535 ATTGAGAAAGAGAGATATTCGTTTGAAGCGCTTGTATAGCACTACAGCTGATTCAG 4594
Db 1094 ATAGCAGACAG 1146
QY 4595 AGATCTGTCAAGCAACCTCTGCAACACTCATTTTTCAGTCACTACAGAGAGAGAG 4654
Db 1147 AGCGCTGCTGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1206
QY 4655 TGAAGA-TTCAAGTTCAAGGTCTGAGTCCCTTACTGTGCG---TAGCAAGCGTACA 4710
Db 1207 CGGACAGCGCGGTGCTGCGCGCTGAGCTGTGCAAGAGCGGTCGCGGTGAGATTGG 1266

QY 4711 CTCGATTGACATGAGTTCCATCTGTTTCAAGAAACGACCTTAAAGTAGCGTCA 4770
DB 1267 CCAAGTTGACCGCGCCCTGGCCGCGGAGAAAGGACCGCGGCGCGGTGCG 1326
QY 4771 ACTTCCGATGAGCTGTTTCAAAATGAGACTGTTGAAATGTCGACAGTATTTCTTG 4830
DB 1327 TGGCGCGCACTGGGAGTTTCAAGACCGACCTGTTTCAAGACGACCGACCTGGAGCCCTCG 1386
QY 4831 AGATTCTGAGAAACGGGCTTCAAAAGTTGCGGACACCAAGTCTCAATATCTTTGA--- 4887
DB 1387 GGGCCAGGCTCACCGCCCTGCTGCGCTGCTGCGCCGCGACCCCGACAGCCGATCGGAC 1446
QY 4888 CTGATGACATTTGATCTTGAATAATTTGATGTTTCAACGTCAACATGTCAGTATTC 4947
DB 1447 GGGTGGGCACTCTGACACCGCGGAGAGGACCGGACCTCTTCAACCTGGAAGACACT 1506
QY 4948 CCGC-----AGATGAGCTTGGCTGATGTTCTTCCAGACCCAAAGTCTTGTACC 4998
DB 1507 CCGCGCCCGCGCGGACCGCACTGCGCGGAGCTGTTCCAGGCCCGCGCGCGAGCAC 1566
QY 4999 CCGATAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5058
DB 1567 CCGACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1626
QY 5059 AGTCTGATATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5118
DB 1627 GGGCCAAACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1686
QY 5119 CAGTATTTGCCCCAGGCTCATGTAGACAAATGTCGCGTCTTGTGTGTGAAGCGA 5178
DB 1687 CCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1746
QY 5179 ACTTGGCTATCTTCTCTCGAT 5201
DB 1747 GCGCGCTTACCTGCGGCTGAT 1769

RESULT 15

US-08-861-774E-17/C
Sequence 17, Application US/08861774E
Patent No. 6297007
GENERAL INFORMATION:
APPLICANT: Waters, Barbara
APPLICANT: Miao, Vivian
APPLICANT: Ho, Yap
APPLICANT: Tong, Seow
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
FILE REFERENCE: 9993-006
CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 94
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 1172
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Clone ps32
US-08-861-774E-17

Query Match 0.7%; Score 74.8; DB 3; Length 1172;
Best Local Similarity 54.1%; Pred. No. 6.8e-12;
Matches 198; Conservative 0; Mismatches 162; Indels 6; Gaps 2;

QY 5917 CAATTGACAGCTGACCACTGAGAGCTATGCTGATCTGACCAAGCTTG 5976
DB 688 CGATCGCGCTCGCTGACCACTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 629
QY 5977 TTGGCAATGGTGTGATGAGAGAGCTTGTCTCACTGGCGATGGTCTTGGCGGCGCTA-- 6034
DB 628 TTCCGCGCGCGGATCGGAGAGCTGTACATCGTGGCGAGAACTGCGCGGCTATG 569

QY 6035 -CAGTGACAAAGCCCTTGAAGAGACCGTTTGTGACATTTACTGTCAATGACAGACAG 6093
DB 568 TCGATATGCGCGCTTCAACGAGCGCGGTTGTATCCGATTCATTCGGTGACCTGGCT 509
QY 6094 TGAAGCGTATTCGCACTGGCGGATCGAGTGGTGTACAGATTGAGATGGCTCATGAGT 6153
DB 508 CCGGCTGTATCCGAGACCGGAGCTGTGTGCT---GGCTTCCGAGCGGCACTGACT 452
QY 6154 TCTTGGAGGTATGACACCCAGTTCAAGATTGTCGCAATCGTATGAAATGAGTGA 6213
DB 451 TCAATCGGCGCGGATTCATGAGTCAAGATCCGCGCTTCCGATGAGCTGGTGAGA 392
QY 6214 TTGAAGCGGCGCTTTCGCGGACTCTCCGTCGAGATGCTGTGTCCTTCAAGAGA 6273
DB 391 TGAAGCGGCGCTGCGGATTCACCCGCTGTGAGACGCGCTGTCTGCGCGGAGG 332
QY 6274 ATGAGG 6279
DB 331 AGCGGG 326

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Job time: 803 secs

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